

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

CTCTCCCCC CCCCTCTCTC TCTCTCTCGC ATACTAACTA GGTTTGACTG TATTACTCGT      60
ACCAGATTTA AAATTAGACT AGCCTTGCCA CAACGCCCTA CTGAGAGGTA CTGTCGAACT      120
GTAGACAGCA TGATGTTCTT TGATGGTGAA AGTCTAAATC TGGACCGTGT TCAGAGATAC      180
CAAATGATGA GGCTGAAAAG GGGAAAGGGG GTTCTTCAGT CTCTTCTTCT TCTTCTTTTT      240
ATTTTTTTTT CCATGATGTT TTCTCTATGG CCACTGCAAA TGGTGTTGTC ACCCTTGCAT      300
GTTGCCAAC                                         309

```

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Met Phe Phe Asp Gly Glu Ser Leu Asn Leu Asp Arg Val Gln Arg
1           5           10           15
Tyr Gln Met Met Arg Leu Lys Arg Gly Lys Gly Val Leu Gln Ser Leu
20           25           30
Leu Leu Leu Leu Phe Ile Phe Phe Ser Met Met Phe Ser Leu Trp Pro
35           40           45
Val Gln Met Val Leu Ser Pro Leu His Val Ala Asn
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

AGGTCTCTCT GGTTCCTTCT ATATCATCAT TTTATTATTA TGCCTAATA TAAAGTACTG      60
GCTCATAGGG CCAGGGTATT ATTATAGAAT ATTATNTTCG CATGTAAACA AAGATATCTT      120
TGCTTTAAGA TGTGAGAAGA AATGAATTTA CTTTGTTTGC ATTAAGTTAN GGAAGAGTTG      180
TAATATATAC TTTAAGAAAG AAGAGAAGAA AACTAGTATC TNTAAGCGGT AAAAAAAAAA      240
AAAAAAAAAA AAAAAAA                                     257

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

CACGAGGATT GATTTCATC TTGCCTCTCC ANAAGGCAAA ACCTTAGTTT TTGAACAAAG      60
AAAATCAGAT GGAGTTCACA CTGNTANANA CTGAANTTGG TGATTACATG TTCTGCTTTG      120
ACAATACATT CAGCACCATT TCTGAGAANG TGATTTTCTT TGAATTAATC CTGGATAATA      180
TGGGAGAACA GGCACAAGAA CAAGAAGATT GGAAGAAATA TATTACTGGC ACAGATATAT      240
TGGATNTNAN NCTGGAAGAC ATCCTGGAAT CCATCAACAG CATCAAGTCC AGACTAAGCA      300
AAAGTGGGCA CATACAAAC CTGCTTAGAG CATTTGAAGC TCGTGATCGA AACATACAAG      360
AAAGCAACTT TGATAGAGTC AATTTCTGGT CTATGGTTAA TTTAGTGGTC ATGGTGGTGG      420
TGTCAGCCAT TCAAGTTTAT ATGCTGAAGA GTCTGTTTGA AGATAAG                      467

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Glu	Phe	Thr	Leu	Xaa	Xaa	Thr	Glu	Xaa	Gly	Asp	Tyr	Met	Phe	Cys	
1				5					10					15		
Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Xaa	Val	Ile	Phe	Phe	Glu	
			20					25					30			
Leu	Ile	Leu	Asp	Asn	Met	Gly	Glu	Gln	Ala	Gln	Glu	Gln	Glu	Asp	Trp	
		35					40					45				
Lys	Lys	Tyr	Ile	Thr	Gly	Thr	Asp	Ile	Leu	Asp	Xaa	Xaa	Leu	Glu	Asp	
	50					55					60					
Ile	Leu	Glu	Ser	Ile	Asn	Ser	Ile	Lys	Ser	Arg	Leu	Ser	Lys	Ser	Gly	
65					70					75					80	
His	Ile	Gln	Thr	Leu	Leu	Arg	Ala	Phe	Glu	Ala	Arg	Asp	Arg	Asn	Ile	
				85					90					95		
Gln	Glu	Ser	Asn	Phe	Asp	Arg	Val	Asn	Phe	Trp	Ser	Met	Val	Asn	Leu	
			100					105					110			
Val	Val	Met	Val	Val	Val	Ser	Ala	Ile	Gln	Val	Tyr	Met	Leu	Lys	Ser	
		115					120					125				
Leu	Phe	Glu	Asp	Lys												
		130														

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGTTTGAAGA TAAGAGGAAA AGTAGAACTT AAAACTCCAA ACTAGAGNAC GTAACATTGA	60
AAAATGAGGC ATAAAAATGC AATAAACTGT TACAGTCAAG ACCATTAATG GTNTTNTCCA	120
AAATATTTTG AGATATAAAA GTAGGAAACA GGTATAATTT TAATGTGAAA ATTAAGTNTT	180
CACTTTCTGT GCAAGTAATC CTGCTGATCC AGTTGTACTT AAGTGTGTAA CAGGAATATT	240

TTGCAGAATA TAGGTTTAAC TGAATGAAGC CATATTAATA ACTGCATTTT CCTAACTTTG 300
 AAAAATTTTG CAAATGTCTT AGGTGATTTA AATAAATGAG TATTGGGCCT AATTGCAAAA 360
 AAAAAAAAAA AAAAAAAAAA AAAAAAA 387

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCTCTT GAAGNTGGGG GGTGCNGGNN GGGGAAANCG NNTCTCCNNT CCANAAGCGG 60
 GGGCCNTTTT GTCCGTNNNC TTGTGNAAAA AANCCCGGNG NTGGTGAACG CTGNTNTTAN 120
 TTACTCCAAA CCTCGANTGG NCNNTTNGTG GTNCNNGGCC GAGGNTGANN TGGNTCCCCC 180
 CCCCCCTGNT NNAATNCCNA AACTNTTCN GAACCCGAAA ANAATTNTCC ATTCTGCCNN 240
 NANTGGTTTC NTCCNNCNC TCCTNATTAA AGAAGCNNT 279

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCGGGTGAC ATTCAGCCGG CGGTTCGGGG GGACGGANTC TCCATTCCAG AACCATGGCC 60
 CAATTTGTCC GTAACCTTGT GGAGAAGACC CCGGCGCTGG TGAACGCTGC TGTGACTTAC 120
 TCGAAGCCTC GATTGGCCAC ATTTTGGTAC TACGCCAAGG TTGAGCTGGT TCCTCCCACC 180
 CCTGCTGAGA TCCCTAGAGC TATTCAGAGC CTGAAAAAAA TAGTCAATAG TGCTCAGACT 240
 GG TAGCTTCA AACAGCTCAC AGTTAAGGAA GCTGTGCTGA ATGGTTTGGT GGCCACTGAG 300

GTGTTGATGT GGTTTTATGT CGGAGAGATT ATAGGCA

337

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Gln Phe Val Arg Asn Leu Val Glu Lys Thr Pro Ala Leu Val
1 5 10 15

Asn Ala Ala Val Thr Tyr Ser Lys Pro Arg Leu Ala Thr Phe Trp Tyr
20 25 30

Tyr Ala Lys Val Glu Leu Val Pro Pro Thr Pro Ala Glu Ile Pro Arg
35 40 45

Ala Ile Gln Ser Leu Lys Lys Ile Val Asn Ser Ala Gln Thr Gly Ser
50 55 60

Phe Lys Gln Leu Thr Val Lys Glu Ala Val Leu Asn Gly Leu Val Ala
65 70 75 80

Thr Glu Val Leu Met Trp Phe Tyr Val Gly Glu Ile Ile Gly
85 90

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAATTANAGG AAGANCCTNT TGAAAAAATT TNTGTTTGTN AAAAAGNTAG GGNAATTGTT 60

ATTTTGGAAG TAGCCTNCCC NAGNGNGGAN AGGGGGGNAT TTTAAGNANG NTTTTTTGNA 120

AAATTTTNG NCGNNGGNA GAANCNAAAA AGNGGAATTT GNNTTTTAAG GGGGNTANTT 180

GNTTGTGGTGG GTTTAANACC CTTGCCAAAA NNAAANACCC CCAAGNNANT TNAANNAGGG 240
 TATAANTTAG NATTTTTCCC TGGANTTAAA NAGNANATTA TATNCTGGAA NAAANGNAAN 300
 GGTGTTGATN AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA 345

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGAGATTCAG GACCTGCAGA GTCGCCAGAA GCATGAAATT GAATCTTTGT ATACTAAACT 60
 GGGCAAGGTT CCCCCTGCTG TCATTATTCC CCCAGCTGCT CCTCTGTCGG GGAGAAGAAG 120
 GAGACCCACT AAAAGCAAAG GCAGCAAGTC TAGTCGCAGC AGCTCATTGG GCAATAAAAG 180
 CCCACAGCTT TCAGGCAACC TGTCTGGTCA GAGTGGAAGT TCAGTCTTAC ACCCCCAACA 240
 GACCCTCCAC CCTCCTGGCA ACATCCCANA NTCCGGGCAG AATCAGCTGT TACAGCCCCT 300
 TAAGCCATCT CCCTCCAGTG ACAACCTCTA TTCAGCCTTC ACCAGTGATG GTGCCATTTC 360
 AGTACCAAGC CTTTCTGCTC CAGGTCAAGG AACCAGCAGC ACAAACACTG TTGGGGCAAC 420
 AGTGAACAGC CAAGCCGCCC AAGCTCAGCC TCCTGC 456

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Lys Leu Asn Leu Cys Ile Leu Asn Trp Ala Arg Phe Pro Leu Leu
 1 5 10 15

Ser Leu Phe Pro Gln Leu Leu Leu Cys Arg Gly Glu Glu Gly Asp Pro
 20 25 30
 Leu Lys Ala Lys Ala Ala Ser Leu Val Ala Ala Ala His Trp Ala Ile
 35 40 45
 Lys Ala His Ser Phe Gln Ala Thr Cys Leu Val Arg Val Glu Leu Gln
 50 55 60
 Ser Tyr Thr Pro Asn Arg Pro Ser Thr Leu Leu Ala Thr Ser Xaa Xaa
 65 70 75 80
 Pro Gly Arg Ile Ser Cys Tyr Ser Pro Leu Ser His Leu Pro Pro Val
 85 90 95
 Thr Thr Ser Ile Gln Pro Ser Pro Val Met Val Pro Phe Gln Tyr Gln
 100 105 110
 Ala Phe Leu Leu Gln Val Lys Glu Pro Ala Ala Gln Thr Leu Leu Gly
 115 120 125
 Gln Gln
 130

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TACCCTGCCC TCCTCCCTTT TTTNNACCCC TCTCTTTTTT ATTTTTTCTT TGCTCTTTAG 60
 AACCCAGTGA AAAATACCAG GGTACTGGGG TGCAACTCTT TCTTATGATA GGTCATTAGT 120
 GCTTTAAGCA AAAGATATTA GCAGCTTTGA CTGCAGCATT AGCAATTAGG NAAAAAAAAA 180
 AAAAAAAAAA 188

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

CCTTATGGCC TACTTTAAAA AAAAACCAAT ACCAAAGAAG CCTACAATGT TGGCCTTAGC      60
CAAAATTCTG TTGATTTCAA CGTTGTTTTA TTCACTTCTA TCGGGGAGCC ATGGAAGAAGA      120
AAATCAAGAC ATAAACACAA CACAGAACAT NGCAGAAGTT TTAAAAACAA TGGAAAATAA      180
ACCTATTTCT TTGGAAAGTG AAGCAAACCTT AAACCTCAGAT AAAGAAAATA TAACCACCTC      240
AAATCTCAAG GCGAGTCATT CCCCTCCTTT GAATCTACCC AACAACAGCC ACGGAATAAC      300
AGATTTCTCC AGTAACTCAT CAGCAGAGCA TTCTTTGGGC AGTCTAAAAC CCACATCTAC      360
CATTTCCACA AGCCCTCCCT TGATCCATAG CTTTGTTTCT AAAGTGCCTT GGAATGCACC      420
TATAGCAGAT GAAGATCTTT TGCCCATCTC AGCACATCCC AATGSTACAC CTGCTCTGTY      480
TTCARAAAAC TTCACTTGGT CTTTGTCATG GACACCGTGA AAACCTCCTG TAACAGTTCC      540
ATTACAGTTA GCATCCTCTY TTCARAACCA ACTTCTCCAT CTGTGACCCC CTTGATAGTG      600
GAACCAAGTG GATGGNTTAC CACAAACAGT GATAGNTTCA CTGGGTTTAC CCCTTATCAA      660
GNAAAAACAA CTTTACAGCC TACCTTAAAA TTCACCAATA ATTCAAAACT NTTTCCAAAT      720
ANGTCAGATC CCCCAAAAAA AAAAAAAAAA AA                                     752

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr Ser
1           5           10           15
Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn Thr Thr
20           25           30
Gln Asn Xaa Ala Glu Val Phe Lys Thr Met Glu Asn Lys Pro Ile Ser

```

	35		40		45	
Leu	Glu	Ser	Glu	Ala	Asn	Leu
50					55	
						60
Ser	Asn	Leu	Lys	Ala	Ser	His
65					70	
						75
						80
Ser	His	Gly	Ile	Thr	Asp	Phe
					85	
						90
						95
Leu	Gly	Ser	Leu	Lys	Pro	Thr
					100	
						105
						110
Ile	His	Ser	Phe	Val	Ser	Lys
					115	
						120
						125
Glu	Asp	Leu	Leu	Pro	Ile	Ser
					130	
						135
						140
Xaa	Ser	Xaa	Asn	Phe	Thr	Trp
145					150	
						155

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAGCTTGGCA CGAGGTCTTT AGAAGAACTA CAAACCTGA ATGGAAACT TCGAAGTGAA	60
GGACAAGGNA ATATGGGCTT TACTAGGCAG AATCACAGGG CAGAAGTTGA ATATACCGGC	120
AATTTTGAGA GCACCAAGG AGAGAAAACC AAGTAAAAAA AGAAGGAGGC ACACAAAAGA	180
CATCTACTCT TCCTGCAGTA CTTTATAGTT GTGGGATTG TAAGAAGAAC CATGATCAGC	240
ATCTTCTTTT ATTGTGTGAT ACCTGTAAAC TACATTACCA TTTTGGATGT CTGGATCCTC	300
CTCTAACAAG GATGCCAAGA AAGACCCAAA ACAGTTATTG GCAGTGCTCG GAATGTGACC	360
AGGCAGGGAG CAGTGACATG GAAGCAGATA TGGCCATGGA AACCTACCA GATGGAA	417

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Met Pro Arg Lys Thr Gln Asn Ser Tyr Trp Gln Cys Ser Glu Cys Asp
1           5           10           15

Gln Ala Gly Ser Ser Asp Met Glu Ala Asp Met Ala Met Glu Thr Leu
          20           25           30

Pro Asp Gly
          35

```

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

TCTGTGTTCA GTATAATTTT ATTTTCTCA ACCTTAAATA TGAAGTTAGG AAATAAGGAG      60
GGAAGTACAA AGATTATTGA CTATACAACN TACCAGCTGA AAGAAAGATC TTCATCAACA      120
TCTGTATCTT TCCAGAGGTA TACAGAATTA AAATTNNATN TTCAAGCTTT AATGATCCAG      180
TTTTAAGTCA ACGGCAGAAG TATGTTGAAT ATTTTCATCAC TCAATCTTGA ACTGATTTAG      240
AAGAGACTCT TTGCTGAAAT TGAATTGCAC TTATACATGT AAATTGTCAA CATGTAATTT      300
GGAATTTTCT GATTAATAAA TGTGGTTTTG GACATCTAAA AAAAAAAAAA AAAAAAAAAA      359

```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 675 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

CTCNCAAATC GGCNCGNGCA ACGAACGGCT TGGGCGCGGA CTGGTATCCG GGGACTGTGA      60
CTTGCAAGGT CCGCCATGGA GCCAGAGCAG ATGCTGGAGG GACAAACGCA GGTTCAGAA      120
AATCCTCACT CTGAGTACGG TCTCACAGAC AACGTTGAGA GAATAGTAGA AAATGAGAAG      180
ATTAATGCAG AAAAGTCATC AAAGCAGAAG GTAGATCTCC AGTCTTTGCC AACTCGTGCC      240
TACCTGGATC AGACACTTGT GCCTATCTTA TTACAGGGAC TTGCTGTGCT TGCCAAGGAA      300
AGACCACCAC ATCCCATTGA ATTTCTAGCA TCTTATCTTT TAAAAAACA GGCACAGTTT      360
GAAGATYGAA ACTGAMTTAA TGGGRAGAAC AGAAAAATTT AGTTGSTACT GTAGATTTAC      420
ATGATTAAGA RGCAGCTTTA ATTGCCATGA TCATTCCCTT TTTTGGGAAG GATAAGNACC      480
TTNCGGANAA CAGNACCTAT TTTTGGGATT GCAGNAGNTA AAATATTTCC CNTATTTTGA      540
NTTAATNACC ATAAACNTA CCTATTTAAT GNGNGTATTT TGTGCAATTT TTTTTNAGN      600
TTGTTTTTAA ATTTGTTTTT AAAATGACCT TNAAAATNAA NTGTNNAAAC ACCNTTTAAA      660
AAAAAAAAAA AAAAAA                                                    675

```

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Met Glu Pro Glu Gln Met Leu Glu Gly Gln Thr Gln Val Ala Glu Asn
1           5           10           15
Pro His Ser Glu Tyr Gly Leu Thr Asp Asn Val Glu Arg Ile Val Glu
          20           25           30
Asn Glu Lys Ile Asn Ala Glu Lys Ser Ser Lys Gln Lys Val Asp Leu
          35           40           45

```

Gln Ser Leu Pro Thr Arg Ala Tyr Leu Asp Gln Thr Leu Val Pro Ile
 50 55 60

Leu Leu Gln Gly Leu Ala Val Leu Ala Lys Glu Arg Pro Pro His Pro
 65 70 75 80

Ile Glu Phe Leu Ala Ser Tyr Leu Leu Lys Asn Lys Ala Gln Phe Glu
 85 90 95

Asp Xaa Asn

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CACGAGGGTT TGGTGAGGAA ATTACCAGAG AACTATTAAA GACTTGGATG CTCTTCTCGG 60

CTTTGCTATT AAGTAAGTTG GACAAGTTGT TTGGCTTCTT TGAGCCTCTG TTTTCTCCAT 120

TCTAAAATTC TAAATGGGA GTGTTGAATT AGATCAGTGG CTTTCGAACT TTCTGCTCCT 180

AGTAGTGAGA AATACATTTT ACTCCACTCC CTGGTATGTA CACGCATTCC TGTGTTTTGT 240

GAAAACCTGA CACCATGCTC CTCCCTCACT ACATGTAAAA CACTTTTATT CATTAAAAAG 300

AAACTGACT GGCTTGGACC TACAAATTAG TTTCATTATT TGTTAATGTT TGAAAGCCAT 360

TAAAAGATGA ATATTAAGGT TTCTTTATAC TCAATACTTG TAGTTTGTGTT TGGGGGAATG 420

AGAGGATGCC CTTGGTACCT TTGTGAGGCC TCTCCACTGA GGGTCAATCA TGACTTCTGT 480

TTTAAACCAG CCCATCCCAT CTTCTCCAGC TGCTCTCCTT ATGTCTTGCT TCTCTCCCCT 540

CCAACCTTCT CA 552

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Asn	Ile	Lys	Val	Ser	Leu	Tyr	Ser	Ile	Leu	Val	Val	Leu	Phe	Gly
1				5					10					15	
Gly	Met	Arg	Gly	Cys	Pro	Trp	Tyr	Leu	Cys	Glu	Ala	Ser	Pro	Leu	Arg
			20					25					30		
Val	Asn	His	Asp	Phe	Cys	Phe	Lys	Pro	Ala	His	Pro	Ile	Phe	Ser	Ser
			35				40					45			
Cys	Ser	Pro	Tyr	Val	Leu	Leu	Leu	Ser	Pro	Pro	Thr	Phe	Ser		
			50				55					60			

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGGGCCCCA TCCTTCAGTG CATTGCACAC TTTGCATGNT GGGTCAGGGA AGATTGTGGA	60
GAGAGGACAG TGCACATGGT TTCCCCACN TNGNCTGCGT GGGGGTATGT CCTGCTTCCG	120
CCACTTCCAA CTGTGGCANT TGGGCACGCC CCTNTCAGGG CACCTTCCCT TTTTGTTC	180
GCAAAATGAG GTTGTAATAG TGCCTGCCGC ACTGTNTGGC ACACAGTAAG NTCTCAAGAA	240
ATGTTAGCTG TTGTTGCCGT TAGAACACCA TAGNTAGAAT ACCATACNTG GCATTCACTT	300
AAAAAAAAAA AAAAAAAAAA	318

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

ATTGAGGAAA ACCACAAAAA ACTTCAAAAC AGCTACAACG GGAAAAAGAG AGTTTTGTCC      60
CACAGTCAGC AGGCCACTAG TTTATTAAC TCCAGTCACC TTGATTTTTG CTAAATGAA      120
GACTCTGCAG TCTACACTTC TCCTGTTACT GCTTGTGCCT CTGATAAAGC CAGCACCACC      180
AACCAGCAG GACTCACGCA TTATCTATGA TTATGGAACA GATAATTTTG AAGAATCCAT      240
ATTTAGCCAA GATTATGAGG ATAAATACCT GGATGGAAAA AATATTAAGG AAAAAGAAAC      300
TGTGATAATA                                     310

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Val Pro Leu
1           5           10           15

Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile Tyr Asp
          20           25           30

Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp Tyr Glu
          35           40           45

Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile
50           55           60

Ile
65

```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCCAAGNAAN TTTCAANTTT TTGCCTTTNC TGGCCTTTAN TGGATCCNA AAGCATTTAA	60
GGNANATGTT CCNAAAANTT TGNAAAGNTA AANGTTTCCC ATGATCGCTC ATTTTTTTTTT	120
TATGATTCAN ANGTTATTCC TTATAAAGTA AGNANTTTGT TTTCTCCTA TCAAGGCAGN	180
TATTTTATTA AATTTTTCAN TTAGTTTGAG NAATAGCAGA TAGTTTCATA TTTAGGGAAA	240
NTTTCCAAAT AAAATAAATG TTATTNTTTG ATAAAGAGNT AAAAAAAAAA AAAAAAAAAA	300
AAA	303

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGCTTGNGC ACGNGGCACA AGTAGCTACG NCTGCAAGCA CCTGCCACCA TAAAGGGGNT	60
GCATTTTGCC ACCATAAANG GGNTGCATTT TTTTAAAAAG CCTAGGCNGC TCTAACATCA	120
TCTGATATGG ACACAANGCN AACAGTTTCC NTATNTACAT CCNTACCTCT AAAAGATACT	180
TCAAAGTGAC AAAAACGTGT TCCTTCCCCA CTTAGAGACA ATGATTACA GGGCCCTATA	240
TGTTCTTACC ACATACAGAG GATGCATTTA TTTTGCTCT ATGACACTG CAAAAATCTC	300
TACTGTAATT AATTTGGGTC TATTATTAAC TCTCTGTTCC ATCATAGAAT GTGGCCAGGC	360
CTTACAATGG AGAGCCAGAG TTAAACTTC AAGTGCATC TGTTTTTGGG CTGAGTCA	418

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Thr Leu Ala Lys Ile Ser Thr Val Ile Asn Leu Gly Leu Leu Leu
 1             5             10             15

Thr Leu Cys Ser Ile Ile Glu Cys Gly Gln Ala Leu Gln Trp Arg Ala
          20             25             30

Arg Val Lys Thr Ser Ser Cys Ile Cys Phe Trp Ala Glu Ser
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

AGTTTGTTCT GTAAATATTT NGAAAAGTGA CAGCTNTCAA CTCAGGGTA ACTATTTCTA      60
AAAATGTAAA TANGTATTAA TCCTTGATC TTTTATGGTA ATTTNGCATA TTGATATGAA      120
TTANATAAAA TTGTTTAAAA TAAAAGGTGT CCTTGAATTA CTGACCACCC ATAGATGTNT      180
ACTGTTACCA GGTTTTACAA TGCAAATTTT CACTAATACC TGGGTTTAAT ACAGCTCACA      240
TCACTGAATG TTACACATGA GTTTAAATGG GTTAATATAC AGGTTTTGTT ATAATAAAGT      300
TACTGATTAA ATTAAAAAAA AAAAAAAAAA A                                     331

```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 583 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CACGNGGGTG	AGGCCGACTG	CTGAAGACAG	CTCGCCACCC	TCCTTGCCCTC	CACTCCAATC	60
CAGGGGCTGG	GGCCACATTC	TTTGCCTTCA	TTTATCCTCA	GATCAGGTGA	GATCGACAGG	120
AGGTGTTGAT	GGCAGTGCCA	GCAATTATTG	CTAATCCGTT	TGCATCCTTA	TGCATAGATC	180
TGAATTCAGA	CTTTGTGAAT	TTCCAGAGGT	GTGGGTNATA	TAATAGAATT	CAGTGAGTGG	240
GCATGGCTGA	TCTTGTGCAA	ATTAAAAGTT	ATGGGGCATA	AGAATAGCAA	AAGTTGAACT	300
TCTTTTAAAA	AGGAAAGTAC	CCTGAGAGCC	AGTATTGGTT	GAGGCTCTTC	AGTATGCCCA	360
GGTTGGCAGC	ACTGAGAACC	GCAGGAACGG	CCTGTTGTTA	CAAAAAGGAG	ATTGACTCAG	420
CTGCCCTTGG	TGCATCTGAC	TGACTATGAC	TGCTGAGAGA	TTCCAAGGAC	CCTTAATGCC	480
AGGGCTAACC	TCTCCATGTG	CAGTGAGACC	TCTGGAGGAA	GTGTCATCCT	CTGGCTTTGT	540
GTGGTACTCA	TTATGGTGCA	GTGCGGGCAT	GAAATGAAGA	CAC		583

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Cys Ser Glu Thr Ser Gly Gly Ser Val Ile Leu Trp Leu Cys Val
1 5 10 15
Val Leu Ile Met Val Gln Cys Gly His Glu Met Lys Thr
20 25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCAAATAGG CTTACAGATA CGATATGTTT TAAATGTTTN GTATTTAACA AAAACATACT	60
GAACTGTTT GGAAATGGCA ACAGGAAGAT AGCAAAATGA ATACTAACAT TACGAAAAGA	120
TGAACAGGTA CATGTTCCAA GGCAGGTGGC TGTGAACTTC CTCTGAGTGA AGGCATCCCC	180
TCCAGCACCT TTCAGCCTGC TAGTTAGGAC GACCCGCCGC CACCCTCCAG GACNTCCAGC	240
CCTGCANTGC NTTTCTTTTN TTTTAAATAA TTCTTCATTG AGTTCTAATA TGTAACAAAA	300
AAAAAAAAA A	311

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AAGCTTGGCA CGAGGGCGGT TGAGGCCTTC GGTGGTGAAC GAGTCTCCAG CACCATGTCT	60
GGTTTGCTG GCCCACCAGC CCGGCGCGGC CCTTTTCCGT TAGCGTTGCT GCTTTTGTTT	120
CTGCTCGGCC CCAGATTGGT CCTTGCCATC TCCTTCCATC TGCCCATTA CTCTCGCAAG	180
TGCCTCCGTG AGGAGATTCA CAAGGACCTG CTAGTGACTG GCGCGTACGA GATCTCCGAC	240
CAGTCTGGGG GCGCTGGCGG CCTGCGCAGC CACCTCRAGA TCACAGATTC TGCTGGCCAT	300
ATTCTCTACT CCAAAGAGGA TGCAACCAAG GGGAAATTTG CCTTTACCAC TGAAGATTAT	360
GACATGTTTG AAGTGTGTTT TGAGAGCAAG GGAACAGGGC GGATA	405

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ser Gly Leu Ser Gly Pro Pro Ala Arg Arg Gly Pro Phe Pro Leu
 1 5 10 15

Ala Leu Leu Leu Leu Phe Leu Leu Gly Pro Arg Leu Val Leu Ala Ile
 20 25 30

Ser Phe His Leu Pro Ile Asn Ser Arg Lys Cys Leu Arg Glu Glu Ile
 35 40 45

His Lys Asp Leu Leu Val Thr Gly Ala Tyr Glu Ile Ser Asp Gln Ser
 50 55 60

Gly Gly Ala Gly Gly Leu Arg Ser His Leu Xaa Ile Thr Asp Ser Ala
 65 70 75 80

Gly His Ile Leu Tyr Ser Lys Glu Asp Ala Thr Lys Gly Lys Phe Ala
 85 90 95

Phe Thr Thr Glu Asp Tyr Asp Met Phe Glu Val Cys Phe Glu Ser Lys
 100 105 110

Gly Thr Gly Arg Ile
 115

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCTTTCAATT TACCTTGTGA AAACACCCTT AACTTTTCT TNACCCTTAG CTGAAATGTT 60

NACATAGCTT NTGGTGATAT CTTTTCATGA TTTTATATNT CTAAAAATGG TGATGGATGT 120

GACACCTCAT AAAAGTGAGC TTTGAACTGT AGATAACTCT TAAAGAAAAT GTCATTTTAG 180

ACAATTAAAA TATTTGTGCT CAAAAAAAAA AAAAAAAAAA AAAAA 225

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

CGAGGGCAGG TCAGTCAGGT TCCTGGGCGC TCTGTTACAC AAGCAAGATA CAGCCAGCCC      60
CACCTAATTT TGTTTCCCTG GCACCCTCCT GCTCAGTGCG ACATTGTCAC ACTTAACCCA      120
TCTGTTTCTCT CTAATGCACG ACAGATTCCT TTCAGACAGG ACAACTGTGA TATTTTCAGTT      180
CCTGATTGTA AATACCTCCT AAGCCTGAAG CTTCTGTTAC TAGCCATTGT GAGCTTCAGT      240
TTCTTCATCT GCAAATGGG CATAATACAA TCTATTCTTG CCACATCAAG GGATTGTTAT      300
TCCTTTAAAA AAAAACCAAT ACCAAAGAAG CCTACAATGT TGGCCTTAGC CAAAATTCTG      360
TTGATTTCAA CGTTGTTTTA TCACTTCTA TCGGGGAGCC ATGGAAGAAGA AAATCAAGAC      420
ATACACACAA CACAGAACAT TGCAGAAGTT TTTAANACAA TGGAAAATAA ACCTATTTCT      480
TTGGAAGTG AAGCAAACCTT AACTCAGAT AAAGNAAATA TAACC                          525

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr Ser
1           5           10           15
Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile His Thr Thr
20           25           30
Gln Asn Ile Ala Glu Val Phe Xaa Thr Met Glu Asn Lys Pro Ile Ser
35           40           45
Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Xaa Asn Ile Thr
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

TCAAAAGGTN ACACAAAATT ACTGTCACGT GGATTTTGTC AAGGAGAATC ATAAAAGCAG      60
GAGACCAGTA GCAGAAATGT AGACAGGATG TATCATCCAA AGGTTTCTT TCTTACAATT      120
TTTGCCATC CTGAGGCATT TACTAAGTAG CCTTAATTG TATTTTAGTA GTATTTCTT      180
AGTAGAAAAT ATTTGTGGAA TCAGATAAAA CTAAAGATT TCACCATTAC AGCCCTGCCT      240
CATACTAAA TAATAAAAAT TATTCCACCA AAAAATTNTA AAACAAAGNA AAAAAAAAAA      300
AA                                                                                   302
  
```

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 628 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

CACGAGGTTT CAGACCAGCT TGTGTCAATA GGGTCCTACA GAGCAGCTGA TATCAGCAGT      60
TTTACTAGTA TGCAGGACCT GAAAGAATAT CTCAAAGGGA AAACAATGTT TCATAATGTT      120
CAGGAAGTTA TCTATAGAGC AGCTAAGGAG CTATAATCTT GTAACAGAGT CTACGTGATT      180
GTAGGACAAT AGGCACCACA CAAATATGAG GAAGCAGGTC AGAGAGCGGG CTGACTTAAT      240
GATTAATGCT GAATGTGCTA CAAGCTTGTT TCATTTTCAT TTCTCCTCCT CCCTTTTTC      300
CTGATTAATT TAATAAAGTT CATAGGGGAG GCTTCAAACA CATGAGAAAT TAAAACCTTT      360
ATTACCAGAG TCAGAGCCTG ACTATATTGA TTGAGTGAAG CTTTCCTTTA TAAAATGCAA      420
AGCATGTAAA CAATTCCAAC ACAGTAACAT ATTCATGAGT TTTTAAATTC ATGAGTTTTA      480
  
```

GAGAAAATAT TTTACTTAAA ACCAGCACTT GATGATCTCT GACAATGTTA TGTAGCCTGA 540
 ACCTGGAGTT TTGGCTGATG GGTGTCTCA GCCTGTGACA GGTTTGTAGCT GGCTTTGGTT 600
 CATCTTGAT CACACCCCCA CACTCACA 628

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Pro Glu Pro Gly Val Leu Ala Asp Gly Leu Ser Gln Pro Val Thr Gly
 1 5 10 15
 Phe Ser Trp Leu Trp Phe Ile Leu Tyr His Thr Pro Thr Leu Thr
 20 25 30

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCAGCTAAG GGGAAATAAT CTTGTAACAG GGTCTGGGTG ATTNTGAGGT AATAGGCCCC 60
 AAACAACCAT GGGGAAGCAG GTCAGAGGGC AAGCTGGCNT AGTGTTTAAC ATTGAATGGG 120
 CTGAAAGTTT GGTNATTTT TGTTTCTTGT TTCTCCCCCT CCCTTCTNAC CTGAATAATT 180
 TTATGAAGTT TATAGGGATG GTTTCAGGAC CTCCATTCTA TCTGTTCTG AAATATTACA 240
 AAAAGATTAT TATTGTAGCA CTNATNTAAT TGGGGTTTTA TTTCGTTGTT NGCATGTCTG 300
 TTTCTTCCCC AGTGAGTTGT AAATTGCTTA AGGGCAAACA GACGCATCCT ATTTATCTGT 360
 CTGTCACTAA CATTAAGCAC AGCATTTGGT ATACAGTCAT CACTCTAATA AAGTTTGAAA 420

AAAAAAAAAA AAAAAA

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 636 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CACGAGGGAA AAAAAGAGTT TTTTTTTTAG ATCATCAGCT ATTGTTAGTG TTTGTGTATG	60
TTATGTGTGG CTCAAGACAA CTTTGCTTCT TTTAATATAG GCAGGGAAGT CAAAAGATTG	120
GATATCCCTG CTTTATACCA AGAAAGACAA CACCCACAT TTGCAGTGCC TGAAAACACT	180
ACCAGCCATC TGAAAAACAT GTGACTTCTA ACTTCTGTTC TTTTTTGTAG CAGTGGAATC	240
CCACGGTGAT ATCTGAGGGA TGTGGTTACC TTTTGAGGA GGTGACGGT TTCTAAGGAT	300
GATTCTTTCT GAGTGAAATA TTGTCAGTGT CATTGACCTT TTCATTATTT CAACTATTAT	360
TATTCCAGGT TATCAATACT CTGGCTGACC ATCATCATCG TGAGACTGAC TTGGGTGTAG	420
GAGTTCGAGA CCACCCTGGC CAACATGGCA AAACCCCATC TCCACAAAAA TTGGATAATT	480
TGATAATTAT CATTATTGGG TTTCTGAGAC GTTACACATT TAACATTNTN TTCTGCACAA	540
GTTGCCTTTG TGTGAGTATA CTAACTTTCT GTAGAGGTAN ACTTGTAATC ACAAATAAGA	600
ATAAATTATA TAAACAAAAA AAAAAAAAAA AAAAAA	636

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Phe Phe Leu Ser Glu Ile Leu Ser Val Ser Leu Thr Phe Ser Leu Phe

1	5	10	15
Gln Leu Leu Leu Phe Gln Val Ile Asn Thr Leu Ala Asp His His His	20	25	30
Arg Glu Thr Asp Phe Gly Val Gly Val Arg Asp His Pro Gly Gln His	35	40	45
Gly Lys Thr Pro Ser Pro Gln Lys Leu Asp Asn Leu Ile Ile Ile Ile	50	55	60
Ile Gly Phe Leu Arg Arg Tyr Thr Phe Asn Ile Xaa Phe Cys Thr Ser	65	70	75
Cys Leu Cys Val Ser Ile Leu Thr Phe Cys Arg Gly Xaa Leu Val Ile	85	90	95
Thr Asn Lys Asn Lys Leu Tyr Lys Thr	100	105	

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGCACGAGGA GCGGGAGCTG GTGCCTTCCC GGAAGGGCTC AGAGGCGGGC TCGGGCAAGC	60
ACTTTAACCT TTTAAGCCCA ACCAGATGAG TTGCCTGCAG TTTTGGAGGC CTTTCAGAGCA	120
TTTCACTAGA CCTCTGTCTG TGTCGGTCCA ATGTCTTTAG CCAAGCTTTG ATTAAAGATG	180
ACTTCCTTGT TTGCTCAAGA AATTCGCCTT TCTAAAAGAC ATGAAGAAAT AGTATCACAA	240
AGATTAATGT TACTTCAACA AATGGAGAAT AAATTGGGTG ATCAACACAC AGAAAAGGCA	300
TCTCAACTCC AAAGTGTGA GACTGCTTTT AAAAGGAACC TTAGTCTTTT AAAGGATATA	360
GAAGCAGCAG AAAAGTCACT ACAGACCAGG ATTCACCCAC TTCCACGGCC TGAGGTGGTT	420
TCTCTTGAGA CTCGTTACTG GGCATCAGTA GAAGAATATA TTCCCAAATG GGAACAGTTT	480
CTTTTAGGAA GAGCACCATA TCCTTTTGCT GTTGAAAATC AAAATGAAGC AGAAAA	536

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met Thr Ser Leu Phe Ala Gln Glu Ile Arg Leu Ser Lys Arg His Glu
1           5           10           15

Glu Ile Val Ser Gln Arg Leu Met Leu Leu Gln Gln Met Glu Asn Lys
20           25           30

Leu Gly Asp Gln His Thr Glu Lys Ala Ser Gln Leu Gln Thr Val Glu
35           40           45

Thr Ala Phe Lys Arg Asn Leu Ser Leu Leu Lys Asp Ile Glu Ala Ala
50           55           60

Glu Lys Ser Leu Gln Thr Arg Ile His Pro Leu Pro Arg Pro Glu Val
65           70           75           80

Val Ser Leu Glu Thr Arg Tyr Trp Ala Ser Val Glu Glu Tyr Ile Pro
85           90           95

Lys Trp Glu Gln Phe Leu Leu Gly Arg Ala Pro Tyr Pro Phe Ala Val
100          105          110

Glu Asn Gln Asn Glu Ala Glu
115

```

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

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TTTATTTTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
AAAAAAAAAA AAAAAAAAAA
79

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What is claimed is:

1. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:
 - (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 28 to nucleotide 276;
 - (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AE402_1i deposited under accession number ATCC 98190;
 - (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AE402_1i deposited under accession number ATCC 98190;
 - (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AE402_1i deposited under accession number ATCC 98190;
 - (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AE402_1i deposited under accession number ATCC 98190;
 - (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
 - (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity;
 - (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
 - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.
2. The composition of claim 1, further comprising a pharmaceutically acceptable carrier.
3. A method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition of claim 2.
4. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
 - (b) fragments of the amino acid sequence of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone AE402_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

5. The composition of claim 4, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.

6. The composition of claim 4, further comprising a pharmaceutically acceptable carrier.

7. A method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition of claim 6.

8. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 61 to nucleotide 513;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 322 to nucleotide 513;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AE610_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AE610_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AE610_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AE610_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:5;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

9. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:5;
- (b) fragments of the amino acid sequence of SEQ ID NO:5; and
- (c) the amino acid sequence encoded by the cDNA insert of clone AE610_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

10. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 523;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AH106_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AH106_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AH106_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AH106_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity;

- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

11. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
 - (b) fragments of the amino acid sequence of SEQ ID NO:8; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone AH106_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

12. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 130 to nucleotide 309;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AH196_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AH196_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AH196_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AH196_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

13. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) fragments of the amino acid sequence of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

AH196_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

14. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12 from nucleotide 69 to nucleotide 467;

(c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AI6_1i deposited under accession number ATCC 98190;

(d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AI6_1i deposited under accession number ATCC 98190;

(e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AI6_1i deposited under accession number ATCC 98190;

(f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AI6_1i deposited under accession number ATCC 98190;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:13;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

15. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:13;
- (b) the amino acid sequence of SEQ ID NO:13 from amino acid 69 to amino acid 133;
- (c) fragments of the amino acid sequence of SEQ ID NO:13; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AI6_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

16. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:16;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:16 from nucleotide 55 to nucleotide 337;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AJ13_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AJ13_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AJ13_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AJ13_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:17;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:17 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

17. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:17;
 - (b) the amino acid sequence of SEQ ID NO:17 from amino acid 12 to amino acid 94;
 - (c) fragments of the amino acid sequence of SEQ ID NO:17; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone AJ13_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

18. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 33 to nucleotide 422;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 114 to nucleotide 422;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AJ27_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AJ27_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AJ27_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AJ27_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

19. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
 - (b) fragments of the amino acid sequence of SEQ ID NO:20; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone AJ27_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

20. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:22;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:22 from nucleotide 47 to nucleotide 517;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:22 from nucleotide 116 to nucleotide 517;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AJ142_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AJ142_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AJ142_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AJ142_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:23;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:23 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

21. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:23;
- (b) fragments of the amino acid sequence of SEQ ID NO:23; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

AJ142_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

22. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24 from nucleotide 312 to nucleotide 417;

(c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AK604_1i deposited under accession number ATCC 98190;

(d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AK604_1i deposited under accession number ATCC 98190;

(e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AK604_1i deposited under accession number ATCC 98190;

(f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AK604_1i deposited under accession number ATCC 98190;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

23. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:25;
- (b) fragments of the amino acid sequence of SEQ ID NO:25; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

AK604_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

24. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 76 to nucleotide 372;

(c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AK620_1i deposited under accession number ATCC 98190;

(d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AK620_1i deposited under accession number ATCC 98190;

(e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AK620_1i deposited under accession number ATCC 98190;

(f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AK620_1i deposited under accession number ATCC 98190;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

25. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
 - (b) fragments of the amino acid sequence of SEQ ID NO:28; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone AK620_1i deposited under accession number ATCC 98190;
- the protein being substantially free from other mammalian proteins.

26. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 367 to nucleotide 552;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AK650_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AK650_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AK650_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AK650_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

27. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- (b) fragments of the amino acid sequence of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone AK650_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

28. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 116 to nucleotide 310;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 173 to nucleotide 310;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AM226_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AM226_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AM226_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AM226_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:33;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

29. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:33;
- (b) fragments of the amino acid sequence of SEQ ID NO:33; and

(c) the amino acid sequence encoded by the cDNA insert of clone AM226_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

30. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 281 to nucleotide 418;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 353 to nucleotide 418;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AR417_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AR417_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AR417_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AR417_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

31. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) fragments of the amino acid sequence of SEQ ID NO:36; and

(c) the amino acid sequence encoded by the cDNA insert of clone AR417_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

32. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:38;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:38 from nucleotide 496 to nucleotide 583;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:38 from nucleotide 565 to nucleotide 583;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AU43_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AU43_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AU43_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AU43_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:39;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:39 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

33. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:39;
- (b) fragments of the amino acid sequence of SEQ ID NO:39; and

(c) the amino acid sequence encoded by the cDNA insert of clone AU43_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

34. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 55 to nucleotide 405;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 148 to nucleotide 405;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone AW60_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone AW60_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone AW60_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone AW60_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

35. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
- (b) fragments of the amino acid sequence of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone AW60_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

36. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44 from nucleotide 337 to nucleotide 525;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44 from nucleotide 406 to nucleotide 525;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BA176_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BA176_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BA176_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BA176_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:45;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

37. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:45;
- (b) fragments of the amino acid sequence of SEQ ID NO:45; and

(c) the amino acid sequence encoded by the cDNA insert of clone BA176_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

38. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 536 to nucleotide 628;
- (c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BD140_1i deposited under accession number ATCC 98190;
- (d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BD140_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BD140_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BD140_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

39. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) fragments of the amino acid sequence of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BD140_1i deposited under accession number ATCC 98190;

the protein being substantially free from other mammalian proteins.

40. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50 from nucleotide 303 to nucleotide 617;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50 from nucleotide 345 to nucleotide 617;
- (d) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BD407_1i deposited under accession number ATCC 98190;
- (e) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BD407_1i deposited under accession number ATCC 98190;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BD407_1i deposited under accession number ATCC 98190;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BD407_1i deposited under accession number ATCC 98190;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:51;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above; and
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above.

41. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:51;
- (b) the amino acid sequence of SEQ ID NO:51 from amino acid 1 to amino acid 32;
- (c) fragments of the amino acid sequence of SEQ ID NO:51; and

(d) the amino acid sequence encoded by the cDNA insert of clone BD407_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

42. A composition comprising an isolated protein encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:52;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:52 from nucleotide 178 to nucleotide 534;

(c) a polynucleotide comprising the nucleotide sequence of the full length protein coding sequence of clone BF290_1i deposited under accession number ATCC 98190;

(d) a polynucleotide encoding the full length protein encoded by the cDNA insert of clone BF290_1i deposited under accession number ATCC 98190;

(e) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BF290_1i deposited under accession number ATCC 98190;

(f) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BF290_1i deposited under accession number ATCC 98190;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:53;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:53 having biological activity;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above; and

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above.

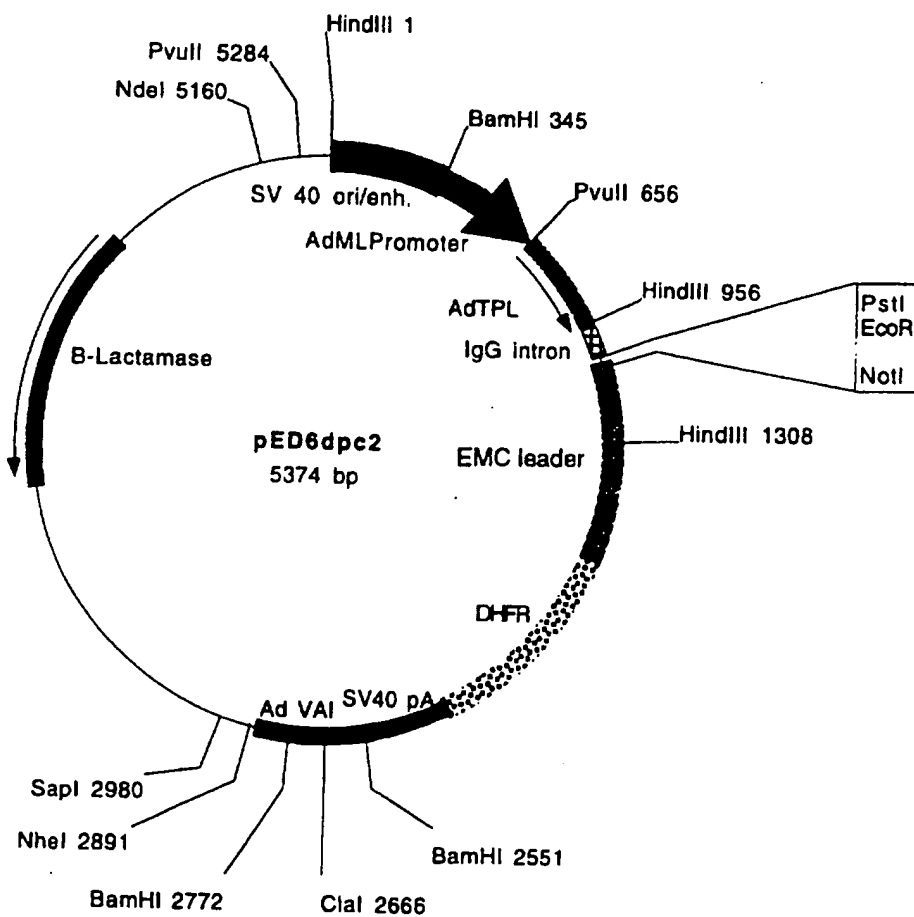
43. A composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:53;

(b) fragments of the amino acid sequence of SEQ ID NO:53; and

(c) the amino acid sequence encoded by the cDNA insert of clone BF290_1i deposited under accession number ATCC 98190; the protein being substantially free from other mammalian proteins.

FIGURE 1A

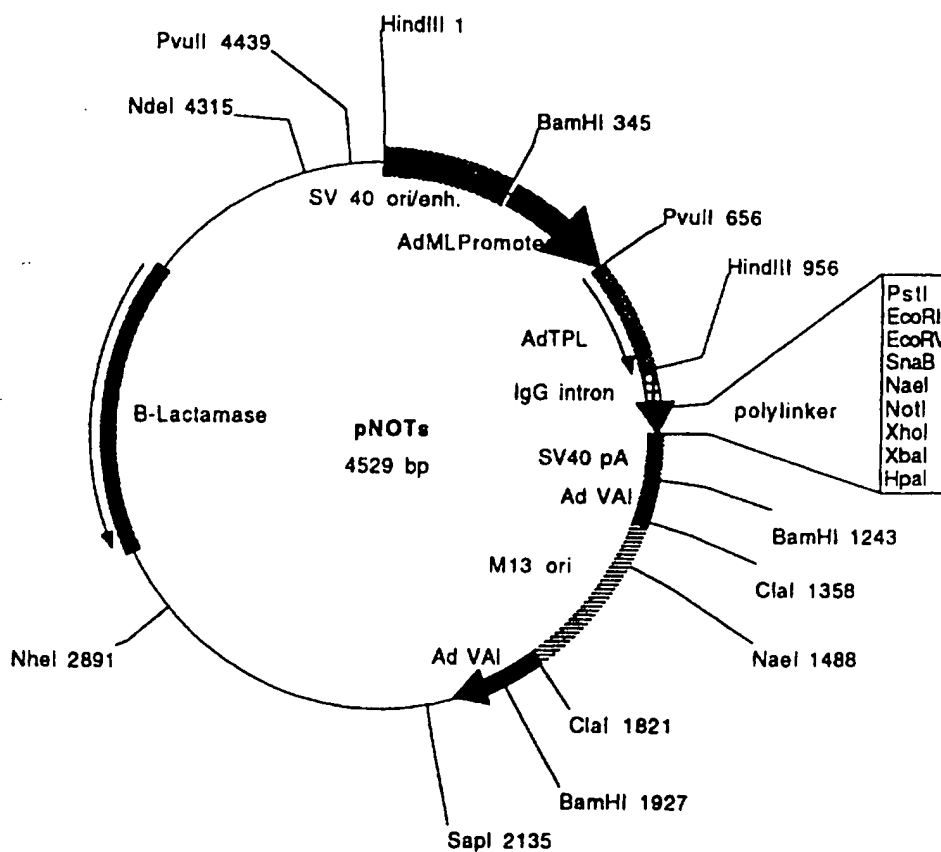


Plasmid name: pED6dpc2

Plasmid size: 5374 bp

Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 1B



Plasmid name: pNOTs

Plasmid size: 4529 bp

Comments/References: pNOTs is a derivative of pMT2 (Kaufman et al, 1989, Mol. Cell. Biol. 9:1741-1750). DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M13 origin of replication was inserted in the Clal site. SST cDNAs are cloned between EcoRI and NotI

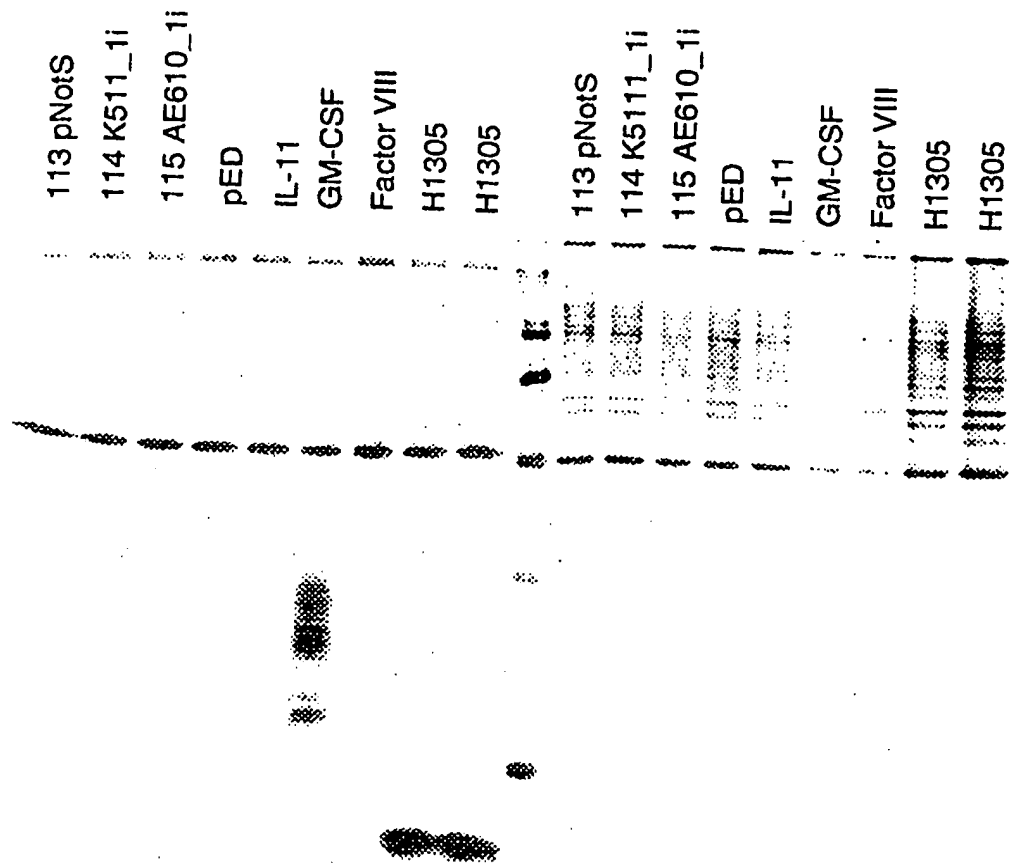


Fig. 2

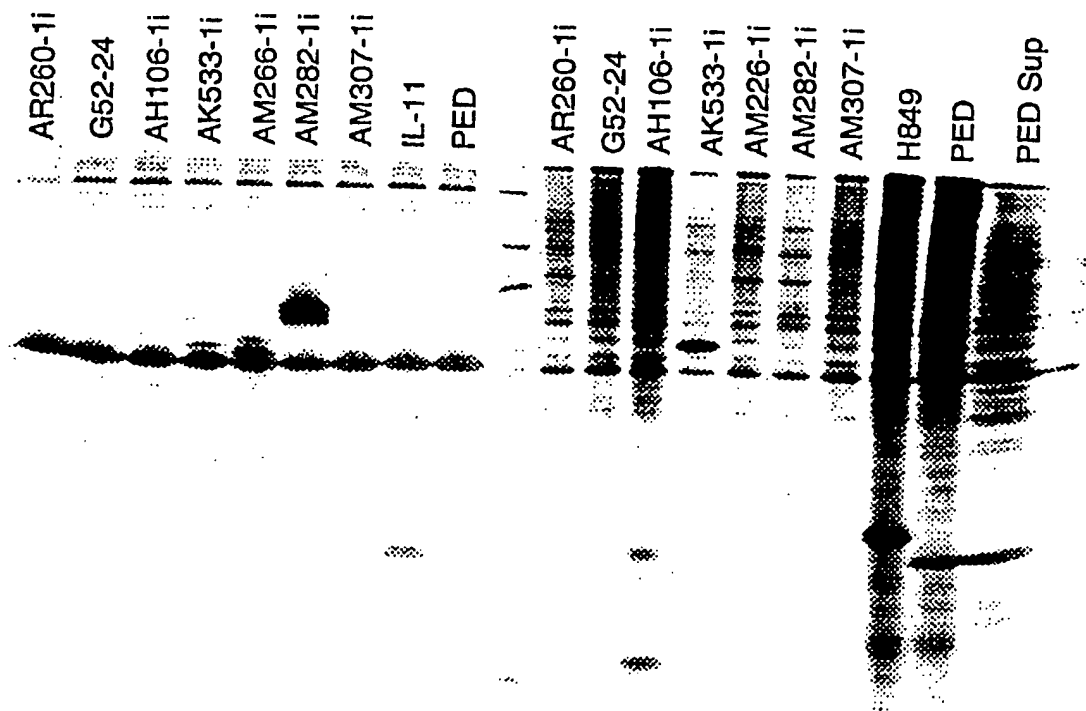


Fig. 3
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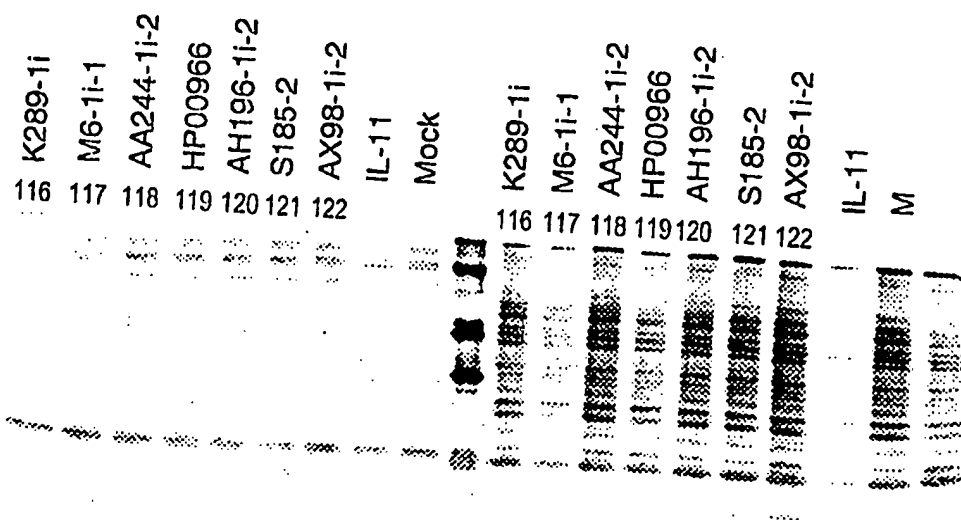


Fig. 4
5/10

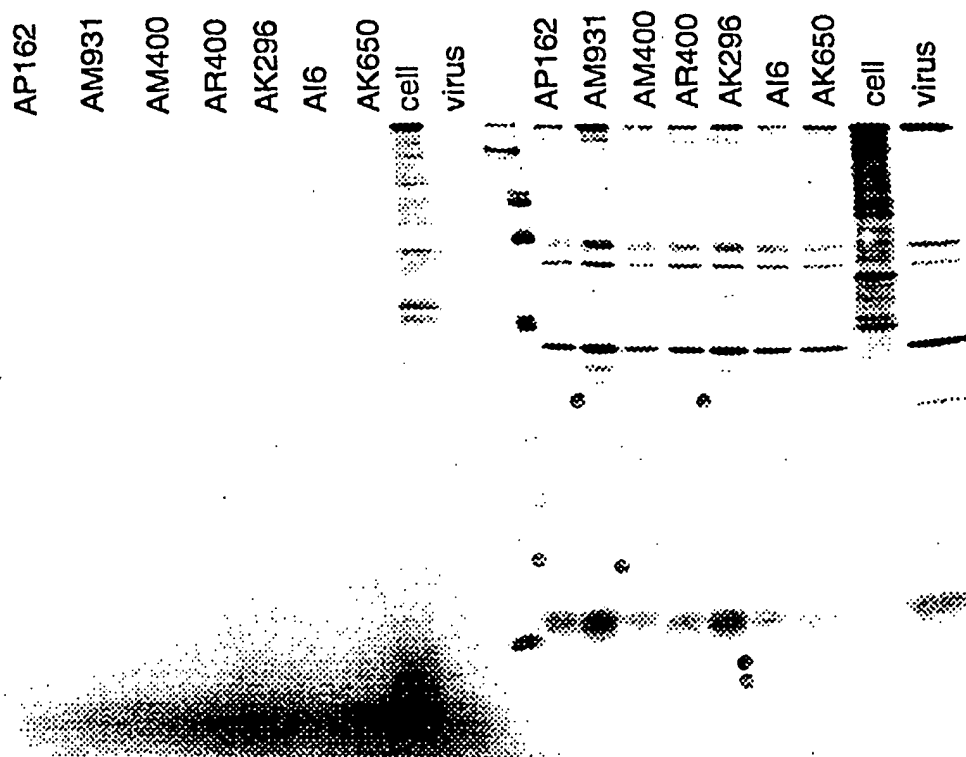


Fig. 5

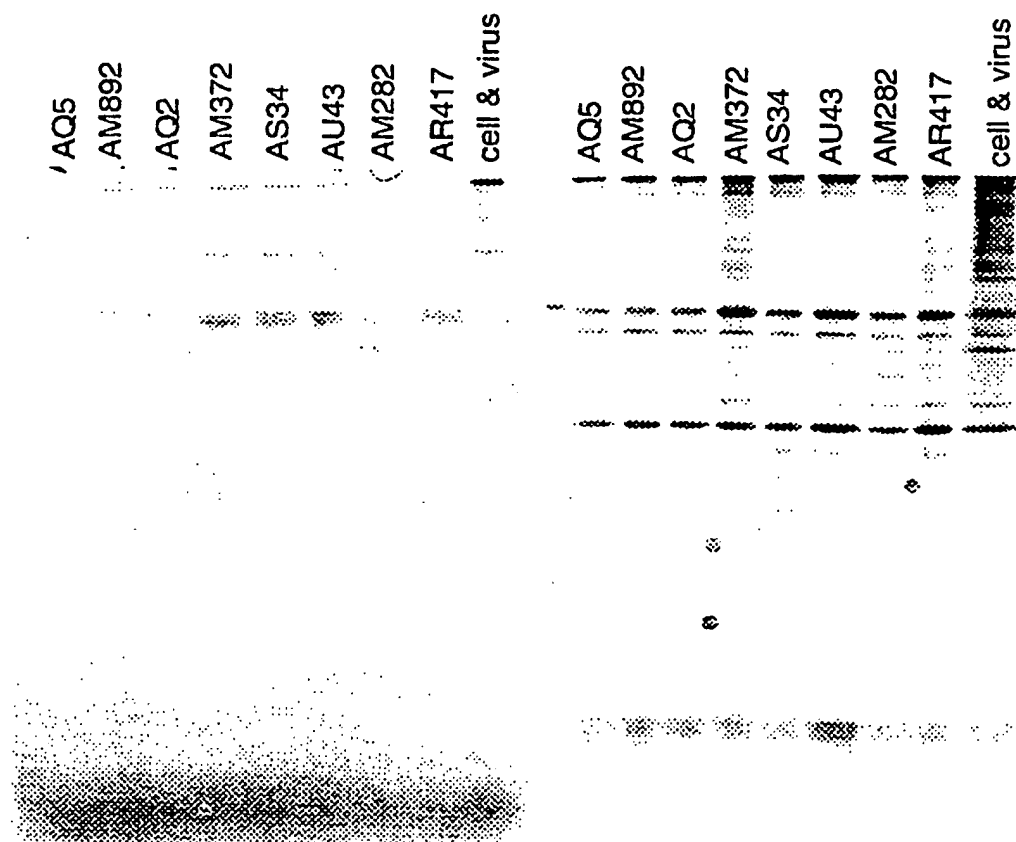


Fig. 6

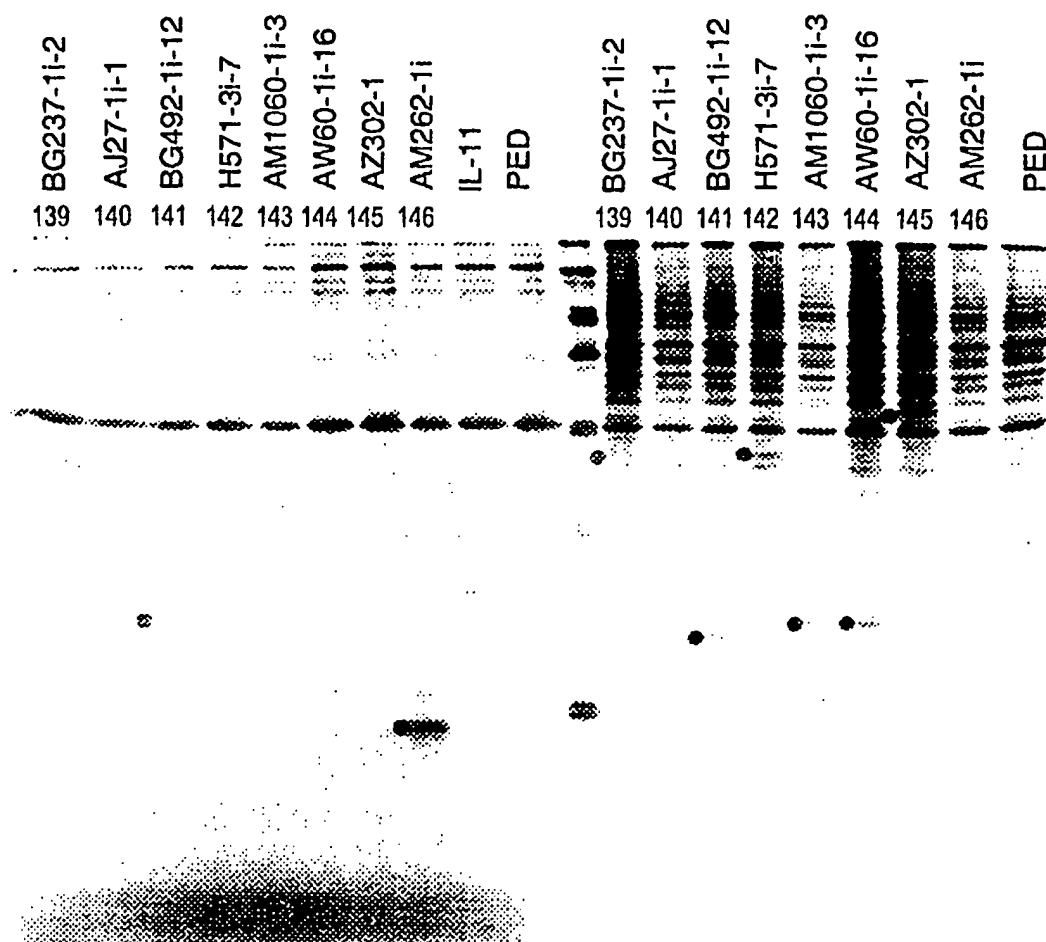


Fig. 7

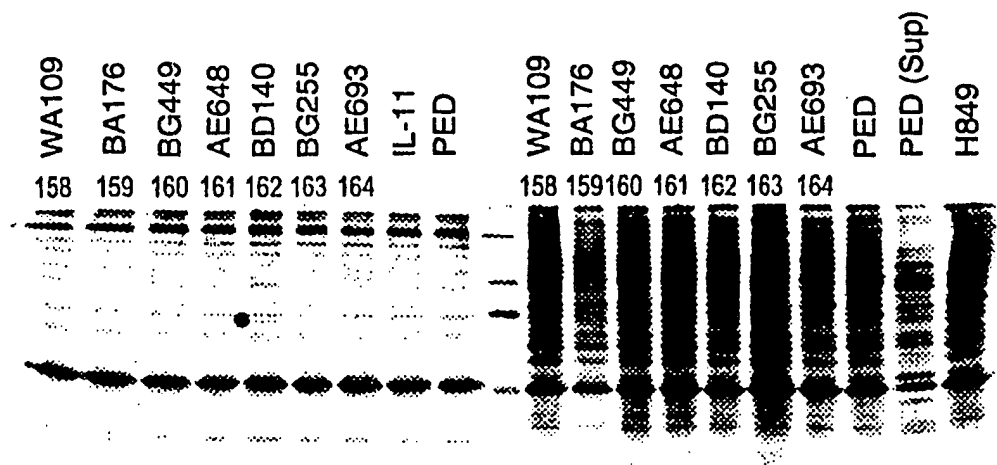


Fig. 8
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<p>(54) Title: BIALLELIC MARKERS</p> <p>(57) Abstract</p> <p>The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference. (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- 10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment
- 15 of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the
- 20 Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- 25 Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- 30 As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with - polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

15 $p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2$.

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($cum p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30

$$cum p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ , to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
5 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.
10

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
20 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.
25

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence. That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by
5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a
10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such
15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a
20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the
25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament
30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTAAATCCACATTGAAGCCAAAGAAAGAACATCACACTTAAACACATGCCAGTTGGGAAGGTCT
						GAAACTCAGTGCATATAGGAACACTTGAGACTAATGAAGAGAGAGTTGAGACCAATCTTTATTT
						GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTGGAAAAGCTTTTGAGGATAATGT
WI-7070	226	C	T	---	---	TACTAGACTTTATGCCATGGTGCTTTTC/TAAGTTTAATGCTGTCTCTCTGTCAG
						AAGCCATTGACGTAACATCTCAGAGGTTATTGTCATGGATTGACTCTGGGACAAAAGGAC[G/C]AA
						AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT
						GATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATCTGAAAT
WI-10744	61	G	C	---	---	AAATGAGGTAAGTTTCAGGCACCTCA
						GGGCAATTACAGCAAAAAGTCAATTTACCAGCATCAAAGTCAGGTGCAAGGAGGTAGAACA
						TTACAGTAACATATGCAATCTTTTGTATATTAGTATATCTGCCCAATGCCCTAGAATA[C/T]AGTG
						GGTCCCTAATAGTATTAGTTCCTTTTCTCCTCTTCTCAATCTCTGAAATTTATTTTATACTTAA
WI-9975	126	C	T	---	---	GGGATTAGTTACCACCAAAATGTGTATGTATCAATTTGATCTTACTGAA
						GCTAGGTTTGTCTGTGGCTGTCTCACTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGT
						GATGTAACCTAGCTAGACCTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAAGTATGCCACAC
						TCACCCCTCTCCAGTTCACTGTATTAAATTTCTCCCATATTAATCAAAAGGGAGTGGACAGGT
WI-8010	247	G	T	---	---	CCCTGGCTGAAAAGAAATAAGAGATCCCCAAAGTGGGG[G/T]CTT
						GCCCGGCTATCTTTAATTTAACTTGATCTTTGGTGTCTCCATCCTAGGATTCTGCCTTATAAT
						CTTTGTCTCTGTGTA[G/C]ATTACCTGATTCTACTTTTGTATACAAAGGCTGATGGCTCACAATGT
						AGTAGTCCCAATCTTCAGGTCCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	G	C	---	---	TCCTGACTCTATAACAACCTCCACACAGM
						GCCCGGCTATCTTTAATTTAACTTGATCTTTGGTGTCTCCATCCTA[G/C]GATTGCGCTTAT
						AATCTTTGCTCTGTGTAGATTACCTGATTCTACTTTTGTATACAAAGGCTGATGGCTCACAATGT
						AGTAGTCCCAATCTTCAGGTCCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	G	C	---	---	TCCTGACTCTATAACAACCTCCACACAGAA
						TATGCACTCCACAAAAGGATATAATTTAAAGTTTTTTCATTAGAAATAAATGATATAAAATAA
						ATATGTTATTAGGCATTTATTACTAATACTAGTCCCTCTTGGAGGAACACCCCAACCAATAGCTT
						ATAAGTACATGTAATTTATAGTAACATAATTTACTATATACATATGGAATAATCATATTTCTCACA
WI-8007	242	C	A	---	---	GAAGAGCTGAACAGACATTCCACAGGATACGACTGTTGGAC[C/A]AGCTGCTG
						TCAGTTGCAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGATGTGTTTGTAG
						TCTATATCACACATATGAGTGAATTT[C/T]GGGGCATGGGAAATACATCTTTTATGAGACATTGA
						ACTGCTCACCACATATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTAC
WI-9823	97	C	T	---	---	ATGCTTCCAATCTGATTTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	---	TCTACATTCATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCCTTCCT ACTTGCTCCTCATGTACAAATTTTCTGCTCGTCTTCAATJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCTTATAGGCCTCTG TCTTTAAACCTGTAATGGTATATTAATCCCTGGGTGTTGAATGCTCTC
WI-9651	139 T C ---	---	---	TCTACATTCATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCCTTCCT ACTTGCTCCTCATGTACAAATTTTCTGCTCGTCTTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CTTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCTTATAGGCCTCTGT CTTAAACCTGTAATGGTATATTAATCCCTGGGTGTTGAATGCTCTC
WI-7676b	309 A C ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGGAGGCTGTGTGAAGGG GCGGCTCTCTGGTGGCTGCTGGTTCAGGGGAGGAGCGTGTGCACTGCAGCTTCTGCTGTGCTG TCCCCCGTCTCCTGGAGGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGGAGGCTGTGTGAAGGG GCTGTGGCTCTCTGGTGGCTGCTGGTTCAGGGGAGGAGCGTGTGCACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGGAGGAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	---	CATTATCTGTCTTGGTCTGTTCATTCACTTCTCTCTCCTCAATGAAGGAGTATTTAAGCATCAIT CATCTGGCCCTTTTGTGAGTTTGAATAATTTTGTGTGATGCTCTATGCACATGATAAATTTGTA TGTCTGTCTTATCTATCTTCTTGTATAGGAGTTTGGCCATGACCTTTATGAGGAGAAAGGGA TCACCCCTTTTGGCTCTACAACTTATAGATAATTTAATAATCTTT
WI-9986	42 T C ---	---	---	TTGGTGTGAACCTCAGAAATATAGGAAATTAAGACAAATTTGAATTA/CJGTACCCAGGAAACAAGAG CCCTGCACTTGACTCCAAAGGAGTCTATTTATCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGATCCAGGTAGTACTCACAAGAACAATGTCA ATATCAATAGCATGCATATGGGTGTTGGATTCTTAGAACCTTATTGCAAT
WI-7041	174 C A ---	---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATAGGCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCCTCAGAGAGCTGAAAGGGTCCCTCGGTCTTTATTT CAGGGCTTGCATGGCTCTATCCCTCTGCTCTC/CJCCACTTCTTTGGAGCAAGGAGATGC AGCTGATTTGTGTAAACAGCTCAATTTGTACAGTGTCTGTATGTAATAA
WI-7224	134 T C ---	---	---	ATAACCCCTTGATGTATCATCCCACTCACTAATATCAACTTATGTCTATCAGATATCCTCTCT ACCTCAGCTTATTTGAAGAAATCCTAAGCATCAAACTTTCATCCATAAAATGTGAGCATTT /CIATTAAGGATGGCTGTGATTATCTTGGGAGGAGAGTGAATCATGCTAG

WI-10826	132	A C ---	---	TCCTATTGCAATTCACAGTAGCCCATGAAGTAGGTATAACACGCTCTATTTTAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGCTCAGGTTTCCTAATAAGCAAAAGACCTGCAJAC JCCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGCTGTCAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145	G A ---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACCTTTGGAGATTCAITTTCTTGAGTGGCACTGCAT GCTCATTCAGTGAAACCTTGCGGTATAGAAATGGAATGGAGAGTTTCAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACGTGCTTAGGCATTGAAACCATCACCTGGTTTGCAATTCCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T --	---	AAACACACAGAAATCATCAAGCACJATJATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTAIG TAAGAAGTAACCTCGAAATAGTAGGATAGTATATCATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATCTATGGAACCTCTCGTACTGTAAATTTTCATTCTATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G T ---	---	TAGTATGTCACTGCCATGGTAAGGACTTTGATCACTAGGAAATAGAACACTTTGAATGGCTTGCC TTTCAATAAAGAGAGTGACATGATTGAACATGTGTTTAGATAAAGGCACCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGAAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGATAATCTAAAAACCAAGAGAAAGAAACTTGAT
WI-4719b	107	T G ---	---	TTCAITTCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTGTTGGGTGAGCGGATT ATGCTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCACACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70	G A ---	---	TTCATTCCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTGTTGGGTGAGCGGATT AT[G/A]CTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCACACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216	G C ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTTACCTTACCCCTGAGG AATACTGAGCTCCGATGCAGGGAATGGGTGGGGTGTAGCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTGCTGGAGAGGGAGGGCCAGACAGGAGGAATCAAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGACCAGGGTTCCAACTTT
WI-9484	178	G A ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTTACCTTACCCCTGAGG AATACTGAGCTCCGATGCAGGGAATGGGTGGGGTGTAGCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTGCTGGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGACCAGGGTTCCAACTTT

WI-7330	207 C T	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTTCGTCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGTGGAAATTCCTCTTTAATTTGGCATATAGGTTT GTGACAAAGAAGTCATACTTTGGTGGTAAGTTTACTAAGGAAAATAACTGAAAGATTAAAG TGAGAGTCCTTGAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGCACAG
WI-9443	211 G A	TTAAACACAGTTTCAGGTTGGTGAAGCAGAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACIT GCACAATTATCTCTTGGCATCATACAACTGGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACTCATGGAAGGCAGTCAGAGTCCATCAGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGACGACAGAGACCTTGGACTACAGATGACACACATGCCACIT
WI-7166	59 C T	TCTCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTACCTGGAT CATCAACAAGATTCTCTGTGCAAAATATTTGACTATTTCTGTATCTTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGGTTTAACTTGTTCGTGTGAACAATTTGCGAAAGAGTCTTCCAAAT TAATGCTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCGAG
WI-7259b	189 T C	GCCTCTCCGAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGAGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCTCGAACAGCTGCAAGCTGCTTCTCTCTCTGAGTTCTCTGGGCT GGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAOCCTGGCCACAGTCCTGGGGAGCAG AGCCAGAGGTGGACAGGTGTTTCAGGGGCCCAACTTCCCTGGAGCTC
WI-7259	188 G T	GCCTCTCCGAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGAGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCTCGAACAGCTGCAAGCTGCTTCTCTCTCTGAGTTCTCTGGGCT GGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAOCCTGGCCACAGTCCTGGGGAGCA GAGCCAGAGGTGGACAGGTGTTTCAGGGGCCCAACTTCCCTGGAGC
WI-7322	275 A G	GTACTTTAGGCTGTGGAGGTGGGCATTTAGTGGTGACCTTGCACAGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCACCCATATG GCCATAAACTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTGGACAGAGAAAGAAGCACTC TGGTTCTCTATCCCTTGTACATAGAGAGTTTGTATGGGCTCTGGCTG
WI-7685	46 T C	TCAGTTCTAGTCTCTGGGGCCACACAGAACTCTTTTGGGCTCTTCTTCTCCCTCTGGATCA AAGTAGGAGGACCATGGGACAGGCTTGGAGCTGAGCCTCTACCTGTACTCTCCGAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCTCTGATCTCCATGGCTTCTCTCTCCCTCTGCCGACTC CTGGGTTGAGCTGTTGCCCTCAGTCCCCCAACAGATGCTTTCTGTCTC
WI-563	87 G A	TGTGACCAATTGTTATTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTGGCCAGAATTTC CTGGGGGAGGGCTCCCTCTGACCTGATCATGTCTACCTAAGCTGCTTACTCTAACAAATACTACTCC TGTGGTATGGGGATCCTAAGCCAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191	CA	---	---	GACCAGGGCACCAGAAAGCCACGGAGGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACTGTCTATTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81	AG	---	---	GACCAGGGCACCAGAAAGCCACGGAGGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCT[AG/TTCCCTCACCACACCTTCCAGTGTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTATTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31	AG	---	---	GACCAGGGCACCAGAAAGCCACGGAGGCCAC[AG/GCCACTAGCCCTGAACCTTGACACCCCTGGA GTTTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTATTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91	CT	---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTTCATGGGTAACAACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGG[C/TTACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC
WI-10870	103	GA	---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTTCATGGGTAACAACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGGCACCTACTTAGA[GA/CAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC
WI-7719b	281	TC	---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAAGTCTACAAATGTCCCAATATCAAGGACAAACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	AG	---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAAGTCTACAAATGTCCCAATATCAAGGACAAACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[AG/TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	CA	---	---	GCCTTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGAA GAGT[C/A]GTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTTA TGCCATTTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---	---	TCCCTTTATGACCCCAAGAGATATTTAATTAACACCAATTAACGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TCAGGTTGGAACATATGCAGTGTCTCCGGCCACACA TCCTGCTGGGCCCCCTACCTGCCCAATTCATCTCTGCCAATAAATCCTGTCTATTGTTTCATCCTG GAGAAITGAAGGGAGGTCAGTGTGTTGTCATGATTTGTCAGAGAACCCT
WI-7842	57 T C ---	---	CACAGCCATGCCCTTGGAGGCGCGCCACACAGATGCTGAATCCCTATCCCATCTGTC/GTATGAG TCCCATTTGCCCTTGAATTAGCAATCTGTCTCCCCCAAAAAAGAAATGTGCTATGAAGCTTTCTTTCT ACACACTCTGAGTCTGTAATGAAGCTGAAGGCTTAGTACACAGAGCTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	CTGCCTCATACGCCACTGGAGTCCACACTTGAATTTGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCAACCCAGCTGTACCAAGCCCGGCGAGGTGCAGCCCTTCTCTCC TGTCTCTG[C/A/C]TCTGACTCTCTTTTGGGTCCTCTGTATGCTACCTCTGACTTCTGTGTCCTCTCTG TGTCTCTCTCATCTCTCTTACTGGGCGCTGGGCTCTAGCCCAA
WI-4767b	173 C A ---	---	TTTCCAGTCTGTTTTATCCTTTTATGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCT CAGGTCGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGAGTGGAGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGAC[C/A]AAATCATAAGGAATTCCTACTAAGA CTCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---	---	TTTCCAGTCTGTTTATCCTTTTATGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTT CCTCAGGCTGGTATCCTAGATCTTCTATATCCATTGAGTGTGAGTGGAGAGAGGGTATG TTTCTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCATAAGGAATTCCTACTAAGAC TCTCTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/G]CAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A ---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	---	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAACTGTGTTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718b	248 A G ---	---	---	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTCAGATGGAAGAGGTGAAATGAAGAGGAACTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718a	42 A T ---	---	---	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGC[AC/TC]TGTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAACTGTGTTGAAACAGAAAAATAAG TCAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7227d	99 G C ---	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTCAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATAGCCCCAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATAGCCCCAGAGGGGACTGAGCTAAACAGTG TTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATAGCCCCAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTCATCTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATAGCCCCAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---	---	---	CCCAATGCCTCTCCACGATGCAAGGACTCCTGCTGCTCCTGGAGTGGGAGACAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGTAATGCTATGTTGATGCTTCATCGAACTGATGCGAAACT TGAATCTGTTACTGAAATGAGGAGAGGAGGACATGTGCTATTGAAGTGAAGCAACACTGTAAT ATCCACAGACTCCCTCCCTGCCCTCCATCCCAACATGATGCTTGAGATTTC

WI-7310a	64 T A ---	---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTCTCGAGGTGGGAGACAAAGGAACCTT/A JCGGAAGAGGAAGCAAGAAAGCGTACTGTCTATGTGTGATCCTTCATCGAACAAACTGATCGGAA AACTTGAATCTGTACTGAAATGAGGAGAGAAAGGACATGTCTATTGAAGTGAAGCAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCCCTTGTACCTGCCTGGACTCCTATGATGGCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGGCTCTGATATCGCTTTGGCATGATTGCAATGGAGGGCAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTG/A/GTGTGATGAAGGTGATGTGGGAGGGGAGCACAGTGT CTGTGGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCCCTTGTACCTGCCTGGACTCCTATGATGGCTGCTGTTGGTTGATAATA TCAGATCATGCCCAAGACGGGCTCTGATATCGCTTTGGCATGATTGCAATGGAGGGCAATGCG GTCCCTGAGGAGAAATCTGGGAGGAGCTGATGTGATGAAGGTGATGTGGGAGGGGAGCACAGTG TCTGTGGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATTCGACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAGATC AGATGTGGCCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAAGGGCTC/TJGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATTCGACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAG ATCAGATGTGGCCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAGGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATTCGACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAG ATCAGATGTGGCCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAGGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTGCTCTATTGGAGCCCTCATATTAAATAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAAG/A/GATGTAGATTGTACATTCAATCCTGAACAAACCTG CCAGGCAAGCTCTTCCCATTTTACAATAAGGAGACAAATAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGTTTGTGCC
WI-1017a	92 G A ---	---	---	AAATTGCTCTATTGGAGCCCTCATATTAAATAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAAG/A/GGATGTAGATTGTACATTCAATCCTGAACAAACCTG CCAGGCAAGCTCTTCCCATTTTACAATAAGGAGACAAATAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGTTTGTGCC

WI-1795b	130	T C ---	---	---	GAAGCAACCAAGAAAGTATCTTATCCCCATCTAGATTATGTCTGGGTCTTCAGACTCCTACGATTAA AATTGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTGCCTTGCGAGAAAGAAAGTTC/C GTCTACCAATTTTACCAGAAATTCGTAGTACAAATTTAAGTATCTCTGTTATCTCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATTT
WI-1795a	47	T C ---	---	---	GAAGCAACCAAGAAAGTATCTTATCCCCATCTAGATTATGTCTGGGTTC/CCTCCAGACTCCTACGGA TTAAATTGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTGCCTTGCGAGAAAGAAAGTTC GTCTACCAATTTTACCAGAAATTCGTAGTACAAATTTAAGTATCTCTGTTATCTCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATTT
WI-10616d	136	G A ---	---	---	CACACAATTTGCAAAACACTTCAAAAGTGAAGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTAGTCTGGTCTCCTATCAGATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTAACCTCTTTTGT
WI-10616c	136	G A ---	---	---	CACACAATTTGCAAAACACTTCAAAAGTGAAGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTAGTCTGGTCTCCTATCAGATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTAACCTCTTTTGT
WI-10616b	141	C T ---	---	---	CACACAATTTGCAAAACACTTCAAAAGTGAAGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTAGTCTGGTCTCCTATCAGATTGCCA CGTAGC/CJCTCCCTTCCCTTCCCTTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTAACCTCTTTTGT
WI-10616a	116	G C ---	---	---	CACACAATTTGCAAAACACTTCAAAAGTGAAGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTAGTCTGGTCTCCTATCAGATTGCCA CCAGTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTAACCTCTTTTGT
WI-1126c	52	G A ---	---	---	CTCTATTCTCTGGGCACCTGCTTCTTTGGGGCAAACTTCCAGTATCACTT/GAJATACTAATAAA AAACCTGTAACTGCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTTCOCAGCAAGAA AATTTATTCTCAAGATATAAAAAATAAATAATTAATTTCAAGTTCTCTCAAAAGGAATATGAATTT TGTTAAATGCAATCCAGCTGAACCTTTTGGACTTGTCTTTATTCCT
WI-1126b	230	T C ---	---	---	CTCTATTCTCTGGGCACCTGCTTCTTTGGGGCAAACTTCCAGTATCACTGATCACTAATAAAAA CCCTGTAACTGCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTTCOCAGCAAGAAAT TTATTTCTCAAGATATAAAAAATAAATAATTAATTTCAAGTTCTCTCAAAAGGAATATGAATTTGTT AAATGCAATCCAGCTGAACCTTTTTC/GGGACTTGTCTTTATTCCT

WI-1126a	97 T C ---	---	CTCTATTCTCGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCACTGATCTAATAATAAA CCCTGTAAAGTCTGCTTGCATTTCAAGATTC/CJCAATATATATCCAGATTTGTTTTCCACGCAAGAAA ATTTATTCTCAAGATATAAAATAAATAATTAATTTTCAGTTTCTCAAAAGGAATATGAATTT GTTAAATGCAATCCAGCTGTAACITTTTGGACTTGCTTTTATTTCT
WI-11183c	124 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAATACTTTTAAACTTGAAAATTTAGAGTAC ATATAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTC/CJACTAACA TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGATAGAGTTTTTAAATAATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---	---	TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAATACTTTTAAACTTGAAAATTTAGAGTAC ATATAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGATAGAGTTTTTAAAT/CJATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAATACTTTTAAACTTGAAAATTTAGAGTAC ATATAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGC/CJCTGTGCTACTAACA TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGATAGAGTTTTTAAATAATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---	---	GCTTGGTTTGGCTTTAGTCTATTGCTCAGTCTTGAGTTCTCCCTTCTGCCTGGCCCTTTTGATTTCA CCCATACCTCTATGCCGTGCTCAGACCAATTTCCCTCTATCTGGAGCGCTTCTCTGTACTTTCTCTG TTCCACCAACCTCTTTTATCTTCAGGACACTCA/GAJTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCCTTTCC
WI-10770a	49 G T ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCTTGGCTCATGACACTTTTCAATCTCTGCCCTGTATCATGG TTATCACTGGACA/C/JAGCCACCTCCCGCAGGCTTAGAACTCCATGAGTAAGGAGCCCTGTCTA ATGCGCGTTCTCCTTATGGTATTACACACAGTATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667b	82 C T ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCTTGGCTCATGACACTTTTCAATCTCTGCCCTGTATCATGI G/CJTATCACTGGACACAGCCACCTCCCGCAGGCTTAGAACTCCATGAGTAAGGAGCCCTGTCTA ATGCGCGTTCTCCTTATGGTATTACACACAGTATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667a	68 G C ---	---	GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

WI-10400d	189 A G ...			ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACIGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTATCTAATTTT TCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTG G G GCCATGTAG TTTTTGGTTCAITTTACTTGCNAATTTATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ...			ACATTTTATTAGCAAAATCAGCAAAATAAATAAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTATCTAATTTT TCTTCCCTTACCTTACTCTCCCAACCA A/C AAATAACGTAAGTACCTATGTCAIGCCATGTAG TTTTTGGTTCAITTTACTTGCNAATTTATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ...			ACATTTTATTAGCAAAATCAGCAAAATAAATAAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTATCTAATTTT TCTTCCCTTACCTTACTCTCCCAACCA A/C AAATAACGTAAGTACCTATGTCAIGCCATGTAG TTTTTGGTTCAITTTACTTGCNAATTTATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ...			ACATTTTATTAGCAAAATCAGCAAAATAAATAAGAAAGTA T/C TGCATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTATCTA ATTTTCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCAIGCCATGT AGTTTGGTTCAITTTACTTGCNAATTTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ...			AAAGGGCTACAACTAAGGCCAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGCCC CACCTCTCACCA C TTTAGAAAGGGCATTTCAAGCACATTCATAGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAAGGTATGGACCAAAAGTCCCAAGTATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ...			AAAGGGCTACAACTAAGGCCAAACCATGA C TGGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTACCACTTAGAAAGGGCATTTCAAGCACATTCATAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAAGGTATGGACCAAAAGTCCCAAGTATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ...			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATTGAT CATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ...			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGA A/C GACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTCTGA

WI-7038a	31	G A	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATACTAGATGCTGGGCTGTCTCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAGACTGTCAGGAAGGTCGGAGTCTGTAAACCAGATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCAITTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGGTTCTGTCTGCCACAGTGAACCAAGCACCAGGTCGGCGCTCCACACA[G/T] CCCTCAGCCCTCAGCTTGCATGTGCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCCTCCTCGGATTGGATCTAGCAAGACCAGACGAGCGGTCTAGAA TCCTGACTGTTAACAAAGCACTCCAGGCAATCTTAAGACCAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGGTTCTGTCTGCCACAGTGMCCAGCACCCAGGTCGGCGCTCCACACA[C/T]AG CCCTCAGCCCTCAGCTTGCATGTGCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCCTCCTCGGATTGGATCTAGCAAGACCAGACGAGCGGTCTAGAA TCCTGACTGTTAACAAAGCACTCCAGGCAATCTTAAGACCAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAAGTACGGTGACCT GTGAGCCCCATTCTG[A/T]GGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCTCTGGGTCTCTATGTCTAGTTTCATCAT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATTAAGAGTGAAGTACGGTGGA CCTGTAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCTCTGGGTCTCTATGTCTAGTTTCATCAT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATTAAGAGTGAAGTACGGTGGA CCTGTAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCTCTGGGTCTCTATGTCTAGTTTCATCAT
WI-6711b	226	G T	---	---	GGCTATTTGTAATGCTTGGTTATTTGACTCCAAAATTGAATAAGTATTTGGGGAAGATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAACTTCAGTTCCAACTCACTGAAT TTCATATACCTCCATTATTAATTAATCAATCATTCAGAGAAAAGACACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA
WI-6711a	361	T C	---	---	GGCTATTTGTAATGCTTGGTTATTTGACTCCAAAATTCJTGAAATAGTATTTGGGGAAGATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAACTTCAGTTCCAACTCACTGT GAATTCATATACCTCCATTATTAATTAATCAATCATTCAGAGAAAAGACACGGTGCCAACTG GGTTTGGTGGTGCCTGCACACCCACAGTGCCAACTAAGTGAATCTCTAAA

WI-10613b	172	A C	ATTGTATGCCAAATCATAATACCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTGAGCCATA TGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTT TTTGCAACTTTTGACAGGCCAGGCAATTTATTTGAC/GC/CCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTCCACTCTATAATTTTAAGTCICGGACTTAGGATGTAG
WI-10613a	44	G A	ATTGTATGCCAAATCATAATACCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAGGCCAGGCAATTTATTTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTCCACTCTATAATTTTAAGTCICGGACTTAGGATGTAG
WI-7587c	133	A T	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAAGATCTGTGCTTCCAAACAGTGACTACCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAAJ/ TJGGAATGAACCACTCCCTGCCATTCCTATAAGATATCCCAAGACCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81	G A	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAAGATCTGTGCTTCCAAACAGTGACTACCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCTATAAGATATCCCAAGACCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28	C T	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAAGATCTGTGCTTCCAAACAGTGACTACCCTTGA AGCATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCTATAAGATATCCCAAGACCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-10881b	103	T A	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCATTGACTTACGCAAACTCAATCAGCAACC ACAGAAAGCTAAAGACATCTTTTAAAGAGCCCTTAAAGACAGCCATTTTAACTTAATTCG TAGTTATGATTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGTTAGGTTCTTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGTGACGCTCTGTAAAG
WI-10681a	41	A T	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCATTGACTTACGCAAACTCAATCAGCAACC ACCACAGAAAGCTAAAGACATCTTTTAAAGAGCCCTAAAGACAGCCATTTTAACTTAATTCG TAGTTATGATTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGTTAGGTTCTTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGTGACGCTCTGTAAAG
WI-7222c	126	G T	GCCTCTCTCAACTGTCTGGACCCAGGCTAGGAAAGGGCTCTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGG/GTAAATA AGGAGGGGGAATCCCTTGAACAGAAAGAACTGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTTT

WI-7222b	255	GA	---	---	GCCTCTCCTCAACTGCTCTGGACCCAGGCTAGGAAAGGGGCTGTGAGATGACTGTGGTCCGCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGGATGGGAATAAAGG AGGGGAATTCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGGTGTATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	GT	---	---	GCCTCCTCAACTGCTCTGGACCCAGGCTAGGAAAGGGGCTGTGAGATGACTGTGGTCCGCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGGATGGG/G/TAATAA AGGAGGGGAATTCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	CA	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCAATCTCCTCCAGTTCAAAATG CTTGCACTCTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAACGCACCTAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTACATAACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGGCCCTT
WI-8054c	237	GT	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTATCTCCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAACGCACCTAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCTTCC TGTACATAACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGGCCCTT
WI-8054b	148	TC	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTATCTCCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAACGCACCTAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTACATAACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGGCCCTT
WI-8054a	131	CG	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTATCTCCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAACGCACCTAAGCCTTAGC/GJA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTACATAACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGGCCCTT
WI-10854b	152	GT	---	---	TTCCACAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAACACACGAAACGATAGTTAACGCTCTGGTAAGTTAT ACGGTGTGCGAGGCAACA/G/TTGAGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTATTTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	CT	---	---	TTCCACAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAACACAC/CTTGAAGACGATAGTTAACGCTCTGGTAAGTT TATACGGGTGTCGAGGCAACAGGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTATTTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127 G A	AATTTATATGTGAAGGTTAGCAAACTATGGCCACAGGCCCAATCTAGCCATGCCTATTTTGTG TGCTGATGGCTGTTGGTGTTCACGCGAGTTGAGCCATTGACAGAGGCTGTTATGAGCCTT CAAAGCCAAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125 A T	AATTTATATGTGAAGGTTAGCAAACTATGGCCACAGGCCCAATCTAGCCATGCCTATTTTGTG TGCTGATGGCTGTTGGTGTTCACGCGAGTTGAGCCATTGACAGAGGCTGTTATGAGCCTT AAAGCCAAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATCTAGATATTTAAA GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60 T G GTGGGTTTT	TTGTTTGTGT GAAATGT	TGACATTATAT AAACGTAAAA	CGGACACGTGTATATACAAATACAGATCGTGGTTTGTGTGGGTTTTTTTTT/GTTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29 A G AG	AACTGCAAAAT AGGAAACCAG	CCACCTGGGGC TDOC	TTCAAGTAACGTGCAAAATAGGAACACAGAG[AG]GGGAGCCCGAGTGGGACAAATCATGGCTACCC TCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCCCTTTAT
WI-8170b	259 G A	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGGTAAAGTTAG CATTTGGTGGAGAGATTTACAAGTTAAGATCATGTGTCATCAAAAGTCAATCCTATCAATCAGAA ATAAGGTAAAAGGGCCCTCAATGAATCTACGGGAAAAACATAACACAAG
WI-8170a	204 T A	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGGTAAAGTTAG CATTTGGTGGAGAGATTTACAMGGTTAAGATCATGTGTCATCAAAAGTCAATCCTATCAATCAGAA ATTAAAGGTAAAAGGGCCCTCAATGAATCTACGGGAAAAACATAACAC
WI-8172	136 C G GACA	CTTTATTAAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCACTTCCAACTACAGGTACATGTTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAAGCTTTTAAATCCTTCGGTAACCTCCCTTTTAAATGTTTCTTGACAT ATC/GIAGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA
WI-8183	56 G A TGC	TGAAATAAAA ACAATTTCTGT	TGTTGTTGAAAT CAAACCTGC	AGCAGGGTTTGAATGATCCCTTATTTTACATGAAATAAAAACAATTTCTGTTGG[G]AGCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGTCGTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83 C T	GCCTTATTGGGATTGCAAGGTTACAAAGTTAAAGACAAAAACCAAGCATGGGATTTTGC CGGAAAT ATTAGCGTTAAAGGAG[C]TTGAGTTGAGTCAAAACACGCGG
WI-8712	44 G A G	CACAGGGAAG AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG[G]AGAGATGGTCAGGCTTCTG TTCTTAAACAGCAGAGCCCGCAACCTAGAGGCGCTCACCTAGCCTCTTAAT

WI-8827	22 C T A C T A T G G	T C C C T G G G A G	G C G A T T A G G A T	GGTGCCCTGGGAGACTATGG[C]TAGTGAACACTAAATCCTAATCGCCATGCATTGGAAATTATT CCGACTATTACTTTCTTTAGTTCCTTTATCCACCCAGTCTTCT
WI-8833	51 A T A T T C T C T G	T C T C C A T G C C	C C T C A C A C A T T	CTCCGGCCTCTAAAGCTCTCTGTAGACTGTCTCTCCATGCCATTCCTG[A/T]JGCCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G ---	---	---	ATTTTATGCCATGTGGTAAAGTTCAATTTTCAGTACATGGGTAAACCCAGGCCCTTTCCCA[G/T] TATATCCAGGTATGCTACAAAGTTCTTTTAACTCTTATCAGAAGTTATTATTACTGTTCCTTAGAGAG GCTACAGGCTAAATTCACITTAGTTGGTTGTCTAATGTCTCATTAATTTATCCTGAAGCTCGTG
WI-8850	21 A G C T T T G G C C T	G G G A C T T A A C	C A A A C A G C C A	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCCTGGCTTTGGCTCTGGCTTGTCTTTTGGTTTCTT TCTCTTACTGGTCTTCTTCTTCTTGTCTTTGCCAGCCACCTAIGCTGT
WI-8853	79 C T A G G A T A	C C C G G G C A T T G	A G T C T T C C T G A	ACTTTCTTGAGCTGAGCAACCTCATCTCTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CAITGAGGATA[C/T]ATGGAAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52 A G ---	---	---	AGGGTGACTGGAAATCACAGGCACAGACTGAGGAAGACAGTCTATGGTGAACA[A/G]JACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAAA
WI-8865a	42 T C C A	C A C A G A C T G A G G A A G A C A G T	G G T A A G T C C G A A G C A T G T T G	AGGGTGACTGGAAATCACAGGCACAGACTGAGGAAGACAGTCA[T/C]JGGTGAACAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAAA
WI-8895	32 A C ---	---	---	GTGCCACAACCTGGACACCACCAACAGAAAT[A/C]CTCCCGTCTTTGAAATTTCCATTAAAGACA CAATGGGGGTAATTATACCAGGGATGCTCCATCGCTCTTTG
WI-8456	93 G C ---	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTTGTGAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATAATAACATTTCTAAGTGTCACTC TCAACTTCTGTATTCTTGCCATGGTCCAGTAACAGTTCACAGGAGACCACAAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACTCCCGTCTGGCTCTCAGTCAACCAC
WI-8496b	157 A G ---	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGAAATGGTAA[T/G]ATTGTATCAGTGCATATTTATGAAA ATTATATCTCAAGTAAGTACCTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCGAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A ---	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGAAATGGTAA[T/G]ATTGTATCAGTGCATATTTCTATGG AAATTCATATCTCAAGTAAGTACCTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCGAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G G C C A G C	G T G C A G G A A G	A A C G C A G G A G G G G A	CTGCAGGCTCTATGTGCAGGAAGGCCAGC[A/G]TCCCTCTGCCCCTGTGACCCACATCCACAGAGCA GCCCTAGTGCCAGGTGCAGCCACTGCCACCCACGSCACACGGGAACGACCCCATGCTGC

WI-12108	40	CT	ATA	TGAAAGGG TAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAGGGTTAACTCAATATCCTGAAATACTTTTCATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTTAA
WI-5989	29	GA	CACAGGCA	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCCTATGTA G3	CAGGCAACGCTCCACAAAGGTACAGGCA[G/A]CGTACATACGGTCTGTTATACCCCATATATTAC CCCTTCATGTCCTAAGAAAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAAT CTTGTTAACTTGCCTCCATCTTTCTTGGTGAGGACACC
WI-12201	61	CT	CCTGCATG	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGCTTTTAGCCTTTTCTCGAGTGTATGTCCCAAGCCCACTGATCACTGCATGCTGCGCA GGTATGGTGGGGGTGATGGACGTGGTTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	AT	TCTGACTT	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCTTATAGAGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	AG	CGCTC	TGGCTCGCTG CGCTC	AGGATCAAA GAGAAAAGGC	TTTTCGTTTGTAAATGATCCGAATGCTTGAGAGAAACCCCTGGCTCGCTGCCTC[A/G]GCCTTTT CTCTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	AG	TT	CATGCCCTTTA AGGATTAAGT AGTT	TCCTTTCTCTTT TGGTAGTGCG	AGCATGTAAGGAGCAGTTTTATTTGATGGTATATTCAGGTTTCTAACCCAGCTGAAAAATTCAAAATA CATGCCCTTTAAGGATTAAGTTTAA[G]CCACACTACCAAAAGAGAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T	CAATT	GTTGAGTATT GTTCTGCTCAT	GGGAGGCTGTG GTACATATTGG	TCTGATGTCATTTATTGGCACAATAATTATCTGATACACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCAATTAGTTGAGTATTGTTCTGCTCATAATTT[C]CCAAATAGTACCAGACCTTCCC
WI-12326	25	GA	CA	GACAGACTTC AAAAGCAATT CA	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAGCAATTACAC[G/A]CTTCCAGAATACAAAGTACTTTAATACATATTTTCAAAC CTGTTTGCATTTCAAACAAAGTTAGCGTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63	CT	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTCAGCATATGTTATTC/T TGAATAAATTTACAAAAGTGAACAGTTGGAAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	CT	ATCACCCA	CAGACACAGC ATCACCCA	GACCTCCCGT G33C	ATACTGGTTTATCCATGTCAAATGTAGTTTACAAAGGGAAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCCACGGGAGGGTCCGGGAGAGACACTTTTCCCTGGG AAAGG
WI-11321	67	AG	TTTT	GGGAGGAAAA TCCAATAAAT GTTTT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGTTTCTGGTGAATCTTTTAAAGCAGGAGGAAAAATCCAATAAATTTTTTAA A/GJAAGGTTTAGCTATTCCCAATGCTATTTAATACAAATGAGGTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40	CG	TGTGCCCA	GGATAAATCA TGTGCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACAAAATGTATCTGAAGAAGTATCTGTTCTTGICC

WI-11352a	69	T C G	AGCACAGCAG ATAGTGGAAA	GACCTCTGGTA GGACACTTAGC	TGACACATGGTTCTGTCTTTCCAGAAAGGAGAGAGAGTCACTACATAAGCAGACACATAGTGGAA AGTCGCTAGTCTACGAGAGGTACATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCAATTGCAATCACCTGTGAACCTATGAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTCAGTCGCTGCTCAGGGGGCTGGACATCCATGTTTGGGAAGAGTTGCCGGGT GATTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCATCTCT AGTCATGGTCA	CTTAAAGCATTATAGTTGGCCTGATGGTGACACAGAGACTTTCATATCTTGTCTTTTAAAGTC TCTTCAGTCGAGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGATAAGATCAGC
WI-11388	88	C A A G T T C	TGTTTGAATTT ACACGTAAC	TGCTTGTATC CAAGTTAAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTC[C/A]TATAATTTTAACTTGGATACAGGCAATGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTGT CTTGACCTTA	GTACATTCAG TGTTTGTAA	TTCTATCATCTCCATTAAATGGGCAGGTTATGTGCTTGAACCTTAAATAAATACTCGCTTTTACA AAACACGTAATGATCTTTCTTGTGAGAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACGTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTGTGTTTG AAATGGTGT	AGCTTATTTT ATATTCACCCA	AAAGAATAAGATGGCATTGTTCAGTTAATTTTGTCTTGAATGGTGTCTTATGATGGGTGAATA TGAAAATAAGCTTACCTCATCCACTCTAAAGGGTAGTTGGTATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCCACCAAC TGAGAAGCCA	TGCCAGGGCCT TATTTG	CTGTGAGCTTTTCCCAACTAAACGGTGAGTTCAGTATGTCTGGCAGCACGCTGTCTTGTCTTGGTG TATCCCACTACTGAATCCCCCAACCAAGC[C/A]CAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T T T A T T T T G C A	TGAGAAGCCA TTTATTTTGC	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTATTTTGCAGTCGCTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAATCTTCTATTTATCTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G ---	---	---	TTTTCTTTTGTGCTCTTTTCTTTTGTAGTAGAGC[A/G]GGAAACAGTTGTCAATACTACCTTCTGTGG TCCCTGTAGACAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G A G A C	GGCAGCAGG AGCAGAC	TGTACTGAGGA GCGGTG	AGGCAACACTGCTTTATAGGCGGGCAGCCAGGAGCAGAC[A/G]CACCGGCTCCTCAGTACACATT CCCCAACCCCTGCTGTGCTCTCCACTCAGGCTGGCAGGGGGCAGCGTAGGCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTGC ATATGTTTCC	ATTGGAAACAACCTTAATAATTTGCACTCTACATATAGAAAGCTGCTTTGAATACTGGGAAAAACA CTATTGCAT[A/G]GGGAAAAACATATGCAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G ---	---	---	AATGGTCTGTTTTTATTGAGAAGCTGTGGTCAATTTGATGGAAAGACACATACGGGTACAAAATTACA GGTGGTTTAGTTTCACTATG[A/G]TACAAATCATTAGAGTCTTTACAAGTCAATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAGACAC	AACTAAACCA CCTGTAATTT GTACC	AATGGTCGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATAC/TTGGTACAAAAT ACAGGTGGTTTAGTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTTGGCTATAGGTCAAGTGGTTCTAAAACTTGAGCTTGAAGAGAACACACTTTGTGGGCTT[A GTTCAAACTAGGACTGATAGGTCCACCCAGATTCTAACTGGTAGTCTGGGGTG
WI-12345	37 C A	GTGGAGGAA AAAGAGGAA	TTGCAGAGGG TTGAGG	GGACAGACCTGATCCACGTGGCAGGAAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTGCAAAA
WI-13416	71 C A A A A	AAATTTTGG AAGTTTTTCAG	AGTGTATAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTATTTCAAATTTTGGAGTTTTCAGAAAAAATAAATGACAAGAACA CATA[C/A]AAATATTGAAATTTATTCATTGAACATATAACACTTAGCAGAGGAGGACTTTTGAT
WI-12310	46 G A A A A G C	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTGGGTCT AAA	TTTGAAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAGCT[G/A]TTTAGGACCCAAACATA TTTAAACATCTCTACACATACAGAAATTCAGTTTACAAATATCCAGAAAGGCAATTTCTTAAGCAG T
WI-12086	72 C T T T G A T T T	CCGGGAAAAC TGCGATTT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATGGAGAAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAAACCTTG GATTT[C/T]CCAAGACCCGAAGACTCCTCCAAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCGCTAGCT
WI-11549	102 T G T T T A T G	GGCATAAAGT TCATAATATTC	GGAAAGTCTGT ACAAATCCCC	ATGCTTCACAGGTTGATTTTGTAAAGAGTTTGTCTATCTAAATTTTATTTATTTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG[T/G]GGGGATTTGTACAGACTTCCCTC
WI-11585	79 T C A A C A A A A	TGGGTTTGCA TCAACAAA	CCATGCTTCA TGATACTCC	TTAGAAGGAAAGAAATAAACAACCGGTAAATGGGAAATCAGTTCAGAGGTAGGAAGGAGCTGGTT TGCAAAACAAAAT[C/G]GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAGAGCAGGGGTAGAGT TT
WI-11604	68 G C ...		---	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTTT G/C]JAGAACTAGGACTTTTCCATGAAAATAATTAAGAGCTAAGGAATTCAGCGCTCACCATTTC TTTGTTACTCTGCAGTT
WI-11614c	108 C A ...		---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAATCCAGAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTCACTGTGAAACTGCAA[C/A]ATATAAGTATTCGTCAGCTAG GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTG	AGGGTGGGAA ATGCC	CAAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAATCCAGAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCAACATATAAGTATTTCGTCAGCTAG GGACTTCGT
WI-11626b	83 T C ...		---	TTGATTTTACTAAGGTTTCCACTGGAACATGAAGGTAGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAATAAA[T/C]TACTTAATAAAGAAATTAGCCATACCACATGTTCCATTGCTGCTAC AAGAACAAAATTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATAATTTTAAATAAATTACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAATGGCAATGA
WI-11627	23	T C	CCTTTCCCTCC ATTGTCCTC	CATTTGCAACC CATCTCAAG	ACCCCTTCCCTCCATTGCTCTC[T/C]CTTGAGATGGGTGCAAAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTCGCATGTCAAGTCCATCCATG
WI-11638	61	A G	GGACTTAAAA AGATCTGCTTA GTCCT	AGAACTTGGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTTGTAAGGTGGACTTAAAAAGATCTGCTTATCCCT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATAATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCAATTTCTTATGGTGGCAAAATAAGCAAACTGTGAGTAAACGAGGCGAGCTGAATAAATTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCACT[C/G]ATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C	GCCAAAAGAC TATTCAGCAA CTG	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGGCCAAAAGACTATTAGCAACTG[C/A]AACTGTCTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCTCAGAGTTCACACTCATATTTTCATATTTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A A	ATTGATTTAG AAGGAAGTGC AA	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTGAAGGAACTGCA[G/A]CTTTACTTGAGGACAAAGCCTTGCTGCAGTTGTTT AAATGTCTCTGAAACAATCAGATTCCTCCAGCCTGGAT
WI-11680	55	T C	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAGCTTTGATTCTCCCCCTTTT[C]TTGCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC CAGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACCTTTGACATCTTTATCACAGCAGGGGACAGT[C/A]AGGTTGGCTTCTCTA ATGCCACCATCTTGTTGTTTCAGAAATCTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA CAGCAG	AGAACAACTT AAGCAAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACITTTCAATAATTAAAAATCGAATAATACTAGAAATAACACAGC AG[C/T]TTTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTTCGTCAGA
WI-11706	60	C T	TGGCTGGAATT TTCTCTCTT	ATCACCAAAG AACAAATCCA	TGCTGATTCTATCGCTTCTACCATCTGGCTGGAAATTTCTCTCTTTGTACAAATTTATTGG[C/T]GGCTG GAATTTGTTCTTTGGTGATTGTCCCTTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTTCTGTTGC	TCATTCTTCT AATTTTACGGG A	AATATCATCTCATATACAGGCATGTTTATAAAAATGAGAGATTATGCTCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAAGCTTGCTTCAGTTGCTT[A/GTCCCGTAAAAATTAGAAAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C A	GGAOCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATAACCTGTCCCCAGCTTTCAGGCACACAGCCAGCCACACTCTAGACACGCCCTTCAC TCCAGTCCATTCTGGCAOCTAGCCTCAGTCTTCACT[C/A]CTCTCTCCCTCTCCACACACTCTCTC

WI-11715b	123 C T	AGCTGGCTGC AGCTT	TCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGAGGAAAGAGGCTGGCTGCAGCTTCTTAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49 A C	GCACACAATG TAAACAGAC AAA	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGAGGAAAGAGGCTGGCTGCAGCTTACGCCAC AGGATGGGACTGGGAAGA
WI-11727	43 G C	AACAATCCTT AAAACAATA TCAACA	CTGTGGTTTG TGTTGCAG	CTGGATTTCCCTATACCTAACCAATCCTTAAACAACTATCAACA[G/C]CTGCAACACAAACCACAGGC AAATGAAAACAGATGCCCCAGACAGACGCCACCACCATGGCACACAC
WI-11728	16 C G	ATCTGTGGTTT TCGGCTG	---	TTTATTATCAAACT[G/C]CAATTCCATTTCCAAATGTAAATGTAAATGCATCAGCTCCCCCATCCACTTT CTCCCATCTTATCTCTTTCCCAACCCTACACTTCTCTCCCTACAAACCGGGTCCAAA
WI-11758	61 A G	GCCTCACAAA GTAATTTCTAA AATAAA	TGATTGGCCCT GTGGTCTA	TTTTCCCTCTTTTATTAAAGTCCGCTATACTAACTAGAGGAGAAATCTGTGGTTTTCGCCCTG[G/G]TAG ACACAGGGCCCAATCAACACAGCTTCTTTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37 A G	GGCTCACAAA GTAATTTCTAA AATAAA	AAAAGTGCTCA TCTGTGAATC T	CCGGCTCACAAAAGTATTTCTAAATATAATTTGCT[G/G]TAGAGTTACAGATGAGCACTTTTCA CATTAGGTGATGCAACAAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C	GGCTCAGAGA GCAAGGGAA	AAAACTCAGA CTGTAAATTTT GTGTG	AGCACATGATATTCTGCCTGGAGTTTCTGTGAGCTCAGCAACACAGAGTCAGAGATTAAAGAATT ATTATTGCCTCTTTTTCCTCCCT[G/C]GTGATTGTAAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G	CCCAACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	CATGACAACTCTTTTATTAAATGGCTCAGAGAGCAAGGAA[G/C]GACACAAAAATTTACAGTCTGA GTTTTGGCGCAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G	TCATCTAATCT GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAA	TAATTCACCCAACTTACCAACCTCTG[G/G]GCTTAGCCTGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A	GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTCTCTCTTCTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T	GTGAGGTATTT AGTATACA	CAATTTTCAGA TTGCTATAGC AAAC	TTTACTAATTTCCCAATTCCTCCCTTTTATAGTTTTTAATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTCTA[C/T]TTGACAGCACAGTTCTTCAAAGTTTGCTATAGACAATCTGA AAATTGGGTTCTGAAC
WI-11906	52 A G	GTGAGGTATTT AGTATACA	CAATTTTCAGA TTGCTATAGC AAAC	ACATTTGAGTAGGAATGACTTTGTGTTATTAACATCAAAAGAAAGAAATCTGAAT[G/G]TGAGGGAACCTG CAGAAATTAACTTCAGICTAATCTCAGAAATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CTCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTG GGTGGTCAAGTACGCTATTCAGAAAATCTCAGAGGAGGACAAATGATAGTCACACTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCAAT/GGTT TTATTAGTATATAAAATGGCTTTACAGGAAGCAATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACTTTTGTCTGGAGACIACAGCTAGTCTAAGAAACTTCCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTCTGGGAAGAGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATTT	CAGCTGTGGTG AATGTTGAT	ACAAAATCACAAGTACAACACACTGCTTATTTTCTTGGTTGAAGATCAGATCTCTGGTTATTTAAAT/ GIATCAACATTCACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A A	TGCCCTACTAC GCTTTTAAAA TTTATT	TGAGGAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACACTGCAGAAAGGCGAGACAACAAATCCTCATAGATTTTCTGGAAATAT TGCCCTACTACGCTTTTAAAAAATTAATAAAAAATCTGTAAACACATTTCTCTTCTTACGA ATACTTCTTTTGGATATGCAATTTCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGTGAAGATCACAAAACAATTTCAACCTCTGTGGTTCAAAAATAATTAAGGATCTTTGTACCTT/ GTGTTTATTTCTGTTTCAACTAAGGAC/TJAGACTTCAGAGGCGATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTTCATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T A C	AAAAGGACAG CCAGATATCA TAAAC	TTTCCATCTTA TTTCATTTCTG TAAAC	CAACATTTATCAACATGGTAGGAAAAGTTCTCACTCTGCACATATAAAAAGGACAGCCAGATATCA ACIC/TJGTACAGAAATGAATAAGATGGAAAATTTTAAACAAATTG
WI-13654	49 A G G T	AACAGTTAAT GAAACACATC G G T	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTAA/GJGTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACTTTTCCCAATTTTACAGACAAAACAGT
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGGAGCTAGGACAATCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAAGTAA C/TJGTGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-11070a	110 G T T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGGAGCTAGGACAATCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAA GTACCGTGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTGTGAGACAGTATTTTGGGGGTGATGTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAATGAATACATGACCATTTTCTCTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142 G A ---			---	CATGGTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTTCTGGGAGGCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTAT G
WI-11076a	106 T C AGGCA	AAGGGGAGC	TCCTGCTCTGG GTATGTGAC	GGTTATTCAAA AATTAGTATGG GACA	CATGGTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTTCTGGGAGGCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTCTACATACCCAGAGCAGGAGAGAG GAGAAAGAGAGGAAGTCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTAT G
WI-14263	49 T C GGCATATCA	CGCAGAAAA GGCATATCA			ACCTTTAAAGTTTCTCCACCTACTCCCGCAGAAAAAGGCATATTCAAT/CJGTGCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGGAGCAT/CJTGAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAAGTATAAAACTCGTA
WI-14267	28 T C ---			---	GATTTGTTTATTCTATCTCGCTTTTCAATTTTGGCTTTTAAATAGAACAG[G/A]CTTTTGATTTTAGTA TATGACATCATCATGATGAATTTTCTCTTCTTACTTTGTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGATGAGTTCA
WI-13892	50 G A TAGAAC	CITTTTCATTT TGCTTTTAA TAGAAC	TGATGATGCA TATACTAAA ATCAAG		ACCTCTTTCTGATGACACTGTACCTGTAAAGGGTCTAGAGAGAAAGATAGTACTCTACTTTGCT TACAATTCAGGATGCAGGGCATGAGAGGATTCCCTCTCTC[C/G]TCCAAAGGAAAGAGCTTTTGGC AATAAATGGAAGAGGAGTGAAACAAAGTAATGAACAAACAGCCCCAGATCAGAGGAAGAGATG GCTTCTCTGTTAATTTCTGGAGCA[G/C]ATTTCAAGCAGCAATATTACTGAACACTTGTCTATGTGCTG G
WI-13951b	88 G C ---	GGAGTGAACA AAGTAATGAA CAAAA		---	AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCCGAGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTTCTGGAGCAGATTCAAGCAGCAAAATATTACTGAACACTTGTCTATGTGCTG G
WI-13951a	39 C T CAAA	AAAAAGGCTC TTGCCCAT	TTCTCTGATC TGGGGTCT	GGAGGGAGAG ACGGGAATA	GAGACCAAAAAAGGCTCTTGCCCATG[A/T]ATTTCCCGTCTCTCCCTCTGACTGACCCCGAGTTCTT ACAAATGAACATCCCTCAGCCCCCATGGCATGGTGTCTATCCCTCTCTTGGGATCTGTGAATATAOCCA ACTGTCTGTCAATGSC
WI-13264	25 G A TTGCCAT	AGCAAAAGGA AGTTAAATAC TGATAGA	CATGAAAGGA CAAAATTTGCAT C		TTAATTTGTCATTAGCAAAAGGAAGTTAAATACTAGTAGA[A/C]GATGCAAAATTTGCTCTTTCATGCA TTTGTGGAGCAAGTACTAAGTTGTTCACTGTCATTTCCCTCTCAAGGAGTTGAGCCCTAGATGAC
WI-13960	39 A C TGATAGA				AACCTCTTTATGTTTAGCTAGCCCCAGTGACTTTTATGCATCTTATACCAAGAACCTTCAAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATACACTTTTGTCTCAGGGTCCACAGGAACCCAGGCTTGGCT
WI-15843	62 C T CAG	ATCTTATAACC AAGAAGCCTT	CTCTGGCTCAG ACTTGCTCT		

WI-13983	52	G A	TCTCTCCACT CCTTAAACCT	CAATACCTCT TAGCCAGTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCT[G/A]CCCACTGGGCTAA GAGAGTATTGTACAGAATATGCACACTCACTGACTTAACAGAATTAGAACATCCAGGCACACTGAGA
WI-13850	51	A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCATN/GTTTACAAACATTGT CAGGGAACATTTACAAGATAAATAAGATGGACTTGCAGGTGTAAGAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGATTCCTGAT[G/C]TTTTCCTTTGCCAACTATTCATTATTGACCAATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAGAAAGGCCCGGAAATATAGTGAGACTCA
WI-14284	55	C T	---	---	ATTTCAAACAATCCAGAACAGGTTCTCACACITTTAGCCCTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCCTTC ACCAAATCTT	ATGACCAGACCAGAACGCCCTGTTCTATATGAAGACAAACAGGTGGCCATACTTTGGTGGAGGGATA CCGCTGCTATTCCAGAT[G/C]AAGATTGGTGGAGAGAGACCATGACAGATGACAAACGG
WI-13522	33	C T A C A C	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATACAAAC[C/T]GAGAACCACTGACTTCAAAATATTATGAGAG AAATTAATCTCCAGGGAAATTTTGCAGAGAAGATAATA
WI-13529	42	T C TTACCA	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCATTCCACAACACATTATTGAACAGTTACCA[C/T]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCCTCGAGGGGTTTATAGCTAACAGGGGAAACAACCTCTC A
WI-13859	84	G A	---	---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTCAGGAAAGGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C	---	---	TGAAAGGATACAGAAAAAATCAACGAAAGT[C/G]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCCAGCTTCCAGTTGCTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTCTCAGCA
WI-13373	52	G A	---	---	TTTATTGTTTGGTAGAAAAACAGGCTCTTAACTGAAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTGACGCCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCCAGAGCT
WI-13477b	61	A G	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAGGACATTGTTTTTTCATTAGCTGTCTTCAAAGGAGAC AGAGAAATAAGATAAATTAACCTTAAGAAAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G A G G	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTGTGGATAAAGGAGGAGATGTTTTTTCATTAGCTGTCTTCAAAGGAGAC AGAGAAATAAGATAAATTAACCTTAAGAAAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACTTTATTTAGCATGCAATGCAATTTATTCTGGCAATAAATAATATATGTGCAGTTATAAAAAT GTTGGGTACTTTTTTCCAAG[AT]AAAAATGTTTCTGAAATGTGCACACTAGAAATATATGCAGAAATCCTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTACCATTAAGAAATCAACA TGTGCACAAAAGAGTAAAAATTTGACCACAAAATTAAGATTTTTTGGGACAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGGCGAGTT AGATTCCA	AAGGTCGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[CA]TGGAAATCTAAGTGCAGAG AATCAAGACCGATGGTGTGAAATCTGGGCGAGCTTCAAAAATTTCTGCCTCCTTAAAAACATTTTAC CCAATTTTTCATTATTGCC
WI-13857	28 A G	TCTGAGTTGATAAAATGCTTTTCTGAAC[AG]TACATTTTAGGTATCTGGCACAATTAACCAAATGT CTGCCCAATTTTGTGTAGCTTTTCATACAGTACAGATTTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[GT]TTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T	TAAATCAGTCTGTGTCAAGAAAGAACAGGACTTGATCAAGTTCAGCCCTCACCACTCTATCAGCA TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTTGCTTAAACCAAGAGAGGA[AT]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCTTTTATCCAAAGATGGGAAGCGGATTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACTTA GCTGCAGTAACTATG/GGCATCCCATCCACTCTTCTCTCTTTTTTGACTGAAACTCTTCAAGAACT GCTGAATGTCTCTCTC
WI-15801a	24 G A	TTTATCCAAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCTTTTATCCAAAGATGGGAAGC[GA]CATTTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAACTAGCATCCCATCCACTCTTCTCTCTTTTTTGACTGAAACTCTTCAAGAACT GCTGAATGTCTCTCTC
WI-13763	59 T C	GGCTGGACACT GCAGTGAT	CCACACCTGC OCT	GCTCGTAATGAGACAGAACGCTACAATCTGTCAACACTGGGCTGGACACTGCAGTGATT/CJAGGG GCAGGTGTGGGCGAGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA TTTTTTTTTGGTGAGTTGTCTTCAATAAGAGCAGAGAAAGAACCTT/AJAGACAAAAGATGTT CTTACACACTGAGCTTTACACAGTACCCAAACATTGATATTTTGTCTTTTCCCGAGGGCAAAAAGA GAGTCTTCCAGAAACCTC
WI-13578	48 T A ACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TCCAAGGAAAAGAAAGAAACCAATCAGTGAGAAAACCTCAAGAAATGGATGGCTGAGGGAG[GA] GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCACTCTCTT GAGTDOCT
WI-13789	62 G A	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	AATAACAAGTTTAAGTTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACAGATCACA AAAAGC GA/TGCACAAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCCTTGGGCA GTACTTTTT	

WI-15625	40	C T	GTTCCTCCACCTACTCCGCGAGAAAAAGGCATATTCAAC[CT]GTGCCCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84	C G A	CCACACTGAA GACTACCAG	TCCCACCCCA CCT	GTCTACATTTCTGTAGGCTGTAATTTTCAGTTTACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCCAGAAC[CT]GAGGGTGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCT
WI-13600	26	G T	TTAATGAGCC AAGCATCCAT	TTGTTACTAGA TGATGG	CTCACATTTAATGAGCCCAAGCATCCAT[CT]CCATCATCTAGTAGCAAAATTTCAATATGCACATTATAT TATACGTGAAACAAAGAAATACGGATTGTAGGGGAAGAGCATAGAGGACCACCACATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89	G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAGAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGGAATAGACAGCCC CTTTCCATTTCTGGAGACAACACA[CT]AAATCTATTAAATAATTGTCATGAGGTATGCACCT GCCCC
WI-13650	76	A T	AAAGATTAC AATATTTCACT	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTTAAAAATTTCTGAGGGATATTGATGAGAACATGATGAAAGATTCACAATATTTTCAG TTTTAAAC[AT]TAAAAACTACTCTTCATATCCTAGCTGATGACTTAAAGTTACCCGG
WI-14319	83	C T A	CAATCAAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTCAAGATAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAG[CT]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAATT
WI-13528	80	A G AAAA	CAATACATTT GCATTTTCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAACTAATCAATACATTTGCAATTTCTTAAAA AAAGAAGACATTT[AG]TTTCAGAGAAACTGTTGTTATCATGCAGGAAAAGCAGAAAAAATTT
WI-13909c	93	A T	ACTTAAACTGGCTTATCTTCACGGTAACTATCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACTC[G/A]AATATCTTTTCAGAGATGTTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C A	TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTTAAACAAATTTAAAAAGGGACAGAAAAATTAAG AATCAACATCATCTCGGAC[CT]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78	T C	ACAGAAAAAT TAAGAAATCAA	GCCTTTCAAG GTTCCAT	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTTAAACAAATTTAAAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTCGGACCATGGAACTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104	G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACTT	AAAATTGACAAATCAACTAGTGTCTTTTGTGTTTGGAGACTACCATTTATTCAAAATTTATTTATGT AATACACTCATCCAGATAATGAAACATCTCGGAAA[CT]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33	G A T C	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTCTG[A/J]TTTGGAAAGACTACCATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTCGGAAAGAAAGTGTGGGAATCACCTCATCTGTGC TGTAATCTGCTTACAGTCTTTGCAAAGACACATATGTTTTGCATAAAGATATAAATGGCTTCAT TTTAAACTAATTTAGTGT[T/C]TTTAAATTATGAACCTTTTGGTGAATTATGAAGTGTACCAAAC
WI-15747	88	T C A G I G I T	TGCTTCATTTT AACTAATTT AGAGIT	CATAATTCACC AAAAGTTCATA TAATTT	C AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATACCTGGCTTGCAC[C/J]GGACACCTTTTACG GAGGATTCGGGACAACT
WI-13752b	117	C T	AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATACCTGGCTTGCAC[C/J]GGACACCTTTTACG GAGGATTCGGGACAACT
WI-13752a	106	T C A G T G T G G A	CCTTCTCGTTA AGTGTGC	CCCTCCGTAAA AGGTGTCC	AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATAC[C/J]GGCTTGCACCGGACACCTTTTACG GAGGATTCGGGACAACT
WI-14339	102	T G T T A C	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGTAGATTAAC[T/G]GGTTTCCAGAAATCTGGATAC
WI-13744	115	C T A A A C T G A A	TGGTGTGAAC GATAAGCACA GC	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAACACACGTAATGGAATTCATGCAGCTTTAGAT TTCCCTTGGCCAGCTAGGAGCTTGTGTATGGTGTGCTGAACAAACTGA[C/J]GCTGTGCTTATCTTTC CTGATCT
WI-14061	68	C T	CCCTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT [C/J]AACCAATTTCACTCCACCAATTTGTAAAAATCTCATCTTCTGGGTCTGGATACCTCAAAAAACAGAT
WI-15719	69	A C A T T C A G C	ACCTTTTCATC CAATTCAGC	TGACTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAAACACTACCACACTGAATATACTGAATTAACCTTTCAACCCCTTTCATCCATTCAG C[A/C]AATTTAAAACTCTTGCCAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T C A A C T T	CTCTAAATCG ATACATCCAA	GAAGTGTGCT TGCTGCTAAT	TAATCCATCAATCTAAATCACACATACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTTGA GGTATTAAATGGTCTCTAAATCGATACATCCAAAACTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G T C A C A	ATTTTATTCAC ATTAAACTTG	GTCTTTTGATA TGTCGCTTAGT TTT	GGATTTTATTCACATTAACCTTGACA[G/J]TAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAAATATACATAGAGATTGAAATTTCTCAATAGCATTTGAAAGGTATTTCCATAAATA TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACACAGTG
WI-13785d	72	G A	TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGAC[A/C]CAATG AACAGTGGTAGTGACACATAGCTGTCAACACAGTG
WI-13785c	56	A C	

WI-13785b	40 C G	TCAAACGTCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTGCAGTAGTGACACATAGCTGTCTACAAACACAGTG
WI-13785a	27 T C TGCCT	AAACTGCAC ACTATAAAAG	TGTTGTGACAG CTATGTGTCAC T	TCAAACGTCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACACAAATG AACAAAGTGCAGTAGTGACACATAGCTGTCTACAAACACAGTG
WI-13793	88 C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCAATAAAATAGTTTTACCCCATTTGATACACATAAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAATACTCTGCCCCATAAATCTATGACTTG
WI-13794	52 A G TTTCTTCTC	TTCTCAGCCT TTTCTTCTC	AGAAATGGGCTC TTAACCTTGTA	TAGTCTCTACAAATCTCTCAATCCATTTTCTCTCCTCACCCCTTTCTTCTC[C/G]TACAAGGTTAAGA GCCCATCTCTCAACAACAACAAAACAACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[A/G]GGCAGCTTTAGAAAAGAGCTGAGACTGAA AAGTCTGCTTGTGACTTCCAAAGGAAGGTAAGTCCCTGTTTGAGCCCCGGGCTGCTCATTTGTTA
WI-13424	66 G A C	TGAGGTTTTTC ACCTATTCTT	TTTTCTCCCC AGGGTCTA	GTCTTTGCACAAAGTCTCCCACTGGTTGGAGTTTCCCTTCTGAGGTTTTTACCCCTATTTCTT[C/G/A] TTAGACCTGGGAGAAAACAACATGTGTAAGTGGCTCAGGACATGAGGCAGGCCGTTTCACAAGAT GCTGGCTAAGGGCTTC
WI-14065	29 T C AATT	TCATTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAGGTCAGAGGCAATTT[C/J]GAGATCCCAGATTGAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTTAACTCTGAACATTTTGAAGCAGGAA
WI-13446	22 G C TCACTCATCA	GCCATGTTCTT TCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACTCATCA[C/G]CCTTCTGATTTTGAATCCCTTTCTGCTCTGTAAATTTTCTTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCTTAAT
WI-13725	56 A C TGGGTGCC	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGAAATGTCACTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCCGAG ACAGCAGGATAAGTTTCACAAAACTTGACCAGGAGTTAGAACCAAGGCATGGTTCAAGGATG
WI-15702d	107 T C	CAATGTTTTATGAAGAGACTCCGAACAATAAAGGCCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACCAATACTAA[C/T]C[GGGTTCTTTGAACAATAAGTTTT TGA
WI-15702c	101 T C	CAAATGTTTTATGAAGAGACTCCGAACAATAAAGGCCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACCAATACTAA[C/T]CTGTAAACAATACTAAATGGGTTCTTTGAACAATAAGTTTT TGA
WI-15702b	90 C T	CAAATGTTTTATGAAGAGACTCCGAACAATAAAGGCCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/T]CTGTAAACAATACTAAATGGGTTCTTTGAACAATAAGTTTT TGA

48	G C A A G	A A C A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A A T G T T T A T G A A G A G A C T C G G A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G G T A A A G G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T G G G T T C T T T G A A C A A A T A G T T T T T G A
113	T C			T T T T T T T T T A T G G A T G C A C T G T T A C A T G T T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G A T C C T C G G G T A G T T T T C C T T C T C T G T A G A T [G/C] G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
56	G C			T T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G A T C C T C G G G T A A G T T T C C T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
62	G A			T G A T T G A G C T T A G A A A G G A A G T C A T G T T G A A A T C A G A G A G G C C A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
86	A G			C A C A T T T T C A G C A A A C A A A T C G A G G T G C A A A C A G G G T T A T T T C A C A T T A A T A T A A C T G G A T T T T T T G T C A A A T A A T A G G G A [A/G] T T C T C T T A A T A A C C A T C T C C T A C T T C A T G G C C A G T
95	A G			A G G C T G T T T T T G A G G C C T G A G G A C C C C A C A C A T G A C A C G T A A G A C T G T A A C C A T G T C A T G T G A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A T C A T C T C C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
61	C T	A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
47	C T	A G A C T T G A G A G C T T A A A A C A	G C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
31	A G	A A T A A A A C T T C C T A T T T C T T	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T T C A T G T A A G A A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A C A G A A C A G G A G G C C T T T
121	G C	A A T A A A A C T T C C T A T T T C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T C T A A A T T T T C A C C T T A T T G C T A A G T T A T A A A A T A A A A C T T C C T A T T T C T T T G C T T [G/C] J T T T T T C T T T C A C C T C A G A A C C C C C T T A
50	A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G A G A A T G A A G G A G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T A T T T G A C G A C T A C A G C T C C T C T C T T T T G T A C T A C G A G A C C C T G C T T A T A G C C C C A C A G A A A T C C T C A T C T G C G G T T G C C A G A C A G

79	102	C T	CACC	TCATTAACA GGTTATGTCA	ATCATCTGTT TGAGGTTGACA	TTATGCTGTTGTTTCTACTGGTGGTGGCTCACTAATATCCAATCCTAGTATGATTTCTTT TACTTGCTCTATTACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[A/C]CCACCATTAAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTGCCGCGAGGCTGGCGAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
02	22	C A	...	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGTTGT	ACCGCAGAGCTGCTGTATTTAAA[A/G]ACAAGCGTCTGGATCTCTGCAGGGGCTGGACCAGCTGC AGTGGGGCTCCGGCAGCTGCTCTCCAGGACTCTTCCCACCACCCC
37	24	A G A	AACTGAAAC GTATTCCTCC	AACTGAAAC GTATTCCTCC	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTATTTCTCTCCA[A/C]ACACGTAGAACTTTAAAGCCGCAAAAGACTCACACCC ACCACCTAGCGGCGAAAAAGGAAGTTTCAGGTGATACAAAGATGCTCTGCCATCACACCTGAAGGAT GGT
144	24	A C A	ATGTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
24	92	A G	...	GGTTGACCTG CATAGATTTT	GGATGGCATG GOCAC	GACAAAGAGGCGAGTTTCTGTAGTTCACAGGGCCAGAGAGTTATCAGAACGGTGGTTGACCT GCATAGATTTTGGACGACTA[C/T]GTGGCCATGCCATTCTCTGAAGTGAATTAATGAACA
25	88	C T	GCCTTCTACC ATGCTTTCACA	GCCTTCTACC ATGCTTTCACA	CTTGTTCTGTC TCITTTGGGC	GTTATTTCTCACAGTCTGGAGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTACAGCTGGCTGCTTTCTCACCATGCTCTCACAT[G/A]GCCCAAAGAGAC AGAACAAAGCTCTCTGGT
36	120	G A	TGTTGGCAOCC GAAAAGCT	TGTTGGCAOCC GAAAAGCT	CAGTATGTACA GTGACATAACA	TTGTTGTTGGCACCAAGAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATCTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTGTTTCAATG
138	23	C T	TCCTTCAGTAG TAGTATATTCA	TCCTTCAGTAG TAGTATATTCA	GCTCATTTCTT TTAGTGTAAAG	GGCAGGTTTATTCATAATTTCAAACTTGGAGCAACCAAGATGCTCTCAGTAGTATATTCA GACAATC[G/A]AATAATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTAAATGGATAATTACT
151	74	G A	GACAATC	GACAATC	TAATATT	TTTTTAAGAGTGCTTCACATCATTTATATTGATTGCACACAAAACCTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA OCTCOC
b	59	C T	TTTTTAAGAGTGCTTCACATCATTTATATTGATTGCACACAAAACCTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA OCTCOC
a	26	T G A T	A	TTTAAAGAGTG TCCCTCACATC	TCATCTGTTCT TGTTGTTTTTG	TTTTTAAGAGTGCTTCACATCATTTATATTGATTGCACACAAAACCTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA OCTCOC

31	82	G A	---	---	TGATTCATGGACAGTTTGGCTCTGTTTGTAGTGAACCCCTCACAAAGCACTCTGCATAGTCGGCTTTCTGCTCTTTAAAC[G]A/GTGCCTGGTTCCCTCTGCCAAACITTTAGGATTGGGCTCCTCAGGGGCTTGTCTGA
34	24	A G	---	---	ATCACACCGTGTCTAAGAACAAC[A]G/TCTTCATGTCCAACTCATATCCCGGGACTTTGTCAACTGCAGTACACTTCTGCTTGAACCTGGCTTCTGGAGGGAAAGCCTCTAGAGGCCAGGTAAGGGGGTGCAGCAGTGGGGGTATATCTGGCTGGCCAGTTGGAACACAGGAG
34	99	T A	CTGGAGGTA	GACTTCTCCAC CCTCTTGC	CAGAAACCTCTTCTGTGTTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT/A/GCAAGAGGGTGGAGAAGICTTGGCAAG
75	103	G A	GGCAC	CCCTTCTTTC TCTTCCCTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAATACCCATCAGAGACAGTGACAAGAGCAGCTGGGGCACGGGGGAGGCG[G]A/GAAGGAAGAGAAAGAGGGGAGGAGCCT
79	96	G A	TGGAGGTCA	TCGAATGACCC TGTAGATGC	TAATTTAAAAACACGCCCTTCCCACATAGTGGGAGGCACTGCACATTTTCTTAGAAGGACATGAATAGTGATGGAGGTACGGTGGAGGTCA[G]A/GCATCTACAGGGTCACTCGAGGAGGAACAG
31	49	C G	ATTGT	CTTATT	CACAAATAGTGAAATTATCTGAGCAAGAATCATCTCTCAATTTAAATTTGTC/GJAAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
36	105	T A	---	---	AATGGGACTTTCAACAAGGGTTTAAACTAATCTAATAACAATCTTACAACACATTCACAGAGCATATAACAAGAATTATTTACAGGCAGCTAATGATTAAT/A/AACCATGAAAAAGAAAAAATTG
73	31	CT	---	---	ATCTAGATGTCAGCAAAATGGGCTGAGACTGTC/TGTGTCTGTAGATGACAGTGTGTATGTTCTAC
37	103	A C	AAATAAAAA	TG	TTCTATTACAAAAATTAAACAGAAATATGGCTTCGCTTTGTGCAAAATGTTTATATACAGTCAATTTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAAAGATAAAATATGTCATTCAGCAGTCAITTTAAAAATAAAAGACTACAGATACAAGGAAATAAAAA[A/C]CACITTTAGGAGATGAAAAACACAAA
38	60	T A	G	TTACTTT	TTAATAATTTACGACAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AAAGTAAACAATGAGTTTACACAATTAATAATATTAAACACATACTTATGGGATTTGTTGAATGA
33	47	C G	---	---	TTTTGTGTTAAGAACAGCATTTTGAAAAATAAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTTAAATTTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
63	CT	CGTCT		CAC	TTAGAAAACTGATAAAAGCAACAACACTTTTGGGAAAGCACCATTGGCAGTCCTTTTGTGCTA[C/T]GTGATAAGTGTCTTATCTCAATGAAGCAACCCCA
15	22	G A	---	---	ACATGGCAGATACAGCTGTC[G]A/TCTTGAAGACCACCCTGACCAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTTTCCCTGACCGTCTGGAGCGTTGAAGGTGACCAGCACATTTGCACATGCAAAA

102	59 T C	GATAACATAA ATGATCATG AGAAATTC	GCCATCTCTC TTTGACTTTT	CCAAACATTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA/T/CIGTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
3	101 A G A	CCCACITGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCCTA AAA	GTGGAAATTTATTAGCCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTTGAACCTCAAGTCATCA/GJTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTTAACCA
159	73 T C	GC GTT T G A C T T G G G G	TCCACACTGC O O O C	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATGGTTTTATTCAAACTCCTAGCGTTGACTT GTGGGGT/CJGTACTCAAAATGGGGGCAGTGTGGACGGGAGGATTGCAACAGAGTTTCATACTG CAA
335	50 A T T A T	CTAGGAGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTCAGGTGGTACTAGGAGGTTGAGGTGTAGATAT/A/TCTTCCCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTTTATCAGCTGAGAAAGGCGAGTCTCGCCATC TTAAAGACCTGCCCCC
a	112 G A	AAAGGCACAC GGGGAA	CTCAGCCTGOC TTGACC	TTCCATTCAATTATGCTTGGCTTTACCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGTTCAGAAAAAGGCACACGGGAA[G/A]GGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
340	18 T C	---	---	ACACAATATAATTCOATTT/CJCGAGTGATTAAACCTATTGTTGTTTGAACCAACAAAACTAC AAGAAAAACATTTTCAAAOCTTTTTTTTCAGGCTGA
308	52 T A	ACCCACCACA CTACCCGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACCTTTAAGCAACAGTTAAAAAGTACCCACACACTACCCTGTT/AJAAAACTTTAAC ATTGTGATGCCTCTGCATCAATTTTTAGAAAAACAAAGAAAAACACAACCTGAAGGCCCATGTA
816	29 A T	---	---	AGTTAAAAAAATCGAGTCAGCATTTTAT/AJAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
'c	71 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/TJTAGGTGATTGATACAAATACGATCCATAA
'b	70 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/TJTAGGTGATTGATACAAATACGATCCATAA
a	45 C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
173	57 C T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAAACTGGGGATACAGCAGTAAAGAATACAAAAAATCCTGC/CJCTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

836	28 T C ---			TCCTTGGAGGGATAGAGACAGAGTGTTCGTTGATTTTCGTTTCGGTTTCAGTTTGGTTGTCATTTGGTTTGTCTAATTTTGCCCCACCCTATAAAAGCAGTGCACCCAGAGGCAG
856	60 A T A A	GGTGACACG GAAATACCTT	TTTGTTTGCTA CTTTTACAAA CTTT	ACATTTCCCTTATGATAGCAACAACCTAAATATGATGGATGGTGACACGGAAATACTTAAATATTTAAAGTTGTAAAGTAGCAACAATAATTTGAGTATATACTATAAGTATAGGATGATATGAAAAAGGTATAAAAAGCTCCAAA
863	61 G A ---			ATGGCAATTTACTTTATAGCAATGAACAATATTTGTCAAAGGGCAATATTTTGTCTG(G/A)AGTTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACTACCTGGC
867	46 T C A	GACATCCAA GGCTCTTAAC	TGGGGCTGCAG ACACTC	TTTTTAATTAACGTAAAAAGGAGGACATTCOAAGGCTCTCTAACAATTCGAGTGTCTGCAGCCCCATTCGGCTTGAGATGTAATGTGTAAACCCAGGGTGA
733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTGAG GCCATTATTT	ACGGAGTCGTCTCTGATGATTCTTTGTCAAAAAATGTTTGCCTGATTCTTAATCATGAAAGAACAATAGAAAAAATCCAAATTGACAGATATCTGCA(G/A)AATAAATGGCCTGACCTCATCAAAAAACATCATGTCATGAAAAACACAAAA
ib	79 A C ---			TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT(C)JAGGTGCCACTAAGGAACTTTCTCCAT(C)AAGCTGCCTGTCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTGCTGCTGTGTTCTGTCTT
a	50 A C C A	CATGTACAGG AAGAGTTGTCT	AAGTTTTCCTT AGTGGCACCT	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT(C)JAGGTGCCACTAAGGAACTTTCTCCATAAAGCTGCCTGTCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTGCTATGCTGTGTTCTGTCTT
907	48 G A G G A C T C T G A C	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGIATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC(G/A)ATTCCCTTGGCAGCAGACATTTGTGAAGCTGCTGTGGGCACACCCATCAATCAGTACTCTGCACTGCAGAGGGGCCACATGCACGATGCTCACGTGTG
911	52 G A C	CCAATACATT CAGTTCCTGGT	CAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAAGCTCAGTGCACCAATACATTCAGTTCTCTGGT(G/A)AAGGTCCCTTTTCCTGGTTTGACAGACATACCTTGCTGTATCCTCACATGGCAGAGAAAGAGGAATATCT
913	88 C A ---			CTGATGCTTTGACATCTGGGGCATTTGCTGTCTTAGAGAGACTACTTCTCTGGGACCAGCCAAATTCCTAGTAGTAGGAGGACTCA(C)CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAACCTACACCTCCAACCACT
914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCCTTGATTGGCTGCTGTAAGCCTGTGAAGTCATGCACATCTGGACAGATTTTCTCTAGCA(G/C)GAATTTATTTGCTGGGCTTGATGGCTTTTCACAGC
926	49 T C ---			GTTTATTTTCAAAATGACACATCCCGAGTTGAAATGGGCACCTTAGCGAA(T/C)JACTTGTGGACCACAGACACTGTCTGAGAACATGTTCAAGACAGTTTTCAAATAAAAAATTTTCCTTAATCAGGTCCA

33	89	C T	AAGGAT	ATGTTTAAACA CAACATATC	TGGAAGAAGATT CCAGGOC	GCATCTTTATTACACAGAACTCATTTATGTCTTAATCATTTAATATATAATATAAGCATGTT TAACACAAACATATCAAGGATCTGGGCTGGAATCTTTTCCATCTATAGAAAGCACTAACCATC CATTAAGCAG
30	55	C T	CTCATGGAT	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCTTTCCACAGGAGGAGTCCCTCATGGATCTGGCGGTATTG GTTGGTTGGTGATTTGGGAGCAACGAGGAGAGCAAA
16	47	T C	---	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTGGCCCCAGACATAACAATCTCTCTAAATCATCTCTA GATCAGGGAGTCTAAGGACCATTAAGGCTCATTAACACAGTACTTTATGGAAGGATT
1	80	A G	---	---	---	ACATTAAACAGCAACAATTAAGGGTCCCAACGAGGTTGGTAGTGCCCTCCACTATGTGAGGACAC TAAGAAGATGGTCTAGTCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
1	32	C T	GGGTCCTAA	CACAATTAA GGGTCCTAA	GGAAGGCACATA CCAACCTC	ACATTAAACAGCACAATTAAAGGGTCCCAATCTGGAGGTTGGTAGTGCCCTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
48	56	T C	G	AGGGAACCTG CTAACTTGTC	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTTATTGCCGTTCTTCAGGGAACAGGGAACAGTAACTTGTAGTCTCTCAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGCTGTTCCCTCCAGCTGA
00	52	A G	TGA	CAAAAAGCTA TTTTCTACAC	ACAGGAATGTC AGAAAACAGT ATAATAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTTCTACACTTGACATGTAATATACTG TTTTCTGACATCTCTGTTATCAACTCTCTGAAAATC
58	83	A G	CAAGG	AATAATTTAT CTCTTCTTTT	AATGCATTCT TTGGGTTTT	GTGATTGATCTGTAATTATTGGATTATTTATCAACTCTAAATTCGAAGTAAATTAATTTATCT CTTCTTTCAAGGGTGAAGAAACCAATGAATGCAATTTTCTCAGTTTCTCCAGGCTTTGAAGTGC AGCAGAAAATTCAGGA
176	35	C T	TCGTTCAAAG	GTTGATTTGCT TCGTTCAAAG	TCAAACATAAAT CTTCCATTCTA AGC	TATTTTAAATTTGTTGATTGCTTCGTTCAAAGCTGGCTTAGAATGGAAGATTAGTTTGGAGAG GGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAGAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
181	31	G T	T	TCAGTGGTGT TATTGGAATTT	CACCTCTGACA TAATACCTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTCTTGGCTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTCACAGGAAGTTTTTGA GAGTCAACAAA
192	80	C T	GAAGCTGCAG	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCT	TGATTACATTTTAAATATGCTACAGCCCATCTAAGCCAAATTCAAACACCACTCTGCATT AATGAAGCTGCAGCTAGGAAAGCTGAGCACAATAGCACCCCACTGATCGGAAAGAAACGTA
102	72	T A	---	---	---	AAATCTCTCTTTCACACACAGATGAACCTTTAATAAATACAAATGCACCTGAAAATGCTCTCTGA TTTCCCTTATTCAGTTTAGGCTCAATGGGCTCTCTCCTCAAGGCTGGACCTCAAGGCCAGTT
100	90	G A	GTCTAA	GACAGAAAA GACTCAGACT	GTTCTAGTTC TGCACAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGATTGAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTATGATGAAGTTTGTGCAGAACTAGAAACAAAATCCACCT

23	68	G A	C A C A A T A C T T C A T G T A C C T A T T T C C T A C C T G	C A C T G G A C A T A T T C C T A C C T G	A T T T G T G A T G T T G G T T A A T C T T A T C T C T T T T T T A T A C A C A A T A C T T C A T G T A C C T A T G A A A T A A G A J A C A G G T A G G G A A T A T G T C C A G T G C A A C A C A G A G G A C T C A C A C C T G T G C A T A G A C A G C A C C
33	91	A T	A A G G G A C G A T T T A G T A T C T A A G T G T T T T	G G C A T G T C C A G T G T T T T	C A T A A G T T G C A T T A T T C A C G T C C A C G C A T C T A A G C T A C T A A G C T A C T G T G T A C A G T A T C A G G A C T G G A G A A G G G A C G A T T A G T A T C T A A A A C A A J A T C A A A A A A A C A C T G G G A C A T G C C C C C T G A A T T G C A A G T T G G A G T T C G T A A G A A T C T A C
70	100	C A T	C C T G C C T T T A T A T T G G A A T T T C G G T C T C T	G G G A G A C C A T G G G T C T C T	A T T T G T G T T T A T T A G C A C C T G A A T T A G G C A A G A G A A C A T T T C A C T G A A G A C T C C A T G C A G T C A A A T T C C C T G C C T T A T A T G G A A T T C T A C J A G A G A C C C A T G T C T C C C C A A G T G A G G A A G C C A G G C A C T C A G C C C T T C
2	38	T A C A	T G A A T G C T T C C A A G T A C A A A T T T G T G A	T G A A A G T A T G T T G T A T A T G G T A T T G T G A	T T T G G T G C T A C T T T G T G A A T G C T T C C A A G T A C A A A T C A J A C T C A C A A T A C C A T A T A C A A C A T C A C A T T G C T T C A A T C A C A A C T C A A A T A T A A A A T A A C C T A C A A A A T C A C A T T G C
2	40	A C T C T A T T G	T T T A C T T T G T T G T C A T T T T T A T T A T	C C A T A A G G T C T C A C A C T T T T C T T A T	T G G G A T A C C C T T T A C T T T G T G T C A T T T T T A T T C T A T T G J A C J A T T A T A A G A A A A G T G T G A G A C C T T A T G G C T T C T G C T T A T G G G C A A T A T G C A A T A T A T A T T G T G T T T A A A A T T A T A T G C A T
33	35	C T A A	T C T G T G A T G C A A T T G A A A T A A A	G C T G C C A A T T A C A T T A A C T T A C A A	T C T A A G A T T T A C T C T G T G A T G C A A T T G A A A T A A C J A T T G T A A G T T A A T G T A A T T G G C A G C A T T G C C C A A A G T T A A G A G G A C T A T T C T T T A A C A A A G A C A G T G C T G A C A T T A T T T C A G G T
33	88	T A T C	A A T G C A C A A A A T C T T G T C T C T A G C A	T C A G A T T T T T A C A T C T C T T T C T A G C A	T T T T T T A T T T G C A T T G A G T G C T T A T T A T A T T G G G A A T T G C A G T G A T T A A C A T T T G T A C A A A T G C A C A A A A T C T T G T C T C T C T C J A J T G C T A G A A G A G A T G T A A A A A T C T G A C C T A G T T G A A C A G C T T A A T G A A C T C A T T G T C C A T
7	58	T C G A T T T T	C G C A C T C T A A A T T A G A G A T A A A T A A G A T G	T G C T G T G G T G A A T A A G A T G	C G G A T A T A A T T A T G T A C C G C A C T C T A A A T T A G A G A T A G A T T T T T T C T G A T A T A C A T T T C J C A T C T T A T T C A C C A C G A C A C A C C A C A C G C A C A G T A G A A C A G T T C C A C A C T G A T A A A T T G C A C A A G A T G
2	17	G A	G C A G A A C C A A T T A A T A A G J A A T C T G C A A G T T T C C C C A A G A A A C T C T G G A A C C A T A G T G C C T A A T G C C C T T T A A A A T C G A T A C T A A A G G A G A G A G A A T A A A A G G A C T G C T T G A T G T G A C A G T C A C T G G T
9	81	T C	T G T A G T C T T C A A A A G A C A T G T T G G C A G A T A G C C A G G C C A C T A C T A T G T G T A T T C C C A G T A T A T G T A C G C A C T A A A A A A A J C J G T G T G C T T G C T G C T G T G A G T G A A C C A T T G C T T A A G A T A A A
6	97	A C C C A G A T C G C	T G A A G A T T A A C C C A G A G T C G C	A A T T G T G T G C A T T T T G A A G A G A	A T C T G G T A T T T G T G T A T C C C A C A A G T A T A C A G A A T A C A G A A T A C T C T A T A A A C C A A C C C A C C C T T C A A T A T T A C A C T A A T G A A G A T T A A C C C A G A T C G C J A C J T C T C T T C A A A A T G C A C A C A A T T A A G A C G
2	59	G T A T G T	G C A G C A A G A T T A C A T C A G T A T A A G G T	C T C C A A A T A G C C T A G A G T A T A G T A A G G T	C A T G G C A G C A A G A T T A C A T C A G T A A T G T A A T A T A A T A C A G C T T T T T C A T T G A A G C T T T J G J T A C C T T A C T A T A C T A G G C T A T T G G A G T G T C C C C A C

100	74	G A ---			TCATTACAGCCAGAAATAACCCAAATTAATTCCTAAATAAGCAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GTTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT GCATTTCTAGTGGACTTTAT
192	92	A T AATTACT	CCCTTATTTTC CCAAATATAA TAAGAC	GTCAACATGTT ATATTTTCTTT TAAGAC	TGGTACAGAAATGTTTAATTACAGAGGGCAGTGATTCAGTTAAATAAAATTAATAAAACCTTTATTTT CCCAATATAAAATTAATAATTA[A/T]GTCTTAAAGAAAAATATAACATGGTGACAGCTTT TCCTTAATTTTATCGGAATCCAGGACACAAACAGAAAAACACCCAAAAACCATGGAGACAGAAG ACGAGACAAACTCTCCCCCACT[C/G]CCTCCCTGCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AG
199	89	T C ---			TCCTTAATTTTATCGGAATCCAGGACACAAACAGAAAAACCCAAAAACCATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCCACTGCCTCCCTGCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AG
206	68	G A ---	TCGGAATCCA GGACACAA	TGGTTTGGG TGTTTTCTT	TCCTTAATTTTATCGGAATCCAGGACACAA[C/G]AAGAAAAACACCCAAAAACCATGGAGACAG AAGACGAGACACAACCTCTCCCCCACTGCCTCCCTGCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AG
230	30	C G		CCTGAATATGC AATTATTTATT ATGACA	TTTTCAATTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACCTACATATAGAATTAACCTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTATATAATAATAATTCATATTCAGGATTTTG TGAAATAGGTGATTGGGA
256	96	C T	GGGAGCCCTA GTTGCAGTAA		GCAAAAGCAAGCTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTGGTGGTGGCTGATACCTGGT GCTGTGTGCATGGAGGAGAGCTCTCCTGTGTCACGAGGGCGTCACATATTTTAAGTGCACATAIT TTGGCAAACTGTCATTC
278	37	C T	GGCCTAAAGG AATGGGAA	TCAAGCGACCA CCAACAC	ATTCACGTTGGCCAAGATCTCCCTTATGTGGCATTGCAIAGJAGACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAATTAACATTTCTAA
293	40	A G	CCCTTATGTTG GCATTGCA	AACCTCAGATA AGTGCAGTGT T	CCTTTGCTCTGAACTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTAGAATCAATGGG[C/T]GACTTTTCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA
315	84	G C	TCAAATGGG	CCAAAGGGGA AAAAGTCA	AGGAAAGAGTGTAAAGCAAAAGGCGATCATTTGGATGGAATGATTATGTGTCCAGGACCTTGAGGAC CTAGAAAGCAAA[C/T]GGAGTGATTATGCCAATCAAAATTCGAAGTTGGAGATATGCTAAAA
325	80	C T C	CTTGAGGACCT AGAAAGCAAA	TTTGATTGGCA TAATCACTCC	AATTTGCTAGTGCAAATGGACCCAGAATTGGAAGGGCTATGTAACACACAG[G/A]TATGCACACCCAC AGCCATGTCAGTGTACAGATCCTCTGTGCATTCAGCTTCTTAAAAACACATCAAAAGGCTGCA
352	51	G A ---			TGACTGTATACCAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAAAACACGAGATAAACACAAT
373	55	C T TAGGATG	TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAACACAGAC	

92	49	C	A	GCACACCAG	GCATGGGTTAA	GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAAACCAGGGGCAAAATACATGCTGGATTAAACCC
				GGCAAAATA	TCCAGCA	ATGCTAATGGGTTACCTTTATTAGTAATCATGGGTCCCTCATAGCATGGTCCAGATCCG
38	38	T	C	GGGCGCTTGGC	ACTTATCCGTC	GTGGACCTCTACAAAGTACCATGGGCCCTTGGCACTATGTCCTACTCTGCTGACGGATAAGTTGGC
				ACTATG	AGGCAGAGTAG	ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
21	42	T	C	CATTATTGAG	GTGTAGTCTT	TCAAAGTGTAATAGCCATTTATTGAGTATTCTTGGTTTGAATTCCTGCTACGTAAGCATGTAAGACT
				TATCTTGTCTT	ACATGCTTACG	ACAACATTACGACCCCATCTCTCAAGAGGAAGCTGGTATTATGGAAAAACATTTTGTGCTTCAGAT
				TGAT	TAGAC	T
10	104	A	T	TGGCAAAATA	TTGAAAATGGT	ATGTTGAGAGTAATATGCCCTACATATTTAGTGTAAGTACACCCAGATATTTTGGGGAGAAGAG
				TGCATAACAA	TAAACTGGCA	TTGTTTGCCTTTTGGCAAAATATGCATAACAAAATATTTGGCCAGTTTAAACCATTTTCAAGAGT
				TAA		
				CATTGCAAT		CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATAAACACCATCATTTCTGCTGAG
				AAACACCATC	GGACCTTATCT	TCCACAGATAAGGTCCCGGAGAAAGGGCTTCCCTCTTCTGCTGGGTGACGTTCCAGCGGAGT
39	57	T	C	GTGGACTCAGG	GTGGACTCAGG	GAAGCCCTTCTGGAATG
				GCATCATATG	GGACAAATGT	
				AACTGTCTAGC	AAACATAGCT	ATGAGTTTATAAACTGGAGACAGCGGCATCATATGAACCTGTCTAGCAGTATTATTCCTATTAGCTA
34	52	T	C	AGT	AATAGC	TGTTTACAATTTGCTCTGAAGGGTCTAGATGTACACCCCGAGAAAGTGGTGAATCTCTGA
				GGGCTTGACAC	AGATTTTAAAC	TTTGTCTGAAGGGCTTGACACAAAGTTCTAACTTTCTTGTGTTTAAATCTCTGGCTTTCTGGCTGG
19	34	T	C	AAAGTTCTAA	AA	TGAGGAGGCACAGCGTGGGCTTTCAGGTATCCACTGTGTTGCCCGCATCTGTTCCCTCCACTCCCCAG
						CCACATCTTGGCTCT
				AAGACCCGT	CCCTCTCCTCA	CTGTCCGGGGAAGACACCGTGCAAAATGGCTTAAAGTGCACCTGAGGAGGGGAGGTCTGTGACTC
39	28	C	T	GCAATGC	GTGCACCTT	CCAAACCCCTCGAATATTTTATGAATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC
					TTGCTACTAA	TCCCCAGATTGTATGGAAATGCCCTAGTGGCATTAAGGATGCATGAGGATGTCCACTTTTAGTAGC
48	41	A	G	CCTAGTGGCAT	AGTGGACATCC	AACCGATGTTAATTCACACTCTCCATGTTAGTGGCTTTACTTGGATTATCTCATTAAAACCCACA
				TAAGGATGC	T	
34	64	G	T	CATGCTGTAA	GGAAACAACA	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC[G/
				TACAGCTGTGC	AGCCTAAATGG	TCCATTAGGCTTTGTTGTTCCATTAGAGAGCACAGGAGGAAATTTAGCATAATCTT
				AAAGGATGAA		TTTATAAGCTGAATGAAAGAGTGCACACAGCGGACACTGTCTAAGTGGAAACAAGGATGAAGCT
30	75	G	A	GCTAATCATG	TCTCTCAGGG	AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGAAATTAA
				GA	AGCTTGC	TCCTG
				CATGTGGCTGG	CCTTCCACCAT	AAGGTTAATGGACTCACAGTTCATGTGGCTGGGAGGCTTCACAAATCATGTTGGAGGCAAAA
15	39	T	C	GAGGC	GATTGTGA	GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
						TATTTAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC
				AGTGGCATTC		CCATAGGTTCAAGAACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATCTCTTAACTCCATGT
16	123	C	T	AATAGCCTAT	TGAAACTCCCA	
					CATGGAGTT	GGGAGTTTCATAATAA

3	62	T	G	TAAAT	TTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTTGJTT GAATTAATAATTTTAAATTTTATAATAAGTGCTAATCGAGACATCACTGGGTATAATTGA TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTCTJCAAAGACTTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA GG
7	74	C	T	AATTT	GAACTCAAAG GAAAAGAACA	TCACTCCOCCA AGTCTTTG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGCTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCA TTTATTGGCTGCTCTGTAATAACAATGTGGTGAACAC[G/AJCTTAATTCAGGACATCTTCCACCTTG TTTGGCTTCCAGTTGACTGCAAGACCAGTGTGAGGCACATAGGCTGATTATCAGTGG
5	95	C	A	GGACTCA	CCAAATTTCTAG TGATAGTAGA	AAGGTGCACGT GCAGG	AGAAATTTTTCCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAATAC CTAGTTATTACACATTCCTCATCTGCTTGCA[G/A]GGAGGGATCTTGGTCGGCTTAACA CCAGCTGGAGGTGGAATAATGCGGCACCCACAGAAAACACACAGCTACACACAGGCCTGCATT TGGCTTATTCJGTGCTGAAAAAGAGGGCCGACCTTTGATAAAGATGICT
3	37	G	A	---	CATTCCCATCT GTCCTGCA	CCGACCAAGAT CCCTOC	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCACACTAGGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTTAAATATGATGATGTCGCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCTTAAGAACCAAGCTTAGGACTAGGACACAACTAGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATTTTAAATGCCGACGCCGACACCCACA
3	100	G	A	GGCTTA	GGCCTGCAATTT GGCTTA	GGCCTGCTTTT TCAGGCAC	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCACACTAGGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTTAAATATGATGATGTCGCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCTTAAGAACCAAGCTTAGGACTAGGACACAACTAGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATTTTAAATGCCGACGCCGACACCCACA
b	97	T	C	---	---	---	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCACACTAGGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTTAAATATGATGATGTCGCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCTTAAGAACCAAGCTTAGGACTAGGACACAACTAGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATTTTAAATGCCGACGCCGACACCCACA
a	87	T	C	---	---	---	CACAACATTCAGAAAGTTTCTGCATTGTCTCTCTGATGTCTAAAAGATTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTATAAGGTTTCTCC[C/A]AGTATGGATTCTCTGATGATTAAATA AGCCCCGAATTCGGCTAAAGGCTTCCACATTCAGACATTTGTAAGGTTTCTCCAGTGTGGAC TCTCTGGTGTGCACAAGAAATGGAATTCGGCTGAATGCTTTCCACACT
	107	C	A	---	---	---	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAACTTAGTTA ATAATCATGTTAAGGGACATTGCCAAAGAGCAACTGATGCCCTCAGTGA
	32	G	A	ATGCAACAAG	GGGAACATCA ATGCAACAAG	AGTTTACAAAT T	TATTAGATAAAACCTTTGTTCCGATTTCAGGATGTTTAAATTTGCTTCTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGTTA/GATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAACTTTT GTGCAAGGCACCTCTGTGGCCTCACAACCTGCCCCCTGTGAGAGGGATGCTGCCTTCCAGCCCTAAAG ACACTAGGGCTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG
	87	T	A	---	---	---	

		GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAAATCAATAGIAGTATCTTTTACAAAAAAGGTTAGAAATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAGGGCAGTGAGACATCAACAA
28	A G A A			TTGTGCTCAACAGATGAAATTCATAACCTTGTCTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAAI[A]GCAACTGACAGTTTTTGAAG GACACCAAGACAATAGGGCT
b	112	T A ---	---	TTGTGCTCAACAGATGAAATTCATAACCTTGTCTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[A]TATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTTGAAG GACACCAAGACAATAGGGCT
a	73	A T ---	---	CTAATATAATCCTGGGCACATGGATCCAAAGAGAGATTTTCAGCAGATTTTCATTATAGTTACTTAA CAGCTAAATAAAGGGTGATTTAACTTACTTACAGAGTCACATAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G]TATCAACCTCCCTAAGCATCTGTCTGGTCCG CAGC
i	165	G T GCTG	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCTGGTAGTCTCTTTTACACAACATTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACGACGCTAAACTCTGAGAGAAAAAC[C]GCTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
.	195	C G ---	---	ATTGTAATTAATAATTACATGGGCCCTATTATTAAAGGACATTGTAATGTTTCCACTTTGTTTTAA [C]TAAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAACAAGTTTGAAAAATGGCG
b	68	C T ---	---	ATTGTAATTAATAATTACATGGGCCCTATTATTAAAGGACATT[G]GTAAATGTTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAACAAGTTTGAAAAATGGCG
la	42	G C ---	---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T]CJAGCAATGGATGCTGTGTCAAGACATACTGCCAATAAACITTAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAC
y	75	T C GTCATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTTCTTGCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGATCAITTTCTCAAGCACAI T[C]ACCCAACTTGAAGGTGATTGAACCCCAAAATATGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGGTTATATTTGATGTTGCCAAT
l	134	T C ---	---	TGCTAAACACCACCATTTATTAAAGGAGTACTAGGAAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC[C]TGGCTAATACACTGCAATATTTTA TGTTTAGCAATATTAGCTGGTCTGTGTATACCAGAGAGCGGTATCTGG
jb	106	C T AGCCACAGC	ACATAAAATA TTGCAGTGTAT TAGCC	

10a	28	T C A G A G	A A C A C C A C C A T T A T T A A G G	G C T G T G T T G G T A G T T T T C C T	T G C T A A C A C C A C C A T T A T T A A G G A G A G T C / J A C T A G G A A A A A C T A C C A A C A C A G C A T G T G A A A C A G T T G G C A C G G T G T A A A G G G C A C A G A C T C T G G A G C A C A G C C G G C T A A T A C A C T G C A A T A T T T T A T G T T A G C A A A T T A G C T G G T C T G T G T A T A C C A G A A G A G C G G T A T C T G G
70	53	A G A N C A T C A C A	C A A C C C C A A A N C A T C A C A	G C T T T T G G A G T G T A T A A T A G T A	G A T G T T T A A T G A C A C A G A T C T T C C C A A G T A A T C C A A A C C C A A A C A T C A C A / N G / A A T T A T T C A T A C T A T T A T A C A C T C C A A A G C A A A T A C T T C A A C T G C A A T C C
36	151	A G A G A	G C A T T C T T C C A A A A C A A A G A	C C T T G T A A G T G A C T A T T C C A A T	A T T C T G A G G C A A A G G T C A G A A A T C A G C T A G C A C T A A T C T T G A C C A A A T G G G T G A G T C A G C C T C A T C A C A G A G A T T T T T T T T A A T T A G A T G A A A T T C A C A T T T A A A A C A T G G T A A C T C C A A G C A T T C T T C C A A A A C A A A G A A T / N G / A C A T T G G A A T A G T C A C T T A C A A G G A C
31	32	C A G C A G	G A T C T A A C A G C T G C A G A A T G	A A A A G C T G G G A A G G A A G A G	C C T G A G A G C A G A T C T A A C A G C T G C A G A A T G G C / A / C T T C T C C T C C A G C T T T T G T G A C A A A A C A A T T C T C T A A G G C A T C A G A A G C A C T G A G T G C A A A A T G G G T T G T C A G G T A C A A G G T C T C
14	225	T C		---	T A A A T A C T G C C A A C T A G C A T T A C G T C C A C T C T T G C A T C A T T A A A A C A A A G G T A T T C C T C C T T G G T A T T T C A A A T G A T G C A T T A T A C A A T A A A G A A G T T A G A C T T A A A T G C A C C C T G A T T A A T T A T G T A A A C T G G T A A T T T T T T A A A A G C A T A A T A A T T G G T T C C T T C T C A T A A A A T G G A A A T T T A A A T A T T C T C T G A T A G C T T G A G G T T / C / A T C A T T A G T A G T G C A A A G T G T G
24	112	A G		---	C G G T T T G C T A C A C T T A A T G G G T T T T T T T A A G G A T T T T T T C A G G C T T T G T C A G C A A C A T C A A A C A A A G G T A C T G A T A C T C C A C A G G T A C A G A G T G C G C C A / N G / C A C C T T A G A A A A A T T A C A T G A C A C G A A A A T G C G C C T T G C T C C T T G A A G A G C T A C A G T A G G A T T T G A C A A C T C A C A G T C T T A G G A A C T G G G C A A A G T A A G G C A A T T C T C A T C C C C T A G A G C T A T T G T G
39	139	T C A A T T C	G A A A A A T G A G A T G C A G T T A A	T C A C T T T G T G G C T T T T A A T T A T	G T C A A A A A A A G C T G A G A A G A G C C A C A C A T G A A A G T G T C A A G A A A C A T T C T G A T A G G T A C G G A C A A A A G A G C T C C T T C A A T C A A A A G G A G T T A C A T A T T A G T T C T C A C C A T G C T A G A A A A T G A G A T G C A G T T A A A A T T C T / C / J A G A A T A A T T A A A G C C A C A A A G T G A A A C T G T T G T C T G G G C C C T A T G T T G T A G A T T C T C T
11	216	T C		---	T C C C A G C T C A T A T T A T T T T G G G C A C A G A G T G G G C A C T C A A A T A T C T G A T G A A C T T G A T G A A C T G A A A A G A G G T C T C T T A A C A A G A T A T C A T C C C G A A G A G A A G T C C C A C C A T A T A A A A T G A T A T G A T C A A G T C C A G A A A A C T T T G C C T T C C C A A G G A A T G T G T T C T A A T T T G G T T C A A A G C A C A C T G G T T C C C A C T T T A C C A C T T / C / J A T G A C A T T G G A C A A T A G T A C T A C T C T T T T C T A C
13	112	G C		---	G C C A G T C T G T A G T A G T C T A G G G A C A T G A C C A G A C C A G A A G C C C T G T C T A T A T A G A A C A A A C A G G T G C C A T A C T T G G G T G A G G A T A C C G C T G C T A T T C C C A G A T G / C / J A G A T T T G G T G G A A G G A G A C C A T G A C A G A T G A C A A A C G G A A C A G T T T C A A A A C A G A G G T A T A
57	74	C T		---	A A A A G C T T T A A A A A A A A A G T G G T G C T A T C T T T A G A A A C A C T T T C A G C A A G A T C A A G T A G C C C A G C T A C A G C C T / C / J G G T G C A T C T T A A C C C C T C T C T T T

7	121	T	G	TGCTCTTTTATTTCACGTTTCACAACACACGCCGTG[G/TTGGCACAGTCTACCAAGTGCCCGCAGCGCCACGCTTGGCGGAAGGTCATCTGTCCTCTATGGACTGATTGAATTTGGATGGCCAGCTOCAGAAATGTTCCACGTGGGGCACTCTGTGGGCAGAGAGGCTGAGCCCTTGCCACACACTGGCAOCCAAGAGGTTGCACGATGCAGCTGCAGTGGGTCCAAAGCCGGGTGTCGTG
37	G	T	AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGCTACCATCCACTATCATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAATAAAGT[G/JATAATTTCTTTGATTAAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTAAAAAAGTAAAAATTTAGAACATATGACGCTTTTCATAATTAAATGCTTTTGATATAGATTGAGG
114	G	C	G	T	G	...	CAGGGTCTGCTCTGCTCTCCAGGCTAGAGTGAGTGACACAATCAAGACTCACAGTAGCCTCAACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/CACACCACACCTGGTTAACTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAACCAACTAAC
51	C	G	CAGGGTCTGCTCTGCTCTCCAGGCTAGAGTGAGTGACACAATCAAGACT[G/C/JACAGTAGCCTCAACCTCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTAACCTCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTAAATTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAACCAACTAAC
12	71	C	T	A	G	C	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTTTTTCCTCTCTTTTCCATATAATACACAAAAATTTCTAAATATCCTTAAAAAGAAAAATATAAATAGTTTCAGTATGTTATGTAGAGTCACATACACTATGGCAAAAAATATTTTATTTAGGGGAATAGGCCCAATTT
188	36	C	A	C	T	C	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[C/JAAACAGCATCAGTAGTGACACTTTGATAAAAAGGAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACATCTTTATGGAAACTGTTTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTGACACACACAAGTAAA
a	108	G	A	C	T	T	TGCTATTCATGACAGACACGTCGAGACAAATATTTCTTATTTTACAGATGGAATAGACCCAGACATTTTCAGTACTTTAACCACTAATAGTGGAAACCCCTGAGACTTTA[G/JATCTGCAAGGGGTTTAATAATGCAAATATCACATATATTTCCATTTTAAACCCATATTTAAGTTTCCATTTTCTTAATAGAAAAATGATAAAAAATGTTTCCCCCAATAT
337	87	A	G	A	A	G	TGTTAAAAAATCCAACTTGTTCACAAAGTACATATGTCCTATGATTTTATGCATACATCCATATACATATATCAAGGTAAAGTCCA[G/JTACAAAAAACAAGCATTTCTATGGCCAGTGTCTACAGAAGTAAGACTGTGCAAACTTTATCGTATAGTCAATAGATTGCACACTAAGGCAGGATGAGGCAGAGCAAGITGTGTC

b	50	G C	---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCTGTG[C/G]TCTCTCGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCACTTCTCTGTCTATAOCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATAATGTATTACCA CTGGAGCTTCACCTTTGTTAC
							GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTT[C/G]TCTCAGGTTGCCTGTGCTCTCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCACTTCTCTGTCTATAOCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATAATGTATTACCA CTGGAGCTTCACCTTTGTTAC
b	34	T C	---				TGAACGTGTGGTTAAAACTAGGCAATTGGTTAAAAATCAATTTAAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCAATTTCTGCTTTT AAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCA CATGATGAGCCTGGACATGTTGT
							TGAACGTGTGGTTAAAA[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAAACAGGCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCAATTTCTGCT TTCAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGACATGTTGT
a	17	C A	---				AGAGGCAGATTGGAAGGTGAAATAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTTCAG AAATGTAAGTGTGCCCTCAACTGTTCTTTACCCACTTAATCTGCAATTTTGAAAACTAGATTGAAT TCCTTGGCAAAACCCCTTGCAATCATGGATAACCCGAGTTAAACCGTTAATTAAAGACATTAAACATGG CCTGGTG
							TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACTCCCATATTC CAACTAAGCAGGAGTGTTCACAAATAAACACATAGGCTCTTTATCTCCTTCTTCAATTTTCTT TCAC[G/A]TTATCCCTCACCCCTGAACGCCCTTCTTCTCTGAGTGACATTTTAAATCCACTTTAC ACATCGGACC
b	141	G A	---				TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACTCCCATATTC CAACTAAGCAGGAGTGTTCACAAATAAACACATAGGCTCTTTATCTCCTTCTTCAATTTTCTT TCAC[G/A]TTATCCCTCACCCCTGAACGCCCTTCTTCTCTGAGTGACATTTTAAATCCACTTTAC ACATCGGACC
							TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACTCCCATATTC CAACTAAGCAGGAGTGTTCACAAATAAACACATAGGCTCTTTATCTCCTTCTTCAATTTTCTT CTTTCACGTTATCCCTCACCCCTGAACGCCCTTCTTCTCTGAGTGACATTTTAAATCCACTTTACA CATTCGGACC
a	126	T C A					GAAGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTAT TTTTTTCAGGCATATAGACATACATATCCATTATACAGAGAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT
							GAAGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTAT TTTTTTCAGGCATATAGACATACATATCCATTATACAGAGAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT
b	114	G C	ACAGAAAAG				GTCAAGTGAGATTTCAGATATTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT
							GTCAAGTGAGATTTCAGATATTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

			GCATGCTGTG TTACTCTATTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTTGTTC/TAAGCCACCTGTGGCATTTCCAAATATGATAATCTCTGCCACCACTACTGCTTTAAACACAAATAGAAATCTGGCAGCAAAATATAGCATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTTAAAAAATAAAAAACCAACACTGCCCA
46	C	T	TGTT	ATCACAGCAG AGTACCTTTCT	AGCCATCACAGCAGAGTACCTTTCTAACTTC/ATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGACTGTTCGTGTATATACCTGTGTCCAGTTAATCCA
29	T	C	AAC	T	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGATGATCAATTTCAAATAAAGATGGTAGTGAGCGAAACAGAGAGGTTTCATTGACTCTAACTGAGTACT/TA/CAAAAAACGAGCAGGTGCTCACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
b	112	T	A	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGATGATCAATTTCAAATAAAGATGGTAGTGAGCGAAACAGAGGTTTCATTGACTCTAACTGAGTACT/TA/CAAAAAACGAGCAGGTGCTCACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
a	74	C	T	---	AACAAAAACAGACACCTCGGCTCTCTCCACAGTCCACATGGGTGCCAAACAATCCACATTCCTACATCTCCCCACTGGCTGCCCTTCACAACTCACCAG/AGIACCTGGCTTACCGGGAAGCATAAAGCCAAAGCATTTAGTCTTTTATTGCAACATGGCTGGCTGCAATAC
3	107	A	G	CCTCAACA ACTGCTTGCTT	ACTCACTGCTTGCTTGATTTAATCAACCTAGCCG/AG/GCTGTGATGTGGGATTAGAAATAAATAAACACAAAAATGAAACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTAAAGATAATAACTTCAA
3	36	G	A	C	TGCATTCAATTGCACCAATAATAACTTCTGTACAT/ATCATTTATTTTCAATTCATTCACAAAAATATAGTGAGGGATGATTGTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCTTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTGGAATCCATCAACTTGAATCCAGAGAAATGTTCTGCATCACTGTACACACTGCTCTTTTCTCTCTTGAACAAAGGC
1	37	A	T	---	CTTCTGACCTGTTTGCAGTGGATACTGTTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTTGTCTCCAG/AG/AGAGTCAATTTGTAGGTGTTCTGGGGTTTTTGTACGTTTCCATTTTCTCTATACACTGCGCTTTAAGGGAGGCTTGACAGAGCATTTATCAGATGGCTGTTTGTCTGCATCTGTGCACCTGAAGTTTATGCAAGAGGTCCATGAGTTTACAGAACTCAAGGAAGAAAGCCCTAGAGATGACACCCAGAAATGAGAGTGGCTTGCTCATGAAATTTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGAATAATCATACTCTATCCACGTGCAAACTGGCAATTAGTTTTGT/ATTTACTAAAAACACAAATGTTFACCTTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTTCTGTGATG
11	70	G	C	CCA CAGTATCTGA AGTTTTGTCT	CTATGATTTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCTTAGAACCTCAG/AG/ATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTGGCCACCTGTTTGTAGGAA
81	178	A	T	---	
791b	76	G	A	---	

31a	44	C G	---			CTATGTATTCCATCTAGCAAAGAAAGACTATTTGGATAAGTTTTC/GIACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCTATCTACTGACCCAAAGGTA AAAAATAAATAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTGGCACCCCTGTTTGT TAGGAA
36c	120	C T	---			CACCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/CCTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAAGGAAAGAAAGAGAGGCAA GG
06b	118	C A A		CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/CCTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAAGGAAAGAAAGAGAGGCAA GG
06a	42	A G	---		---	CACCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGG/C/GCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAAGGAAAGAAAGAGAGGCAA GG
38	48	G C T G		TTATTCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTT TCAAT	CCATCTCTCTCTCCCTCCCTTTATCTCCCTGTTTCTTTTG/C/CATGAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
15	54	T A T T		TCTTCATGAAT TCATCTTTTCTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTTAAGCACGATTTGCTTCATGAATTCATCTTTCAGTTT/T/ATAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
37	41	C T G		TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAAATAATCCAAGAG/C/TCTTAAACCATATTTTGTGTTTA GAACTCCTGTGCCAACCCACTCTTGATGTGAGTGAC
81b	131	A G C T G C A G T C G		TGTCATTATG CTGTCAGTCG	TTACTTCCAGG CTCCAAGTAT	AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCCTGTTTTTCAAGAGGTAGTATATGTCGAAATACTATTTTGTCATTTATGCTGCAGTCG/VGJA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
31a	29	G A A A T T		CCCATGCAATTA GATACTGTAA	CCCATGCAATTA GATACTGTAA	AAGCCAAATTCACATTAGTTGATGAATTTG/A/AAATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTGTTTTTCAAGAGGTAGTATATGTCGAAATACTATTTTGTCATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
92	38	T C	---		---	TCATGAGTCTTCTTCAAGATGCTGTTTAAAGTCCCA/T/C/CAAGAAAGGATCCCATGGCCTAAT GAAGATGACCTCCACCTTAGGATATTTTGCAGACCAA

134	T C ...	CCCAATACTTT TTCAGGTGAA	...	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTCTCATGCTTCACATTTATTTTTT TTTCACTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTCTTTAGTC TTTCAAAATTAATGCCACCATAGAAATAATTTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTTGGTGCAATTACTCTTTACAC
40	C T A	CCTGTATTTTA GCAACATGGG	CCTGTATTTTA GCAACATGGG	CCTTATAACCCCAATACTTTTTCAGGTGAAAAAGGGAAAA[C/T]ACCCATGTTTGTCTAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATTTCTGATGTGGGAAATAT TAGAAATTAAGCGAGAGAGGCA
97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG OCCAGG	TGTTTGTTCTGCACCTCCCAACAGTGGTCAATGAGCCCTCAAGGTTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACCAGCCTTTTAGAGTC/TCCCTGGGCAATTTGTCACCTAGTGTGAGA
b 161	C T	TAAGTTGATTTAAACACTCTGTGCTCTCAATTTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATAACTCTGATGATCTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCATGAT[C/T]CCATTTTGAAAAATTAAGCTTTTGAATTTGTTTCCCA ATG
58	C T	GTTCATAAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATCGGTTCAACCTCGATGATGTTGGGCTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG
b 134	G A	CAGGACCTGGAGCCTTGGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGACGGCTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG/A TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
a 92	C T	CAGGACCTGGAGCCTTGGCTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCTCTATGCA[C/T]GGCTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
b 125	A T TTC	CTATTAAATGA GCATCGTGTCA	TTCTCTTGAGA AACCTAAAAC ACTG	TGCCCTGATTGACACATAGTTATCTGACAGTAAATCATTCTAACATCACAATATCTTATTCTGCCCTG TCACACTAAATTTGGAAGCAATTCAAATGATTGACTATTAAATGAGCATCGTGTCTATTQAT/CAGTGTT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCCGTAACTCAAGTA
a 44	T A	TGCCCTGATTGACACATAGTTATCTGACAGTAAATCATTCTAACATTA/CACAAATATCTTATTCTGCG CTGTCACACTAAATTTGCAAGCAATTCAAATGATTGACTATTAAATGAGCATCGTGTCTATTCACAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTCTGTAACCTCAAGTA
26	A/C	GCCAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA	TGAGAGCCAAATTTTATCCGCAATAAA/C/TCCCAAAGTCCCTCGATGGAGGCATTTTCAGAAATCGGG GCAGGGGAGGCAGAGGTTGAGACAGATGTGAAGAAC

37	165	C T	...			GAGTTAATGAATCCTGTTCCCTCCTAAACACCTCCTGTTCCCCCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTCTCTGTGCGGTAT[C/T]TGCTCCAATCACCCATTCACATTTATTTCCCTATTAT GCTGAATGAACGGTTATATTACAG
93	53	G C	...			GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA[G/C]GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTTCTGGAAGTCCAACTGTGCACTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTGACAAACCTTTGATTGACGGTGAC ACACATGCTTCGAGAAGGAATGAGG
41	80	T C	AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAAACCCCA GAACAGTG	GACTCTGCTCAAGAAAAAATAAATTGAATAATTGAATTAATTAAAGCATCTTTAATAAGCAT CTACAAGGTACTTAT[C]CACTGTTCTGGGGTTTCAATCCTCTCACCTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAATTTGTCTTTT CTC
150	45	T G	TGTCACA	CCAATGACTT ATTCTATATCT	TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTCTTCCATGACTTATTCTATATCTTGTACAT/GJAGAAGTACCACACATTTCA AACAAAGCCAGGCTATGCCAGGGTGGGATTATTTTCACGGTCAATGTAATATGCATGTAAAGACTA TTTTTACTGGCCTTCTTTTATGCATAAAACAAGGATTGCTCTATTTCAACAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGCTGCTACTAGATAATAGTCTTTATAGATATGTGTTTGAATAAAGCCACA AATTATCTATAAAACAAC[C/T]AAGGAACGAGGCTCAAAAGTGAACAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
161	88	C T	...			GAAACTATCCTTTAGTGGTGGCCACATTTCTATTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTCACTGAACTAGTTATCATATAAAGACATGCAAAAACCTTTTCACAGTCTTGT CCTGG[G/A]AATATCTCACAAAATTAATTAATAATTGGCATGGGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
166c	141	G A	TTGTCTGG	TTTTCACAGTC TTTGTCTGG	AGTCGATGCC AATTTATAAT	GAAACTATCCTTTAGTGGTGGCCACATTTCTATTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT[C]ATTCACTGAACTAGTTATCATATAAAGACATGCAAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTAATAATTGGCATGGGACTTTCTGATTTAGCCTGACAGGA TTGTCTCTT
466b	80	T C	GTC	GACTTCTGGG CTATGAAATA	TGCTTTTATG ATAACTAGTTC ACTGAA	TGCTTTTAAATAACAATGACCACCACCTGACACCATAGTCTGTCTCCATTTGCCACGCTTCTCCTC AGTAGAATAAGACAGGACTTTGGCTGGCTGCTATCT[C]A/TCTCCTTCAGAAAGAGCATTGGCCCT CATAGGCATTCATAGATTTGTTGAATGAATGTGCTTTTGGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
814	104	C A	...			CCTCTAACAGAAAACTTGACTTCTCACTCAAAATACCCCTCTCTAATAATTTA/GJAGTAACCA AAATATCTCTCAAAATAAATTAATCTTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCAC
1720b	55	A G	...			

20a	47	A G	---	CCTCTAACAGAAACCTTGACTTCCTCAACTCAAAATACCCCTCTCTGAGJATAATTTAAGTAACCA AAATATCCCTTCAAAATAATCTTTAATTAGAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
25	123	A T	---	CACGCTCTAAGGCAGGATGGCTTATGAGATACCTTTGCATTGCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTCAGATGAAGGCTCAGGGTCTGJATGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTACAAGAAGAACTACCAAGGGTTAGTTTGCAAT TAAGAAATGCCAGCTTTTGCTGTCATCATCTTGAACATTATCCACATG
18	74	C G	---	CCACTCAGTAAATCAATTTGTAGCACCTTATTTCTAAGATTCTAATTTTATATGTTTACCCTTT GTCATTGJTCAGACCAAGTACATGTTTTCACAGCCATCTTTCTTTCTGGAAATCTTTCAGAAT TACAGTTATGATGCTCTTTTATATCCCA
43	91	T C	---	TGAGGCTATGATTGCAGATTTGTAGTGACTAATACTTATTAGCAATTTCAATGTTGGGCACCTGT CGTTGTGTTTATATCCATCTCTGJATTTTAAATTTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTGCTCCCTATTGTACCTTTAATATTGCATTTCACACCTTCTCTTTTGTCTTTAGGGA
31	39	T C	---	AGGGCCCTTCACAGATCCGTCAGCTCAACACTGCTCTCTGJAGTGAGCCTGTGAACCCACCAAGAC GGCTGGTCATCAGTGTACCTCTCTCTTTCCGGACAATCTTTAAAGAAAAAAAGAGTGT CTTTGAATGTATCCATTTTATCCCAAAATAATCTGTTTAAATAATCTTTATAGGCCAAATCCAAT GTGCTGAAATATCTGCCAAGCATGTCTTCTACACAAAAGGATTGCAAA
17b	84	C T	---	CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATCTGTTCTCAACATCTTATTTTCTCAAAAC ATTTATCTAGCCTGTATGJAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
17a	83	A T	---	CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATCTGTTCTCAACATCTTATTTTCTCAAAAC ATTTATCTAGCCTGTATGJAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
15b	115	C A	---	AGATAACCCCTGGAAACTAGAGAAATTAACGTGTTGACATCTCACCAGACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACA/CJ/AGCCAAGAAAAGCC TGATAITTAAGAGGCACTTGCAITAA
15a	42	C T	---	AGATAACCCCTGGAAACTAGAGAAATTAACGTGTTGACATCTCACCAGACTGGAAGG AGCTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACACAGCCAAGAAAAGCC TGATAITTAAGAGGCACTTGCAITAA
13	146	C T	---	CCTGTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCCTCCCCATTTCTTTGTCTTGA TTCCCCAAACCCCAAGGTCTCACCCCAATCTGATCAATGCTGACTAGGTGCTGGCTGGTCAGGGTAA AGCATTTATGJCTJAGACACAAAGACAAAGAGGTAAAGTTGCTGCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

		19	139	A	T	ATCT	TGATGTAATGC TATGTAGCAA	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTGTTTATTTATGTGTGCTATAAATCAATGGTTCTTA ACATTTCAAATAAGATCTTTTGTCTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTAATJTCCCTAAGCACAGTAATCAAGGCCCTTCTACCCCA
		2	122	T	A	TTT	GCGAGAAAAG AAATCATGAC	GACTGTAAAT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTATTTGGCGAGAAAAGAAATCATGACTTTTAAATAAATACC AGACTAATGATTAATAATAATTAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTTAGTGGCCT CCTTAGA
		3	39	T	C	ATAAAT	TGTCATCTTGA CTCGTATTAA	AAATTTCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTATTTGGCGAGAAAAGAAATCATGACTTTTAAATAAATACC AGACTAATGATTAATAATAATTAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTTAGTGGCCT CCTTAGA
		b	170	C	T	TTTACATG	CCTTTAGATAT ATTGGAATTGT	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTTGGTGACACTCTGTTTATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATGCTGTTGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
	a	54	C	A	T	CAGGGAAGG	GTAGCAGGAT	CAAAATTATAT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGC/AAJATTATAATA AATAAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTTGGTGACACTCTGTTTATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
	289	29	T	C	CAAAC	TCTT	TCTCTGTGCCC CAAAC	ATTCTGTGTGT ATTGAATGGAA TTAA	CCAGGGATTCTCTCTGTCCCAAACTCTTATGTTAAATCCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAGACACCCCTTATATTAGT
	119	40	A	T	ATTCTTT	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	GCTTTGGAATG TATCCAAAAGT TT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATCTTTTATJACCATAGGGGTGTGGCTTATCT TTTACCTGGCAATGGCTTTAGGCTCTGTTTATAATTTGGTATCTTTTGGCCACAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTAAGATTAACACTGGTCAGATGTTTAAAACTTGTGAACCTGCAGC AGCAACGTGTACAACTTAGTGAAGGTGTAATCAGAAGCATCTATATTACCAGTCAACCCCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTCTTATGTTAACTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAGGATGTTTAAAGGCCAGCC AGTGAGTTGTGCACAAATTTGGAGACATCTGTGACCCCAACTTAAACACTTCTCCCACAC/CTAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA
	572	61	C	T	

38	31	C	T	TGAAGCAACC	CAAGATATTAT	GAGGAAGCTGCCTGAAGCAACCAGGCTGTGTTGCTACCCCTCTTAGAGAAATAAATAATATCTT
				AGGCTTGT	ATTTATCTCT	GAGATAGGAGGAGCAGCCTGAGGACAGCTGGGTTTTGTTCTACCCCTGGAAGCAGAAATATCC
					AAGAGGGG	TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCTTTTCAGGG
31	32	A	G	CTGCTCAGGT	GGGAGTTAGGA	T
				GTCAAGAAGTT	GTCAAGAAGTT	CCTCCCGTTCTCTGTCTCAGGTATGACTCCCAAGJTGCAACTCTTGACTCCTAACTCCCATCTCGGTG
				GA	GA	TCTGCTTCCCAGGGGACGATCTGACACAGCCTTTGCTTGCTGTGACAAACAGAACATTGCAGAAG
146	A	C	GCAA	GTTACCCAGA	TGCGGCTTCCA	TGATGCTGGTGACCTCCAGGATA
				GTAGCT	GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTTAGCGGTGCTCAATAAATATATCTTTTTTCATATT
						TTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTTT
						CTAATAGCAAJACJAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
82	A	C	AGCGATGAAATTTATGTTATGCTGACTTAGCGGTGCTCAATAAATATATCTTTTTTCATATT
						TTCCAAATTAATAJACJCTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG
						TCTTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
						AGCGATGAAATTTATGTTATGCTGACTTAGCGGTGCTCAATAAATATATCTTTTTTCATATT
						ATTTTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGT
						CTTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
						CGTTGGGAATTTCTATCTCACCTAAATATGCTGCTGCTCAATAAATATATCTTTTTTCATATT
						TTGCTTTAAGTACTTTAICJGGAAGACCTTGACTGTGGATTTTGAGTTTTTCTTTTATCTTAATA
						AAACATGCATATTTAAGTTGTCAGCAAGATGTACTATATGTTAATATCTGATATCAGCATCCCTT
84	C	G	TACTTTA	C	TATGTAAT	TATGTAAT
						CGTTGGGAATTTCTATCTCACCTAAATATGCTGCTGCTCAATAAATATATCTTTTTAACAAACTTC
						AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGAGTTTTTCTTTATCTTAATA
						AAACATGCATATTTAAGTTGTCAGCAAGATGTACTATATGTTAATATCTGATATCAGCATCCCTT
33	C	A	AATTATG	GTAT	TATGTAAT	TATGTAAT
						GTGTGAAACTCCAGTATCATTTCCCTCAAACCGCTTAAATCAAAATCACTTTTTTCTTCTGTGA
125	T	C	ATCC	CCATGGCTGTA	CCATGGCTGTA	GAGCTCAAACCTCAGTCTGAATGAAATTTGCTGCACAAATGTAAACAAAGATGATCCTATJ/CJACTGGG
						ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
						TGACTCAAAGGAAACACACACAAAAAGTTTACCACAGTGAATATGACCAAAATGAGAJCJAAAT
58	C	T	TGAGA	TTTGAGGTTTT	TTTGAGGTTTT	TTGTTAAAAAAAACCTCAAATGAAAGAGACAAATATAGTTCAAAGATTCAGGTTCAATATTTGT
						ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTCTTTTCTTTTCTTTTGTGJGJCTTA
						GAAATCCATTTTGTCTTTTGGCCAGCATCCCTCTCCCATATTTTAAAGGAGAGAATTCACCTTTTTCT
						CTGTTGGATGATCACAGGTTCTGCTCTCCCAATCCAGAGGAGGACTACTATTCACCCCATGGGGTCAT
56	59	T	G	AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAAACC

154	T G T T T T	TTAACCAAGA GTTTTTCATTC	CTAACTTAAAA ATCCTCAATCA AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTAAGCCCTAAAGTAGTCTTTTAAACCAAGAGTTTTTCATTTCTTTT TTTAAAAAAGAGCAGACAT/GJTATATCATGTTCTGATAAATTTTTTATATATTTTGAATGAGGATT TTTAAGTTAGCAT
95	A G T T G A A A A A	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTAAGCCCT/GJAAAGTAGTCTTTTAAACCAAGAGTTTTTCATTTCT TTTTTTTAAAAAAGAGCAGACATTTTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
5	25 A G ---		...	CAAGTGTCTGGACCTTGATAGGTG/GJACCGCTGAAGGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAAATATAGATCTTGTCTCTTTGGGTTTACCCTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATTCAAAATAGCCATGGGTTGGACAAAATAC AAGGTTAGTGTCTCTCTAACTTTAATGGGCATA
133	C T A A G G	TGCCCTGTGC AAGG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGACATAAGGCAATACTAGCCCCATACAGAGTGTTTTATGTTAATATTATGAAA AAAGTCAAGAGAAAGATGATATAGTCTGTAGAAATCTTGAAATCTGATGCCCTGTCCAAAGG C/TJTGCTACACATGAATTTAGAGATTGAATGAAAATGGCAAAATTCAGAAAAGGG
77	T A A	AAATGATTCTT TCTGCTCAAG	CTGTTCTCACA TTCTTTTGA	GGTAGGATGATCTAGAAATGCCACTTTACAGCCACTGAAATATATTGCTCCCAATGATCTTTCTG CTCAAGAGT/AJTTTTTTTAAAGTTATCTACTTATTATCTGCTTTTTCAAAAAGAAATGTGAGA ACAGTACAAATGTGTTTCAGTATAGCAAAATTAATAAAGTAAGAAAAAGAGCCAAAT TGGGC
144	A G T A T G A G T T T C	TGCAAAATGCTT TATGAGTTTC	GGCATTTTGTA AAGGAGGAA	TAGAGAGGCTTTTTCAGTTTCAGGTTGGAGGGGGTGGTGAGATTCTTAGAAGCACTGGC TATGTACAGAAAGATAAATCTCTGAGAAAGAACTCAGTTCTAAAGTGTTCAGTCTTGCAAAATGCTTTA TGAGTTTTC/GJTTCCTCTCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT T
23	T C C	TGAATTCATCC AGAAAACAG	TCTCTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT/CJGAATGACAAACAGAGAGAAAAAGAGATTAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCTCAGTGCATGGAGCAGTG
115	T C G C C A T T C T A G	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCCAACTCTGTCAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTTCTGTGTGT GCCACCAATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCAGT/CJGGCTGCTGGCAGTGT TTCAGGCTGTGCCCATAACTAA
40	A G C T T G C C A	TGGCTCTGCTA CTCA	GAAACTCCCAC ATAAATAAAT	CAACCAATTGAGATTTAATTTTGGCTCTGCTACTGCCA/GJATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATTGGTAAATAGTATTCCTCTCCCTGCTTAGGTTTGAAGAAAGTTGAA

25	C T A	G C C A C A G T G G A A T C A T T T A C	T T T T A G C A T T T G C T G A T T T C G	A G C C A C A G T G G A A T C A T T T A C A C T A C T G G A A A T C A G C A A A T G C T A A A A T T G G G C C T T T G G A T T T T G T T T T G T T T T C C A T A G A C C C A C C G T T G A A C T A T T G T T A A C A T T T A C C A G C A T A C C A C T G C G G C T G G G T C A C A A C T T G G C T A C C A G G A A C C T G A C A G A C T T C G T A A T T G C T T T C A C A G G C T A C T G G A A A G C C
75	C T C A C T C	T T T A T G C C A T A T T A A T T C A T T A	C T A G A T G T A T T T G C T A A G A A A A T A T G A T G	T T G C A A G T T G T T T A T G C C A T A T T A A T T C A T T A C A C T C T G T A C A T C A T A T T T C T T A G C A A A T A C A T C T A G A C A C C T G G C A C T C A G T A A G G A T A T T C C T G G C A G A T A A T C A T T G T T A T C A T T A G A C A T T G C A G G A A C C A C C A T A T G G A T G G A T A A T G T G T T G T T A A T G A A G G C A A G C A A T T A T T G C A T G C A T T T A T A C G A A A G G A A T T A A A T A T C T T C C T T A T A G T T G A A T T T A A G T A A A A A T A A A G T T A T A C A T A T A T A C A A A A G T T G T A A G T A T A G T A C A A A T G A A T T A G A A A A T T G T C A G T G G T T G C T A G T A C A G G A A T C A A A T T T G G A C T A T G A A C A C A C A T A G T T G C T A A G G A T A T T C C A C A A A T T A T T T C A T G A
26	A C	---	---	C A G T G G C T G G C T A C T G A C A A A C G T A A C A T C G T G G C A G G T G G C A A G G G A G A C A T T T A C A G A G G T C C A T C T C T A G T G T C A C C A G C A G G G C C A G G A A G G T T G A T C T G G A G T G G G A C A C A C T G C T A G A C C C C T C C C A G G T C C C T C A A A G G T G G G T G A G G C C C T A C T G C C C T G C C C T G G G A C G A G G C A T C A G G C C C T A G C C T C C T G G G A C A G T A A A G G G C C A C C A C C A C A G A A A A T G C C T A G G T C T T G T A G C A A G A G A G A A G C A T C T T C A T G G C A G G A A T T C T C A T T T C T G T G T T C T T A G G G T T G G C T G G C C A C A G T T C A A C T A G C C C C T G C C C C T G A T C C A G C A A C A T T T C C G T A A C T A C C C C T C T A G A A G T C A T G C A A A G A G A A A T G A T G A
78	A G G	G C A A G G G A G G A A C A T T T A C A	C T G T G A C A T C A G A G A T G G A C	G G A C C A A C A G A A T T A C T T G G C A T C J A G G G T T C T T A A A A C T A T T T C G C A G A A C A T T A G T A A A G T T T A A A T A A G G A T C A G G C T A C C A G G A A T A C A G T T A G G A A C A T G T G G A T G A A T A T T C T T T A G T A G A G G A C T T C T A A A G G C T A A T A T T T G G A T A C A T T A G G C T C A T T A T G A A T C T C A A A A G G A G C A T G T A G T A G G G C A T A T C T A A
89	C T G C T A G A C C	G G G A C A C A C T T G G G A	T T G A G G G A C C C T G G G A	A C A G A A A A T G C C T A G G T C T T G T A G C A A G A G A G A A G C A T C T T C A T G G C A G G A A T T C T C A T T T C T G T G T T C T T A G G G T T G G C T G G C C A C A G T T C A A C T A G C C C C T G C C C C T G A T C C A G C A A C A T T T C C G T A A C T A C C C C T C T A G A A G T C A T G C A A A G A G A A A T G A T G A
10	C T G C A G G A A T T	C A T C T T C A T G G A A C A C A G A A	A A C C C C T A A G A A C A C A G A A	G G A C C A A C A G A A T T A C T T G G C A T C J A G G G T T C T T A A A A C T A T T T C G C A G A A C A T T A G T A A A G T T T A A A T A A G G A T C A G G C T A C C A G G A A T A C A G T T A G G A A C A T G T G G A T G A A T A T T C T T T A G T A G A G G A C T T C T A A A G G C T A A T A T T T G G A T A C A T T A G G C T C A T T A T G A A T C T C A A A A G G A G C A T G T A G T A G G G C A T A T C T A A
128	T C	---	---	T A T G C C T C C C A A G A G C C A T C C A C G C T G C T C T A G C A C A A A A A A A T A G A T A C A T C A T T C T G A A T G G G C A C A T T A A T C T G C A G G C T C C C G C J G C J T T C T A A G T C A C C T G C A G T T A G G T C T G C A G A C A C T G T G T A T A C C A T A T A A A T C T G A T T C T G A G C A G G A G G G G C A G A T G A G A A G G G C T G C T C C G T G A A A T A C T A G T C G G
132	G C A G G C T C T C	C A T T A A T C T G C A G G C T C T C	G T G A C T T A G A A A	G A T T T G A G T A T T A C A A A T T G C C C A A A G A C C A T T A A C A A G A T T T A A T A G T T A A A G C C A A A C T A T A A A G A A T T A A C T G T T C A A A A G T G T T A A T C J C J T T A A T A C C A A T T T A T A G G C C A C C A T T A A C T T C T G A A A A G G T C A G C A T A T G C A A C T A A A T T C T A A A G T C C A G T
134	C T G T G T A A T	A G	A G	G G A T G A T G T T C T G T G G C C C T T A T C J A A A G C C C T C T T G C A T C C C A A A T G T G T A A A T T A T T T A T T C T T G G T A T T C T G C T A C C C A T A G T C A C C T G C A A G T G T C C A C C C T
37	T C	---	---	

		TGTTACITTTGA		TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGCTCAGGCTTTAGATAAGTTGTTACTTTGA TTCITTTGCTCTGACAGCCAGTTAGCTGTGATTGTCAGAAAGTTACATTTGTTGTTG
6	81 A	GGA	AGCTAACTGG	TTTCATCATGCTGCTTTCCTCGAAATTTCTTTATTGAGGGGGAGGTGGTAGGCACAGAAGC CAGTCATACGTTTAAATTGACCCCAACCATTAAGAAATAGCATTTCA
0	77 G	CCAGTCATAC	TTTTAAAGCA	CAATGATCCCCCAACATTTCCAGGAAAGGTGCTGCTGTTCTTCCCAGCTCTGTTGGTGGCT GTCAATCTTTGACATTCCTTGTCTTGACGTGTATATTCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCCGGTGTCTGTG
1	55 G	GTCTGTCTT	CAAGATTGAC	GGGGGCACAAATTTAGCTACAGTGCATATTAAAGATAACATAGAAATATCATAATACTTGGTTTAC TGAAATCTGAAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTACTATCCAAAC/CCTGAAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTAAGAAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAAACCCCA
5	122 A	C TACTATCCAA	TTCA	CACCAGCCACCCCTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCACAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG(G/A)GCTGTG GTGCCAAGGACGCATTATG
7c	192 GA	---	---	CACCAGCCACCCCTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCACAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG(G/A)GCTGTG GTGCCAAGGACGCATTATG
7b	179 GA	---	---	CACCAGCCACCCCTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCACAAAAATCCCAATG(A)CTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
7a	128 GA	---	---	CACCAGCCACCCCTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCACAAAAATCCCAATG(A)CTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
0	71 GA	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG(G/A)GTGAGACCAATAGCAGAGTTGTACCTGCAGAACT
5	123 TC	TGTTAGGAA ATAATGACAA GAAAA	TGGTTACAAC GTACCAACAT G	CTGTAACTTACACACATCTCTCTGTAACTCTAGGTTACTTGTATATACAAACACAAATGTAATGCT ACATAAATAATTTGTCATCTATATTTAGGAAATAATGACAAGAAAAAGGCTT(C)GTACAT GTTTGGTAGAGTTGTACCAAGCCATTTTCCCCCAATATTTTCAATCCACAGTTGGTTTAAATCCACAG AAACCACGAATG
3	46 C/A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAGGCTGCAGCGGTTGCAGAGTCTGGGGGAGAAAG(C/A)AACGAGATAAAGCATG GCAAGACCACCGTGAAGATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAGGTGTGACAGAAACAGAGGAGCGTT

[illegible]

19	51	C T	...			GAAAAGCAGGAAGCCAGGAGGACAACTTTTGA AAAAGTCTTTAGCAGCAGC/TJTTCTGGATCCG AATTTTAGTGTGATTTGGCAGGCAATGCGGGGTAACTGTTCCAGTGTTCAGTGTTCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAATTAAATGAATGTGAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
16	116	G A	...			GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTTCATCATCTCTGCTCTG/GA/GCCCCCAGGATAAAGCA GGCA
37	49	T C	CA	TAAGATAACC ATACTAGGTAC ATCOG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTAGTCTTCTGACAA/T/CJGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAAAGACACAGT CATTAAAGTGGAGAAGCCAGCATTTCTAATCAGGCTCAGTGAATCTGCCAAACCAACCCCTTCTGCTATAG CATC
38	25	A C	G	TGACCAATGTG TTTAGAAGCA CTCTCC		CAATGACCAATGTCTTTAGAAGCAG/ACJGGAGAGGACACCCGACGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTAGCGCAGCCACAAAGGTGAGGAAGCAAGGGTGTGGGCCACT
01	114	A G	...			GGACATTGTCCTCAGAAAGTACATTCAAGCCCTGGACGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCGGCTTCTCACCTGACAAGTGG/AGJATCATGTGCTACACTGC AGTGTATAATGCTGCAT
14	99	C T	CC	TGATTCTCTC AAGACTCACA TGAAGGATGG		CTGAGGAGATTGATGCTACTTTACCTGAGGAAACTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATCTTCTCAAGACTCACAGC/TJACCATCCTTCAATGCTTAGACCTATACTAG ACTCAAGTCCCGCAGCGCCCTTAAAGGTAAAGGTAAAGTACAAAGTGTACCCATGGGAGGTATGTAGGCTA CAAAAGAG
19	33	G A	A	CCAGAGCGT CCTATGAATC ATG		CCACTCCAGGCCAAGAGCGTCTATGAATCATG/ACATTTGTTCTGTTATGCTGTTACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
91	84	A T	GTCAATGCATG	TGAGTTCTAT TAAGTGACAAT ATTGTT		TAATTCACATTGCTCTGTTGTGCAATTTATGCTTCTTATGTAACACAATCACCACAATTGAGG TCTTAGTCATTGCATG/ATJGTATAACAATATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
60	117	A G	CAACAGAA	CCATATAATTTA GCAACAATAT AGCC		TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTGAGGTTAGTTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/AGJGGCTATATTAGAAA ATTCTACCTGCATCCCTGGATCTGAACGTTCTTCATGATACT
68	32	A G	AAACA	GGTGAGAGTC AAATTGATAC GATTTTCAGA		CGTTGCTGGTGAGAGTCAAAATTGATACAAACA/AGJCTGAAAAATCTGTTGGCAATCTATTAAAGG CAAAATATACCAGCAGTGGTGTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

7	68	T C T A C C T A	T G A A T A A G C A C G T A T T A A A T T	A A G G C A G C A A A T C A T G A T G	A T G C C T G C G A T A T A C T T T C C A A A T G A C T A G T A T G A A T A A G C A G G T A T T A A A T T A C C T A T T A T A T T T A T T C J A T C A T G A T T G C T G C C T C T T T C C A A A T T A C T A C A A A T T G A T T G T C A C A T G A G G C A C A T G A T C C C A T T A A C C C A A A T A G
3	51	A C A A A	A G T C A A T A T A A T A T G T G T G	A T A T G T T G A T T A G G T A T A A C A A T A T G T G T G	G C C A T G A G C A G A G G C T G A A C C A C T C C C C A A G T T A G T C A A T A T A A A A A A C J C A C A C A T A T T G T T A T A C C T A A T C A A C A T A T A A T G T T A T A G A T T A A C A G T C C A C A G C A A A C A A
3	24	C T C G C T G T	C T G T C A C T G G T C	A A A G G A A C A C A G G A A C A G A C	T T C T G C T G C A C T G G T C G C C T G C T G G T C T G T T C C T G T T C C T T T C A A T G T T C A A C T G C T T G T A T C T G T C C C A C T A A G G T A T C A G G T T A T A T G G G C A C A G G A T G A G G G C T T T G T A G A C C A G A G T T T C T T G G A A T T G C A A C A T T T G G G C A T
3b	117	A G	T A A G T G C A T T A A C T G T A C A A G T C C A C A A A T A C C T C T C C A C C A A G T G C T A A A G C A G T T T A A T A A C A G G T C A A T A T A G T C T T G T G A A C A G G G T G G A A G G A T C C T G T A A A A G G A T A A A T A T T G T T T C C A T A T A T T G A A G A T G T G
2a	94	G T A G G	T C A A T A T A G T C T T G T G A A A C	C T T T T A C A G G A T C C T C C C A C	T A A G T G C A T T A A C T G T A C A A G T C C A C A A A T A C C T C T C C A C C A A G T G C T A A A G C A G T T T A A T A A C A G G T C A A T A T A G T C T T G T G A A C A G G G T G G A A G G A T C C T G T A A A A G G A T A A A T A T T G T T T C C A T A T A T T G A A G A T G T G
5	68	G C C A C C T	T G C T C C C C A T G	A G T T G T G T A A G G	T A A T G T C C T G G G G A G A T A A T A G A A A G G T C C C A T C C C T C T G A T A C C T T G G T T G C T C C C C A T A C C T G C J C C T T A C A C A A C T T G A A G T A G G C C C C A T C C A A C A C T G T C A G A A G A G T A T A C T G T C G A C
8	57	C T	A C A G C C T C T T C A A A T G G C A A T C A A A A G C A C C A G T A A A A G C A G A G G C A A A A T C T G G C J C T C A C C A T T G G A A A G T C T T C G A A G G A T A A G G G A G T G A T G A C T G C T A G A A G A G A A T G A T T G G C C T T
5b	71	C T	A G T C A C T G C C T A G A T G A G T A G A C C A T G T T G T C T T T A A A T G T A C A T G G G C A G G A C C G G A A T G G G A T G C J T A C T A T A G A T A A T C T T T T A A A T G A C T C T C T T G G T C T C T T C A A G A T A T C A C C A G C C A C C C A G G A C A C T G C C A T A T C T
3a	58	C T	A G T T C A C T G C C T A G A T G A T A G A C C A T G T T G T C T T T T A A A T G T A C A T G G C A G G A C J C T G G A A T G G G A T G C T A C T A T A G A T A A T C T T T T A A A T G A C T C T C T T G G T C T C T T C A A G A T A T C A C A G C C A C C C A G G A C A C T G C C A T A T C T
7	158	A G	T G G G C A A A G T C G G G T A T G G C A A G T C A G G G T G G T T A A C T T G G A T G C C A C T T C T G C C T G T C A C C T T C T C T A G A C T C T T G A C C C T G C A G G A G A T C C C T G G C C T C C T G A G T T T A T C A T C T C C C A C C T C A G C C C A G G G C C C T G A T C T G T T C A G G C C C A G J A T C A C G G C T C A C A C T G T G G G A G G T A G A A T G A C G A G
6	117	T C	C C A G T A G G C T G C A A G G A C T C A A T T C T G G G G C A A G T C C T G G T G T G T A G G G T C A G A G G C A G C G A C C T G A G G G A C A C A A A C C A G T G G G A C A C C A G G G T A C T T G T A T C A C C T C C C G C A A C C C C A A G C A G C A C A G C T T G C A G C T C A G G A A A G A C T C C T A C T T C C A C T T G A G A A A A G G A G A G G A A G A A A A G A G G A C T T T G A C A C A C A A C T T G G A

10	110	A G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTTCTTAAATTTGGTGGCCATAGTACTGGCTTCTGTGTGCAATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAGCACCATGTGGCATCC/GTGTGATGGCTGCATTTGTCCAGTC AAATGAGACAACTTCTCTAT
12	226	T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATTCTCTGTACACA AATAACTTTATGGGAGACAGCATTTGTAATTCAAATCAATAAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT/CJCCCTCTGCTAGAAACCAATTGAT
35	105	G C	AG	GAATGGATGGG TCATCTCTCT	CAAAGGTTAGTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAG/GC/JAGAGAGATGACCCATCCATTCTCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
8b	99	C T	TTG	AGAAAAGAG AAGAAGGAA AAA	TGTTTAAACCATAACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAATTTAAACGCCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/C/JTCTTTGCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTAACTATT
8a	38	G C	CTACGTGTT	TTTTAATTTTC TGGGGTGTCT	TGTTTAAACCATAACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAATTTAAACGCC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTTTTCTTTTCCCTTCTCTCTTTTCTG CCCTCTTTAACTATT
16	69	T A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTGACTTTGCTGTAAGCAGAGAAGCACTGTGA CT/AJCATTTATTAGGCCCTCTCTCGCTGAGCCCTGCCTAGAGCAATTTGTAAACATATGGCATTTGGG ACATATCTCTGAGCCCATCACTATTGTGACAAGATTCTCTTTTAAACA
12	119	A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAAGAGTCTTGGGAAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAATTAATACTGAATACCTGTGTGAATCATTTGCTTTTACJACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
16	61	A G	CT	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAATTTATGCCTA/JGJC CAAGTAGACAACTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTTTGTCATTAAAGTCTCTATTCA ATTACCATTTATCGGGTAAATTAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTTGTCTATGCT
7	77	C A	GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGGGGCAAAATTAAGCATATGAAATACCAGTGTGGCAGAGGGCATG AAGCAAGAGG/C/JCTTTCATCTGCCCTTGGGGTTTTCAGTAACAGTGAACATGCTTTGCTCTOC CGGATGAAAGATACCCCTCTATGACTCAGCAATTCACACTCCTAGGTATGCACCCATAACATGGGTG GCAAAAT
19	50	C T	TTCCGAATG	TGACTAGGTG TACTTACAAGA AATCATC	TCACTGTTTAGAAATTTCTCTCTCAGTGAGACCATTCTTTCCGAATG/C/JGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTGCTACCTGAAATTTGTTATTTTTTAA AAATCCTCCCAATATTG

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					TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACTACCATTTGCTGTATTGCTCTTCAGIGT ATCCAAGGATGTCACATTTTGGAACTCTGTAGATCAGAAAAAAGTGTCTTTAAAGTGTGAAGTATTAA ATTAGATTCTATTGATA[CT]GATGTTCTTTCAAGAGGAAATTTGTGAAGAGGATTCCCAATT TGCAATTCATGGC
155	CT	ATTAATTAG CA	ATTCCTCTTG AAAGAAACAT CA		TCATTGACATTTTAGAGTCTTCAGTCTTTATGCTTATTCTTAGGAAAAAAGTGGTAGGAGAA CACAATTGAGTCTCTCCAGATGCAGAGATACTAGAAAAATGC[CT]GAACAGAAAAAATAACCA GAAGATTCATTATGGTTTTTCCAGAACGATTAC
113	CT	AATGC	GAATCTCTTG GTTATTTTCT GTTG		AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATCAGTGCATAGATCATCTTGTAAAGTTC[CT]G JTGAAAAAATTTATGCCAAAAATTTAAATTTTATCCAAACTTTAAGTCGAGATTATAATTGATATTT AAAAAATATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
65	AG	TTCC	GGATAAAAT AAAATTTTGGC ATAA		CTTACTCCAAAGTGTTCAGAGACCACCTTCATCT[CT]TTTTTGGATTATGAATAGAAAGAGT AGGTGTTATTCTCTCTTTTACCAGGTGAAATTTGAGGCTCAGAGACAAGGTAGATGAGGCCCA AGGTGAGTACAGAGCCA
38	TC	CACTTCATTG	CTACTCTTCT AATTCATAATC CAAAAA		TATAATGTTTTGTTCCATAGTTGCCATAGTAGGTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGCCCTGT[CT]CTCTGGCATA CATATAAAGGAAGGCTAA
121	GT	GCCTGTT	GA		TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTATGTCC[CT]GACATGAATAACAATCTTAT ATAATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGCCCTGT[CT]CTCTGGCATA CATATAAAGGAAGGCTAA
43	AG	GC	AATAAAT		TTTTTCCATTTGTTGATTCCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGTTAAT AATATAATAATGATGTTATATATTAACAATTTCAACTCAACAGGAATCCATTTCTGGTAGCAGGT ATA[CT]GGACTCATTTCTCTTGCATCTATTCTAGGTATTTCAGCCCCGAGATCTACCCAGG
139	TC	GTAGCAGGT C	GATGCAAGA AGAAATGAGTC C		AAATGAGTAACCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAGATAACAAGA[CT]ATGAAT AAATGAGTAGTGGAAATGCTTGATAACTGGAGTAGTGCTT
56	GA	AAAGATAACA CA	CAATTCCACTA CCTCATTTATT CA		AACATTTTTTAACCATGCTACATTTACAAACACTGAAAGACAG[CT]G/AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACCTGGAAAGGAG
44	AG	---	---		GCCTTTTGGAGTTAAGTCTTTTGGAGTGTCTTTTTTTTCCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAGAAATAAGCGCTGG[CT]G/ATGATAAACACATCTTC
93	AG	---	---		CCCTGCTATAGGTGAGTTTAAAAATCCT[CT]G/ACCTGCTATGGTTTGGTTGTAAGCCACATCCACT GAGGTATTTCTGCTGCATTTTCTATATCACTCAGCTTTCAGATCCACTCCACTCAACTTGCAG
29	GA	---	---		

					GGATAATCAGTACAAATATGGGGACCTTAAACTGCTGTGATGACGAGTGGAGGGCTGGGCAGTG CCGAGGCGAGGGAGGACAGTGGGACAGGGATGCTCAGTGGTGAGCCACAGCCCTGGCTCTGGA TGGGGCATGGGAATGACAGGTTCCACATCATGCACAGAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTCTGCCCGCCCTA/C/A/C/TGGAGATGTCCTCTAAA
2	232	C/A	---		CATAGAAAGGAGTCTTGAGTATTGTACAGTTTGAAATTCCTTTGAGATAATTGATTTTCATATT TGTGGCTTCAACCTCCATTACCTCTTGTCATTCCCAACATCTTTATAGAGAAATAAAACCCAAATTT CT/C/TTCACCATTTAGTTTGAATATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTACCTTTAATAATTAAAGGAACAAT
4	138	C/T	---		CATAGAAAGGAGTCTTGAGTATTGTACAGTTTGAAATTCCTTTGAGATAATTGATTTTCATATT TGTGGCTTCAACCTCCATTACCTCTTGTCATTCCCAACATCTTTATAGAGAAAT/A/G/AAAACCCAA TTTCTCTTCCACCATTTAGTTTGAATATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTACCTTTAATAATTAAAGGAACAAT
4	123	A/G	---		TGAGTCTGACGACGAGTTGCAGCCAGGGCCAGTGGGAGGGGTCTGGGCCAGTGCACTTCCGGGGCC GCATCC/C/G/TTAGTTCCACTCCTCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATTCTTTGTTCCCTGTTGGA GTTGTTCAAATGTTCTTTTAA
5	74	C/G	---		GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAT/C/CAACAGCAAAACAAACCCACA CAACCCAAACCGTCAACAGCATAATAAATCCCAACACTATTTTATTTTCATTTTCATGCACAACC TTGCCCCAGTGCAGAAAGACTGTTACTTTATTATTGTTTCAAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
2b	42	T/C	---		GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAAAACAA/A/C/ACCACA CAACCCAAACCGTCAACAGCATAATAAATCCCAACACTATTTTATTTTCATTTTCATGCACAACC TTGCCCCAGTGCAGAAAGACTGTTACTTTATTATTGTTTCAAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
3	56	A/C	---		GTGGCCATCGATCTGGACCGTCCCTGCCACTTGTCTCC/C/G/ATGAGCACTGGGTACAAACATCCA AAAGTTCAACAAACAGCACTGTGTCTCATGGT
17	41	G/A	ODC	GGCCACTTGCT	TATACCACCTCCATTTGATGATGGAATGCTGCTGTTTCATGACCACTTTATGGTAGATGGGTACAGAA AGCACCCAGTTTCATGATAGGCAGTTTCAGGTTCATATGTTGACTGATGACCCAGAGTCAACATTCAG TTTCCACCAAAGCCAGTAACAGGCCAAGAGCTGTCTCTCAAAG/A/G/AGAGTAGTTATCTGCAGA AGATGGAGGGCTTGTCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
28	180	A/G	---		GGTCCACGAAATTTGCTGGGAATCT/C/T/GTTTTTCTTAAAGACTTTTGGACATGGTTGACTCC CGAATCATCCGACGGTCTCCTGTTTTTCTGGTGG
05	26	C/T	GGGAATCT	CGAATTTGCTG	GGTCCACGAAATTTGCTGGGAATCT/C/T/GTTTTTCTTAAAGACTTTTGGACATGGTTGACTCC CGAATCATCCGACGGTCTCCTGTTTTTCTGGTGG

46	GA	---	---	TTTTGTTGCTGTGGACACCCACTGCTCCAGGATGAAAGGAGAG[G/A]ATGAGATCAGTTTGGACACTTCCTTGAAATATAAAGAATCAACAGTTACAGTCATGTTGGGACTTCTCTCTCTCCAAAGTGCATCTTGGGGAAAGGGCTCCAGTGTATCTGGAACAGTTCTCTTTCAGGTGGGACTCTTGATCCAGAGAG[G/G]GACAAAGCTCCTCAGTGAGCTGGTGATATATCCAGACAGAACCCAAAGTCTCCGACTCCTGGCCTTCTATGCCCTCTATCCTATCATAGATAACATTCACACAGCCTCACTTCATTCACACTATTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTAGATAAGA
78	AG	---	---	GCAGAGAGAGAACCATGCCAGGGGAGAGGCCACCCAGGCATC[G/G]TGACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGTGAATATACCAAATTCIGCATCTCCAGAGGAAAATAAGAAATAAAGATGAATGTTGCAACTCTTAAAAAA
43	CG	AAGGCACCCA GCCATC	GCTCCTGGCTG GGTCA	AGCAGCCATCACATGATCTGTTTTCCACCCTTCACTGAAAGACACCATTTATAGTTACCCAAGGGCAGAAAGTAGAATTACTATTCATTAATGTTTGACACAATTTGGAATTGTC
53	AC	TT	TCTACTTCTG OCTTGGGT	AAGGGCATGAGACTATAAAGCAGTAGACAATCCCAATACCATCTGTAGAGTTGGAACATGCAATCTTTAAAGTTTATATGTCATATTTAGGGCTGTAGACTTACTTCTCTATTTCTTTTCCATTGCTTATCTTGAGCACAAATGATAATTAATTAACATTTATACATCACCTTTTGTACTTTTCCAAAGCCCC
293	TG	---	---	TTTACAGCTCTGGCATTTTCTCGCCTAGGCCCTGTGAGGTAACTGGGAT
38	AG	GGTAAAGTT CTTTTGCTCT AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCGGAGGTAAAGTTCTTTTGTCTAAAGAA[G/G]AAGGAACTAGTCAAAAATCTGTCCGTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAATGTAACTGT
249	CT	---	---	GGAGTTGCCCCCTCTAAGGGAAGGAGATCTTTATCTTCTTGGTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGGTCTACTTTGGACTGAGAGAGGGAGGCCCCAGGCTGGAGCAGCATGAGGCCAGCAAGMAGGCTTGGGTCTGAGGAAGCAGATGTTTTCATGCTGTGAGGCCCTGCACCAGGTGGGGGCCACAGCACGACGATCTTTG[C/T]
157	CA	---	---	GGAGTTGCCCCCTCTAAGGGAAGGAGATCTTTATCTTCTGTTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGGTCTACTTTGGACTGAGAGAGGGAGGCCCCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAGGGCTGGGTTCTGAGGAAGCAGATGTTTCATGCTGTGAGGCCCTTGCAACCAGGTGGGGGCCACAGCAACGACGATCTTTGGT
34	CT	OCTGAGCCCTC AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACATGAGAGCCCTGAGCCCTCAAGAACTC[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC
61	CT	CCTAAGCATTG OCTGGC	GCTTACAGGAG AGACTAGACA GGAA	TGGAGTTTCATGCAAGGGCAAAAGGCAGTGGCATGCAAGCTGTTAA
93	TIC	---	---	CTGTGAGGGTGACGTAGCATTTACCCCCAACCTCAATTTAGTTGCCCTAAGCATTGCCTGGC[C/T]TTCCTGTCTAGTCTCTCCTGTAAAGCCAAAGAAATGAACATTCCA
				CCCTGTTCCCATGCTGAOCTGTGTTTCTCCCCAGTCATCTTCTCTGTCCAGAGAGGTGGGGCTGGATGTCTCCATCTCTGTCTCAACTTAT[C/G]TGCACTGAGCTGCAACTCT

b	44	C T	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCCTCCCATCATCTTTCTGTTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGCTCAACTTTATGTGACTGAGCTGCAACTTCT
					TCTGAGAGAAATGACTTGTGGGAGACACCTGCAGATCCTCATGGTTTGTGACAGACCCCTGGTGGCT CAGTGGCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGTCCCG TCCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC AIC/AACACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
b	206	C A	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCTGCAGATCCTCATGGTTTGTGACAGACCCCTGGTGGCT GCTAGTGGCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGTCC CCCTCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAC CACACACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
la	56	A C	---	---	CTGAATCCCTCTCTGCTGGCTGGATCCGGGGACCCCTTGCCTTCCCTCTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAGTTGTGAAGCAGAGAGAAAGCTGGAGGAGGCCGTGGGCCAAT GGGAGAGCTCTGTATTATTAATATTTGTCGCCGTGTGTTGTTGTTA
3	54	C T	---	---	ACATATCTGAAAATGTTGAAGCCTAAGCCAGGAATAAAGAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAGCTTGATTACACAGACTTCATGC
1	62	G A	---	---	GTGTGAGACCATCATGTGCTGCTAGTCTAGGACCCCATCTCCTATTATTCAGTCTCTCTATATA CCCTCTAGAACAGAGAAAGCAATTTTAGGCAGCTATGGTCAAAITGAG
4	47	T C T			AAGGCCAGATGCACATCCCTGGAGGAGACATCCATGTTCCGAGAGAAACAGATAGATCCCTGTATT TCAAGACCTCTGTGCACTTATTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
3	52	A G	GAAGAACAGA	A	AAAGAACTACAGAGGACGATGTCCAAACAAAAAATGGCATCACTGTCAAAAATGGAGTCCACT TCTCCCCGCA[G/A]ACCTAGGTCAGACTTCCCTTTCATCTT
6	76	G A	CGCA	T	TTGGACAAACCTAGAAATTTCTCCCTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGAAATAA CTCAGAAATATTGCTGCTGCTTAAAGCA[G/A]TACCCCCCTACACACACACCCCTGTCTCTC
3	94	G A	CA		TTTGGATTGATATCGTGAATCTCTCAGCCGAGAAATGGGCTGGATTGCTGCTTGGTTAATACAT CTTCCCTAAAGAAAGATAAACACAAAATCCATTCAGGTAGCTCGGCACCACTAAGAA
5	48	C T	---	---	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGGCCAC[G/V]GTCCCTAATGACACCCACTCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAAGGGAGGAGCGAGCGACTCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG
4	37	A G	AGGAGCCAC	CATTAGGGA	

68	G A ...	GCTAACACITTT TAAACCCGT	...	CATTATTTTG AAAGCTATTCA GACA	ACTGGTGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCAGAGGGCTTGCTGGCTACTGG [G/A]TGTTAGTTGCAGTCTGTGTGCTCCCTCTCTTATGACTGTGTCCC
142	A G CTC	GTATATTACA ATGATCACCG	...	CCACACAGAAC TATTGTAAAC AA	TTCTGAAATATAACACGACATTGAGCTATTTAAACTGTAAATTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACATAAAACATTAAATGCTAACACATTTTAA ACCGTCTC[A/G]TGCTGAATAGCTTTCAAAATAAATGTGAATGGT
70	G A ACTGA	TCACGTTGGTCTCTCAGATTCTGAGGAAATGCTTTGTATTTATATACAAATGATCAACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGAGGGCTGTTTTTGT
314	C A	TTACAGAAACTTGCCCTGTGCTGTCCCTCATGCTAGGGCGGAGGGTCTTTCTCTCTCTTCC TACCTACCCCTTTCTCTTGGCCAGGGCTCGTATCTCTACCTTTCTTGTCCCTGGCTGGCTGCAC AGAGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCACAA AGTCTAAGGGAACCATGGCTGCCCTGGGAGGAGCAACCATAGTCCCT
96	G C	TTACAGAAACTTGCCCTGTGCTGTCCCTCATGCTAGGGCGGAGGGTCTTTCTCTCTTCC TACCTACCCCTTTCTCTTGGCCAGGG[G/C]CTCTGATCTACCTTTCTTGTCCCTGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCA CAAAGTCTAAGGGACCATGGCTGCCCTGGGAGGAGCAACCATAGCT
182	T A	CCAGATGTGCCATCACGTTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTCCACTAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATTTTGAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTTGAAGAATATATG[A/C]AGAAACACAAAGGCTT GAT
78	C T OCTTGCCA	CCAACAACAT OCTTGCCA	...	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCATCTCCCAACAACAT CCTCTGCCA[C/π]ACACAACAACGTAAGTTTCATTTGGGCAAA
104	T A	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTCAACTCT TAAAGACATCTTAAATCCTGAATGTAAACAATTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
75	A G	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTACATTTTGTATTAT GCTCTTA[A/G]TGATTACAGACTGATGCCAGACAAACCTTGGGAAGA
79	T C TTGG	CTTAGAAAA TCTGCTTTAAC TTGG	...	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGGGCATCTGTGTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAATCTG CTTTAACTTGGT[C/π]ATCTCTAATTGTTCCCTAGGAATGACTGTCCAAAG
107	T C GTTCC	TGCTGGGCTGT GTTCC	...	GGTCCAGAAGA GCTTCC	TGCTCCCTGTCCATCTGAGTGGACCCAGGACCCCTTTGAGGAGGTGGGTGAAGTCTGCTCTT GGCAGGAGTTTGTGACACTGCATTGCTGGGCTGTCTC[C/G]CGGGCTCTTCTGGACCTTGACCCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCTGGGAGGGTGGGTGAATAAAGGCATACTGTCT

4	131	T A A A A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGAGGGGAAAGAGCAGAGTTAGAGAAAAAGCCACCGGAGGAAAGG AAAAACATCGCCCAACCTAGAAACGTTTTTCATTGGTCATTCGAAGAGAGAGAGGAAAGAAAAA TT/AJACAACTTTCATTCTTTCGACGTTTCATAAACATTTCTACATA TCCTGCAAGAAGTCTCAAGCCTTTTGAATTTTGCAATAAAGTACAGCTTTCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAAATTTAAGTGAGA[A/C]TCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAAATCTAAATTAIGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTCA GTGGCCACTACATGTTATAGAAACCATCATCTGTGCACACAGCACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAAAAGTGCCCATTTAAAGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAAT/AJTTCAGAAC TACACAATGAATGCTTTTATTCGGTATGCATCCACATTTAGCATTTAGTGGTCTGAAACAGCAAG TGGAAAGACGAGCAATTTGCCAGGAGGTCAAGCCCAATTTGCGGATCTGCTGTGCACACCGG GTTCTTCTTAATCCCTGCTGAGGATCTTG[A]GAAGCAGCAGCAGCACCAAAACCAAGGCATGCA CCGGATTCAAGGTCTTTTGTCCAGTTGTCAGATTCCAACTAGACCCCA AACAGTACCAACCAACCATGACATGACAACTGCCAGGAGGCTTGTCTCCCTCCCTTTCGCTCC ATGTGCCTAGTCAGCAAGGTGCGGGAGGCACCGATGTTAGCTTGCCTCCAAAGGAGATTACAGAGA GAGGCTTGGGAA[A/GC]GGAAAGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAACCTGGTATGCTGAA ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGTTGTTGGCTTCCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGACGAGGAGCAACCGTACCTGAGAGGGGATGGGGCTCTCTACAAAA GAATATTTGGGGCAGAACCCCTGGAACCTGGCCACAGGACATCCCAATATCCCTCCTCCTCAGGG CTCACCCCGACATCTCAGCCCAATGAAGGCTCTGAA GGTGAGACGGGTTTATGTGCACATTTACACAGCTCACAGGCTGCGGTGGGTGGCGGCCATGCTC CTGTGTCGGGCTGCTCTACAAGGGGTTCACTTTCTTCCACCACACTATGTACAGTCAGTGTCCAA GGTGATGGGCTACAGTGTGATCAGTGTGATGCTGTACACACATTTTACATAAATTACACAGACTC ATACATGAAAAA[A/T]AAGAGCCTAAGGGCTGTATTTTAAATGAGAAAAA AACTGTTTACAAAAAGGCTTTCACAACTTCATTACTGAATGTAAAGTCAATGACTGTGTTT TAAATATGTACCAAGGAAATACAAATTTGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACCTGCACAAAGGTGCAGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG [G/A]GCATCTTCTCACCTTAACCTGCAGCTGTGCAAGATGCCTCAGTGTG
5	148	G C			
21	41	G T			
25	215	T A			
20	202	G A			

3	184	G A ---	---	TGGGGTGCCTTTAGACTTCATTTCTAGAGCAGGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAATGGCTTGTGTTCCAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAGGCGATGTTCTTAACGTGCCCGTGAGCAG
3	204	G A ---	---	ATGTCAGAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCCACTAATCCACA GATCTGAAAAGTACAGCTCTCCAGGTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGCAATATGATCTCCCTAAAGCCCCAGATTCTTACTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
3b	201	G T ---	---	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAAGCTACATCCTTGCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
3a	85	T C ---	---	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGT[G/C]GCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT GGTTTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAAGCTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
1	149	G A ---	---	TTCAAGTGATAAGGACAGGCTAGAACAGCGTTCCCAACCCCTGGACCAATACAGTGTGGACCAAA TAACCTTTGTTTCAGGGGACTGCTTACACATTTGGGATGTTAGCAGCCTCCGTTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACCCCTCCCCAACCAATCATGACAATGAAATGTCCTTAGACATT GCCAATATAOCTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGGTT
5	110	G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCCAATGGTGGGATTGAAAGAGG GAAGTCGATAATTTTAAACATATGGTTTCTTGGCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACCTAGTGACCCCATGGCTAGAGTTCCTGAC CCCTGCTACGGGAACATTGAATGCA
3	199	T G ---	---	ACCAACCGTTGGCAAGGCTCCCCAAGACTACGACCCCACTTGGTGCTTACCTATGCCGGGTG GGATTGAAGAAATAACCAATAAATAATGCTACAAATTTTCCAGTAGTTACCAGGCCACCGCCTAT TGGAAGAAATCATAAATGTAACCCCTACAATGATTGCTCTCTGGCTTGGTCCAGGCATAGAGTT[G]GGCCTACAACCCATTTTATCAATTGAACCCCTCAGAACCATCCAGTTGGGGCT
1b	157	G A ---	---	TGGTATTTTCTTTCTTAAATGTTATGATTAAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAATAAAGTATAGTTGAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGAATGAGAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCAAAGGAAGTTAAGT

1a	48	A G ---	---	TGGTATTTTCCCTTCTAAATGTTATGATTAAATAGTGCTCTTTGTJAGJGAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAATAAGATATAGTTGAAACCTCTAAACAATTTTAGATTTTAAAGGCC TAGGAAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAAGCACAACAGAAAAAAGAGTGCTGT GGCTAAGGGAAGCCAAAGGAAGTAAAGT
6	61	C A ---	---	TTCTATTAAATCCTGTGCCCATTCGAAGACTGCAITTCAGTCTGCATGAGCCTTAGTTTCJAJTAA AAGCCCCCTCACACCGAGGGACAATGTTCAAGAACTAAATGACTGACGTGAGCAATTTCTCTGTATTA TACAAACTGGGACCAAAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAAGTTATTAACTT
1	153	C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATATAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTTCTAACGCTCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTTG TGGCAGGACTGTGCTTCJAJTTCCTGTTGGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
6	221	G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAACTCTGAGGCTTTAATGGTCCCTTGCTCTAAC GCTTTTGGTATACCTTCTCTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTGACTTCTTACATTCCTGGAACACTAGATGAGTTAGGCTCTCTTTCATCT CAATTGAAAATCTAGAAJGJAJAAACACCTAATTTGGCTCATCTTGGATCA
0	49	C T ---	---	TTTTTGTTAAGTCTTGTGAAGCCACACAGAAAGTGATCTACTCTCTTTACJCTJAAAGTTACTTTGCA TATATTTTATGGGGATGATTCTATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATCCATTTCCCT TTGTTCAAGGAGTTCTTATTGGCTCTTTCTTAACCCCTTAACCATCTGCTTATTCTCTGCTTGACA CATGCTATTATCAAGGTGACATT
5	31	A C ---	---	GAAAACCTCGTTGGCTCAAAGGAACTGTAGJAJAAATTCCTTTTATTTTATTTTGTCTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTGATGGCAGCTGCTCTTTTGTGTGGTAAATCCTCTAGT GGGCACCTTGCAAAAGCAATTTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAAG TAGCAATGGAAGAAAGGTTAATGGA
12	41	A G ---	---	AAGGCCAGTGGGAAAGCAGACAAAACACTCCAAGAATACJAJGJAGATATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGCGCATGTGACACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGTGCTTGGCCAGTCCCATAGTAGGTTGCCATAAATAAAC AGTGACTAAACTGAGGTAGAGTCACAGAAAGAAATTTCA
52	179	C T ---	---	GATTCCTTGGGACATGCAGAGCAGATACGGCAAGGCATCTTGGGCAATTTGGAAGGAACGAGCCCTA ATTATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAGTGGGACAAAAGGCTTGTCAJCTJCTGTGACAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

1	167	A G ---	---	TGTTGAGGAGCTGTAAAGGCTGAAAGAAATAGTCTCTGCTCTGGTCTTTCGTTGGAAATGGATGAGTCTCT TTTACAAAATTTTCTCTTGGCCATGGGTGTTATGTTTAGAATCAIGGAGTTGGAAGACTTAGATTCA ATTGGGGCTGTACAGTTTACTGGAAGTTGTA/GTGAACCTTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
1	198	GA ---	---	GGTTTCATTTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGTATACACCTACAAAACACACATTAAACCTCCTCCCACTCTA CCCGCCAAAGTCTACCTTTTGGTCTTTTATTTCTGCTAATGACCATACTATTTTCCCAATTAGA[G/A] CCATGTCATTTTCAGAAAAGCAGTATA
3	164	CA ---	---	TTTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCATTTAATT TGCACCTTACTTTGTTGGCTACACACATTGCTTCCAAATTTGTAATTTCCCTAACACAGCAAGCATAACT GATGTGCCATCTTTGTATTCCTTAAAC[A/A]AAAGAAAAGTGTCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCACTTCTGTATTTCCCTATTCAGCATTTCAATGATTA
3	72	A G ---	---	AAAAAACAACTTCATTTGACATTTCTAAGAAGATAAGAAAAACACGATCCACTGTGTGTTGCTT GATTTA/GGGAGATAAAACCTGATCTCTAAGAAAATTTAAACAAAGCAGTACACTAAAATAGCCT TTGTGTGTGTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAATATGTTTCATATCA CTCTAACTTCCACATAGAGCAATTAATATAGCA
5	111	CA ---	---	TGAAGGACCACTTCGAATGCCCTACCAAGGTAAAGTAAATCGGAGGGGCGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCCGGTGC[C/A]AAAAATGTTAACACTGATGC TGCTACAAACGCCACATAGAAATCGGTGGTAGATTGCGGTTCTTAGTAGTAGCTAATGTTTAGATA TGATTGTTGAATTAATTGTTGCTGTGTTCTGGTG
8	177	A G ---	---	CAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTGATGTAAGGTGGGGCAGGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAG[A/G]TCTCCAAATTTCAAGGGGCTCCC GTGGGATGGTGGAGCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
1	34	T G ---	---	GGGATTCATGTGTCTGTCTCATCCAATAAGCAC[T/G]CATGACCTCAGCCCCATCTTTCTTCCC TATGTTCCAGAGACAGAATAGACTGGCCCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGATCCTTTCTAGTTGA
7b	88	T G ---	---	GTGAGAGCGAGGCTGAGCCTAGAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGATTTGAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTCTGTGTTGTTGTTGGGTATCTGCCAGTGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTATAAAGTATATAATTTTTTATGTTTGTGTTCTGA

a	44	T C	...	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCT/CITTCGTTAACTGTATGTAC ATATATATATTTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAAGTT ATTCCTGTTGTTGTTGGTATCCTGCCAGTGTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCAATTTGTAATAAGTATATAATTTTTTATGTTTTGTTCTGA
	197	T C	...	TCCAGAAATTTCCCTCTTCAGCTCATTTTGTCTCTCACAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCAATTAATTTCCCTTCAACAATAATATTTTACAGAAGCAGGACAAATATAGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAACAATTTT[C/JAG TTTGCAATAGAACTAATCTGGTGAAATTTACCTAAACCTTGGTTATT
b	57	GA	...	AGCCGAGCTGGACTCATGGATGTGACCCCTTGTCCCTGCTCTTCTGCCCTGGG[C/AJCTCATGTA TCTGGCAGCTCTGGTACCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGAAGCT GAGAAGGCACAGGGCAAGGAGCCAAAGGACACAGAGCCTCAGCCAGGATCCGCTCCTCATTTT ATTGGTGATGATGGAATGGAATGAAATCAGGGGGCTGCTACTAGAGCC
	69	GC	...	CTCTCTCTTCATCCCATCACCCCTAAATAGGTAGGTGAGGAGGCTGGGAAGAGGTGGAGGAGG G[C/JAGAAGTGAAGGAGATAGGAAGGATATACCTCTCTGTTATTTTAAAGAAACATTGTTT GGTGGCAGCAATCTCCCTGTCCTATCAGTGTAGAGGCCCTAAATTTATATCTATAAATATATAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATATTGTCAAAAGTTTAAAT
c	242	T C	...	GAAGGCAGCTGGATCACTCCGCGAGTCTTGGCAGCGCTTGTGTGGACACAGAGCTCCTCCT CAGGGGCTGGCAGCTCAGCTCTTCTGTATGATGTTTGGTTAAACACTGTCAATAATAGAGAT GTGCCAGATTTAGATTTCTTACCCCTAATCTGTTTAAATATGTAACCTTATCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAA[C/JACAACCTTT
	310	T G	...	CTCCCTCTCTATGCTCTCAGCAGCAGTGGGGCACACTGTTCACTCTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAATAAATACGTACATTTTCGAGGTAATGGTA
d	131	T A	...	TTTTGAGTCAAGACTTAAGGGCCCAATGAATTAATATACATACTGCATCTTGGTTATTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCAACACTTACACCAAC[C/A] ACTGAATGAAGAAGTATTTGGTAACCAAGGCCATTTTGGTGGGAATCCAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
	99	T C	...	TACAGTTCAGCCGTTGCCCACTCATCTGCGCGCTTGTCTTGGTTGGGGGCAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTATG[C/JAGCCCCAAAGTACAGCCTGGACCAACCTCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGAGCTGAGCCCTGAGCCAAATGGGACAGTTACACTTGACAGA CAAAGATGGTGAGATTGGCATGGCAATGMAACTAAGAGCTCTCAAGTCA

3	101 A G ---	---	TTTCTAGGCTGTACAGTCTGATGATGATTTTTTATAAAATATTTTATACATCTTGTGAATTTGGATCTTT TTTACTTTGAGCATATATTTAGAATATGTGTAAGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGAGGTTTCAATTTGGAATAGTTAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CTACCAAAATAGCCAGTAGTATCTGAAAAATGAAAAATAAATGAAGTAT
6	137 G T ---	---	GGCCAGGAGATTAGCAACAAGGATTCATTCTGTTACTTGGCCCTTTTATCTTCCCTCTTGCCC CAGTCCCTTCTCCAGCTTCATGTAAGCTCTGCACAGACAAGACTCAGTGTCTGTCAGTGTCT [G]TCTACTCCTCAGGTGCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTTGGCAAAATGTCATCAG
	252 C T ---	---	ATTGAAGATTGGAGGGCTTTGCAGAGGAAATAGATTTCAATTGGATCCCCAAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTACGCCAGCTCATTGGCCAGAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAATTTTAGTTTAAAAATGTGTCATTTTGTCTGATTTGGCATTCCT[C]
	218 C T ---	---	GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCCCGGATCAAGTCTGGCAOC CATGATGGAACCTCTTGCCATGTTTAGTACCTGGACCAAGTAGTATCCATCTGACTGACTTTTAAAA TTCTAACAGCCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC[C]TGTAAACAAAGCATAGAAATTTCTGAACAAC
3c	146 T C ---	---	TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTTG[C]CCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
3b	146 T C ---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTTG[C]CCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
4	165 G C ---	---	GAAGACTGAGTTTCCAGGAGTTGCAGCCGTTTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCACCCAGTNCCTTCCAAAGAGGCTCTCAGACTACCTCCTCCATCTCCCT CTCCCCACACACACAAATACAGAGATTG[C]AATTTCAGGAGCCAGTTTCTAGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTCTTAGTTTCTCAANTGGGAAATGG
6b	25 A G ---	---	AGCTTTTGAATCCAAAACCCACATGAGCTTGAAGTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAAGAAATACAGAACACCCCTGTGGCTGCCTGAACGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCTCTCTGCTATCCCTGATGACTGGGCAAA

				TTCAAAATTAACACCAATGGGTATATTATAATTTINGCTCTATCCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCTTCTATTGTCTTGACGTATTAAAGTATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCCTACCCCTACTTGGCTCTGACTTCCCTTCTGCGCT GAACCTTCTCTGCTGGCTGTCCGCTTCTCTCTGCTGGCTCCAAATAC
66	GC	---		TGAAGCCCTCTCTATACCCCAAGTGTCTTTATCTTAAATGCTGTGGTGCAGATATCTACCCCTTA GGATATTGTGAGAAATCAATAAGTTTATACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTAGCTATTJAGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAATCTGTCATGGTTT
b	156	AG	---	TGAAGCCCTCTCTATACCCCAAGTGTCTTTATCTTAAATGCTGTGGTGCAGATATCTACCCCTTA GGATATTGTGAGAAATCAATAAGTTTATACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTAGCTATTJAGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAATCTGTCATGGTTT
	156	AG	---	AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTTCATCTCCJGJTTGTGTTTGGC CAATAATATCTCCCGAGGAGCTCTCTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCCACAAAGCACACATTAGAACTTA
b	119	GA	---	AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTTCATCTCCJGJTTGTGTTTGGC CAATAATATCTCCCGAGGAGCTCTCTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCCACAAAGCACACATTAGAACTTA
	113	AG	---	AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTTCATCTCCJGJTTGTGTTTGGC CAATAATATCTCCCGAGGAGCTCTCTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCCACAAAGCACACATTAGAACTTA
	119	GA	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAAGGAAATGATAAGAGCACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCACTGTTATGGCCTGAATTTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTGTACATAA
b	123	CG	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAAGGAAATGATAAGAGCACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCACTGTTATGGCCTGAATTTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTGTACATAA
	123	CG	---	TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTGTACATAA

198 T C	---	AGGTTCTGGACTGATGCTGGGAACAATTGGGTCGAGAAATTCCTATTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAGGTATCCTAGTCCATCCCTTTATAGGAACCTTCTGATCTATTGGGA AGTCTCCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAAGGAATATTCJG ATCCCGCATGCAACATTTATTCAGTGAAACATGATGAAATGAACATAAT
205 G A	---	CACATCCCAAGGGCTCTGGGGGANGAGCGTGGGACGCTGCCGGGAGCGATTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCATCCATCTAC TCTG/AJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
205 G A	---	CACATCCCAAGGGCTCTGGGGGANGAGCGTGGGACGCTGCCGGGAGCGATTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCATCCATCTAC TCTG/AJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
90 G C	---	GGCTGGGATGAGAGGTCTACTTGTGTTACTGGAGGTTTCTACTGGCTTGCTAGAACTAGNAAAGNA GAAAGACAGNAGATTGGCTAACG/CJCATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAACACANTAGGTGCACACANNNGGGTT TTCTCTGGTCATAGAAATCTCTAAAGGGAATCATGACAGATTTCTTGGCTTTA
90 G C	---	GGCTGGGATGAGAGGTCTACTTGTGTTACTGGAGGTTTCTACTGGCTTGCTAGAACTAGNAAAGNA GAAAGACAGNAGATTGGCTAACG/CJCATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAACACANTAGGTGCACACANNNGGGTT TTCTCTGGTCATAGAAATCTCTAAAGGGAATCATGACAGATTTCTTGGCTTTA
167 C T	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCTCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
155 G A	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTACC CTGAGGAATTTATCAAAGATG/AJTTAAGTTATCTCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
181 T C	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATATGATGTCCTAGGTACATTTGTTTTATTGTTCTG CGAATGTTGTATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTTCTGTGTTG CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCTACTATTCJGCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTTATTGCTCTGGCTTCATTTTGAAATNG

17b	204	G A	---	---	TTGCCATTATTTAGAGATAACCCACACACCTTGGTGTCCAGGGTTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATCCAGCCACCGCAAACTTCTCCTCCTCCTGCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCAGCTTTGTTAGGATGAACCTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
18b	147	C T	---	---	GCATTGAGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGCTATGTAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAATACAAATGATGGTCTCCTGAGTGTCTGAATGCGCCAGGTGGC TAAGTGTGGGGC/TTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
18a	124	C G	---	---	GCATTGAGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGCTATGTAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAATACAAATGATGGTCTCCTGAGTGTCTGAATG/G/GGCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
14	124	T C	---	---	AAGTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTCCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGNT/CJGNCAANT AAAAATGATTTGAAATTTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
15d	202	C T	---	---	TTCTCAATCCAAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTG/TTATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAAATNACACTGTTTAAANTGNNTATG/C TTAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
05c	46	C T	---	---	TTCTCAATCCAAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTG/TTATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAAATNACACTGTTTAAANTGNNTATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
15b	153	T C	---	---	TTCTCAATCCAAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/CJTNACTCCACTNATGCTNACAAAAATNACACTGTTTAAANTGNNTATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
05	202	C T	---	---	TTCTCAATCCAAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAAATNACACTGTTTAAANTGNNTATG/C TTAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

				TTCTGCATTGGAATAGTTGACCTCTATGAGNNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCCTGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCCTGAGGC
b 248	A G ---		---	TTCTGCATTGGAATAGTTGACCTCTATGAGNNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCCTGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCCTGAGGC
			---	TTCTGCATTGGAATAGTTGACCTCTATGAGNNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCCTGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCCTGAGGC
240	A G ---		---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGGGCAATTCGTGAGATTGCTTT CCTACCCCTCTTAAATGTATCTTNCNTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTGTTTCTCTGTAAGNTGTTT
b 118	T C ---		---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGGGCAATTCGTGAGATTGCTTT CCTACCCCTCTTAAATGTATCTTNCNTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTGTTTCTCTGTAAGNTGTTT
			---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGCAACCNCTGTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCTTGTCTCTCTACCCCTCAGAACTTCTTGAAGGCGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
ib 169	T C ---		---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGCAACCNCTGTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCTTGTCTCTCTACCCCTCAGAACTTCTTGAAGGCGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
5	165	CT ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGAAGAACGCTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTACGAGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTCTGAAAGTTGGTAGCTACAGGCTCCGCCAAATGTAGT TCTTGNCGTGAAGTCTCTCTTACTGAAGAGGCAATGGTCCATCTCTAAG
7b	162	T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGAAGAACGCTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTACGAGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAAGTTGGTAGCTACAGGCTCCGCCAAATGTAGT TCTTGNCGTGAAGTCTCTCTTACTGAAGAGGCAATGGTCCATCTCTAAG
7	175	C G ---	---	TCTTGNCGTGAAGTCTCTCTTACTGAAGAGGCAATGGTCCATCTCTAAG

41b	136	G A ---	---	TATCAGCATGATTGGCTGTGGACACAAAGTCAATTTGACITTTGNTGNNNTCTTTCTNTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTNTCTTTGTTAAATATACCCCAAGC G/AJGGATTGTGATGGATCTGTTATTTCTCTGTCTGTGGACAGAGAGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCGAGCCCACTTGCACTTAGCAAGTGT
49e	192	G C ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAATTTCCATCTCTGA(G/C)TTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
149d	264	C A ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
349c	192	G C ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAATA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
349b	264	C A ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
349	264	C A ---	---	CTGACAAATGTCATATCTCACTCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
1403b	57	C T ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTTTCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTTGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTCA TAATCCCAAGTGCCAAAGGGTTGATCTGATTGT
1403	58	T C ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTTTCCGAAT TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTTGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTC ATAATCCCAAGTGCCAAAGGGTTGATCTGATTGT

c	31 C T	CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGGGCAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGAGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGCGAGGCCCTTAGGTCGGTATTAAATGTTGCTTTGTAGAAAAGTCGC
b	31 C T	CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGGGCAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGAGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGCGAGGCCCTTAGGTCGGTATTAAATGTTGCTTTGTAGAAAAGTCGC
			CCATGAGCAACAGCATGTTCTACTCTGTGATGTGTATGTTAGGGGGCATGTATCTGTATTTCTT TTTATTCTCTCCAAAAGAAATTTCAATATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA TGTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGTATGTGCTTCCGTGGTNAOCTTCTCTCCACCATCACTGTGTTTT
	172 A	TGCCCTACTCTTTGTTGATCCCAACCATTACATTTTGTAAATGGAACTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGTCAACCTTTT/CJATTGAGTCT CTGCCACATGCTAGTAACGTGTGAGTGATGGTGCATCAGTATAATCTGAGCCTCCCAAGGTACAGC CTTTCACTACTTATCATATATTGGCTAAGGTATTCATCATATTGGCTAAG
2b	122 T C	TGCCCTACTCTTTGTTGATCCCAACCATTACATTTTGTAAATGGAACTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGTCAACCTTTT/CJATTGAGTCT CTGCCACATGCTAGTAACGTGTGAGTGATGGTGCATCAGTATAATCTGAGCCTCCCAAGGTACAGC CTTTCACTACTTATCATATATTGGCTAAGGTATTCATCATATTGGCTAAG
2	114 C T	GCGAATTTAATGACTCCAAAGGTAGTAATCTCTTCCCCCAAAAAAGGTTTAAAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACTTGGAGTAAAGGTGTGCTGTTTCTGGCAAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG CTACATTCACCTTATGATCTCCAGCAGGTTCTTCCA
0	97 A G	GGTACACAAAGAAATGCTTCTGGAATCTAC/AGTAGCGCTTAACATTTTGGCTGAGTATTATC TGTACATGTGTAATGTGAACCACTGAAGCTGGGCAAGAACAAATCTAGGAAAAGTACAATTAC TGGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTATGTTCCTCATCA ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAGAAATATCATATAAAAAAT
10	31 A G	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/AGTAGGTAGGATGAGCATCACACTTGGGAGGACATATTTCTGGAGTACATATCCTG GGTGTAAATTTCAATATATCTACTAAAGCATGACTTCTAGAAAAATTAATTAATCTTGTCTCTCAA GGAATGGGAATACCTAATAACAGTCTTATTGAGGAAAAATACTGGAATCA
33c	77 A G	

103b	77 A G	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATAGJAGTAGGTAGAGCATCACACTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGTAAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATCTTGTCTCAA GAAATGGGAATACCTATAATACAGCTTATTGAGGAAAATAACTGGAATCA
137b	112 C T	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TTCGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGGAAGTCTGGGGAACGTTTTAGCTTCTGCTGGCT
137	112 C T	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TTCGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGGAAGTCTGGGGAACGTTTTAGCTTCTGCTGGCT
340b	79 G T	TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT/G/TGAGAACTGAAATATTCAGCACATACAAGTGTGACAACCACTTGTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTTACTAAAGAGTTCTTAAGAGCCATGAAGAAATTAAGACT ATCGCA
840	79 G T	TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT/G/TGAGAACTGAAATATTCAGCACATACAAGTGTGACAACCACTTGTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTTACTAAAGAGTTCTTAAGAGCCATGAAGAAATTAAGACT ATCGCA
879b	110 C T	GGGCTCAGTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTTCTTTTCATAACTACTCCCCG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/TTCGTGCAAAATAAACTCCCAAA AAGTGTAGTCCACAGGGTTTAAAGTTC/TGTTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAG/AAAAAAACATTGAAAATCTCCACAGAGCCCTTTACCCACT
879	110 C T	GGGCTCAGTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTTCTTTTCATAACTACTCCCCG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/TTCGTGCAAAATAAACTCCCAAA AAGTGTAGTCCACAGGGTTTAAAGTTC/TGTTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAGAAAAAAACATTGAAAATCTCCACAGAGCCCTTTACCCACT
900b	119 C T	TGTTCTCTGGTCCAGGACCGGCTAAGTCTTGTCTGCATAATGAATAATCACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCACTTACAGCTGCAAAAGAGG/C/TGCTCTGAGAGGT AAAGTCCCTGCCCAACCGGCACAACTAGAGAGCAGCAACAGGTTTGAACCCAGCTCTGCT GACTTCAGATCTGTGCTTAACTGCCATGAGAAACCACTTTCTTTGCTCC

10	119	C T	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGCTGCAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTCCCTGCCCAACGGCAACAAGTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTCCATGAGAAACCACTTTCTTTGCTCC
13c	165	C T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAAGTATAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGAACCCAGCC[C/T]CTCTGAANCTGGTCCACGTGGAGATAGTGAA TACAGGGCACCCGNTGAGCAITTCAGATGACTCAAGCCCGGCTGGAGTAT
13b	165	C T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAAGTATAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGAACCCAGCC[C/T]CTCTGAANCTGGTCCACGTGGAGATAGTGAA TACAGGGCACCCGNTGAGCAITTCAGATGACTCAAGCCCGGCTGGAGTAT
43	164	C T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAAGTATAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGAACCCAGCC[C/T]CTCTGAANCTGGTCCACGTGGAGATAGTGAA TACAGGGCACCCGNTGAGCAITTCAGATGACTCAAGCCCGGCTGGAGTAT
60c	270	A T	CCAGGTGAGGCTGAAGAAGGAGGAGGCAATTGCTGTTGGAGTGAAGGATCTGGAGAAGCACCCCT GCAGAGCTTCAATCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAATAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACCTTAAAATGCACCTCCCAACTTT
60b	270	A T	CCAGGTGAGGCTGAAGAAGGAGGAGGCAATTGCTGTTGGAGTGAAGGATCTGGAGAAGCACCCCT GCAGAGCTTCAATCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAATAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACCTTAAAATGCACCTCCCAACTTT
177	203	T C	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTCTTCATAGAGTNTGTTTTAGTCTCGTAATACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAGCCCTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTTT /C/TAAACAAACACTGGCTGAGGCTGTTGG
112	102	T C	AAATCTAGAGCCAGAGTCAAGTCAAGTATTAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATCTGCACAAACTAGCTAAAATC[C/T]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTGAGTCACTTTTTTCTACTCTCAT GGCTTCAACCAATGCTTCCACTGGATC

					CTTTAGAGGTGGTCATTTGGTTCCTTCTGGAAAGTGATTGCTGTTTAAAGAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTC/TCTCA CCAGAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGATATCTCAGCTTCTGAGCCCTGTTACTGCAATCC
3	127	C T	---		ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACAC/GATGTGGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCATTTGGTTAGGCTACCTTCCTGTAATTGCTTCTGTTTTCAAAGGG
32c	166	G A	---		ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCAATTGGTTAGGCTCA/GCTTCTCTGTAATTGCTTCTGTTTTCAAAGGG
32b	219	C G	---		ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA/GCTTCTCTGTAATTGCTTCTGTTTTCAAAGGG
32	219	C G	---		CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAGAGTGACCTTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGCTC/TCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
54b	188	C T	---		CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAGAGTGACCTTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGCTC/TCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
54	183	T C	---		TGGGATTAACACCTGTTTCTTCTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTCAAGGTTTCCGTCCTT/TCTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCAAGGTCATATGGCTGGGCTTGGACGAG
73d	129	T C	---		TGGGATTAACACCTGTTTCTTCTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTCAAGGTTTCCGTCCTTGTGATAT CATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCAAGGTCATATGGCTGGGCTTGGACGAG
73c	165	A/C	---		

3d	129 T C ---	---	TGGGATTAAACCCTGTTTCTTCTCCAGTTCAGTGGCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTATGCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGCTTGGACGAG
3c	165 A C ---	---	TGGGATTAAACCCTGTTTCTTCTCCAGTTCAGTGGCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTC/JTGA CATCTGATCTTCCCAACAGGGCTTATTTC/JTGGCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGCTTGGACGAG
3b	165 A C ---	---	TGGGATTAAACCCTGTTTCTTCTCCAGTTCAGTGGCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTATGCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGCTTGGACGAG
3a	129 T C ---	---	GACTTCATGCTCATGAACAAGCAATTTGCTTAATTTACAGACATTAGAACAAGCTTTC/JGJTC CCACTTCCCTCCCACTATCACTCAACCTCTTCACTCCACTTTAAAGAGGTTTCTTAGGTCTCTGCA ATCATGGAAGCCCACTACTCTATTACGCTTCCCAATGATGCAGCCAGTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACAGCTGAATAATGAATATCGATATAC
38b	60 A G ---	---	GACTTCATGCTCATGAACAAGCAATTTGCTTAATTTACAGACATTAGAACAAGCTTTC/JGJTC CCACTTCCCTCCCACTATCACTCAACCTCTTCACTCCACTTTAAAGAGGTTTCTTAGGTCTCTGCA ATCATGGAAGCCCACTACTCTATTACGCTTCCCAATGATGCAGCCAGTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACAGCTGAATAATGAATATCGATATAC
68	60 A G ---	---	CATGCTGTGAACCTCTGTGCTGCTGCTGCTGGGAAATTAGAGCAAGGAATTGTATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATC AGAAATGAATAGAGCCCCATTTAAATTATATCAGAGCTTATGTCCACTTCTGCTGCTGCCATCAC TGGGCTTTTACAAGGAGGCTTT
70b	131 T C ---	---	CATGCTGTGAACCTCTGTGCTGCTTGTGCTGGGAAATTAGAGCAAGGAATTGTATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATC AGAAATGAATAGAGCCCCATTTAAATTATATCAGAGCTTATGTCCACTTCTGCTGCTGCCATCAC TGGGCTTTTACAAGGAGGCTTT
370	131 T C ---	---	TGGGCTTTTACAAGGAGGCTTT

14c	49 T A ---	---	TTAGCACATATCTGTTGGGACTTAAGTGGACAAAGGCATAAAAAT/AJ/CAGCACCTGGGGCA CAGAGGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCCTCTCATTCATTAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA
34b	41 A G ---	---	GAG TTAGCACATATCTGTTGGGACTTAAGTGGACAAAGGCATAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCCTCTCATTCATTAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA
34a	38 G T ---	---	GAG TTAGCACATATCTGTTGGGACTTAAGTGGACAAAGGCATAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCCTCTCATTCATTAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA
71b	62 T C ---	---	GAG ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTAACTCCTCTCCTTAAACCTTAAG ATTCTCTTTGTTCCCTGACATCTGAAGGCCACGCTGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATTCTGAAGAAACCTTTTACTAGGGATTGTCT
71	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTAACTCCTCTCCTTAAACCTTAAG ATTCTCTTTGTTCCCTGACATCTGAAGGCCACGCTGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATTCTGAAGAAACCTTTTACTAGGGATTGTCT
95d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA /TAAATCTTTCTTTCTGGT/GC/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
95c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA AATCTTTCTTTCTGGT/GC/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
95d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA /TAAATCTTTCTTTCTGGT/GC/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT

35c	151 G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
35d	133 A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
35c	151 G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
95b	151 G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
95a	133 A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
47	85 C T	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACGAG ATCTCAGTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTTCCTACTCTCTCTCTGAGACTTCTTCTCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACTTTGCAAGG
34b	68 T C	---	ATCTGTAATGTTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATCTACTTAT T/CJGACAAAGCAAGAACACACACAGAAAGCCCTGTGTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT
34	68 T C	---	ATCTGTAATGTTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATCTACTTAT T/CJGACAAAGCAAGAACACACACAGAAAGCCCTGTGTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT

192b	106 GA ---	---	GTITGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTCTGCACCTCATOC TCCCTGTCCTCCGTCCTCCCAAGCCTATGTTACTGGTATGCTGAGTGGATGGGATGGATTA GCCATGAATATTTTCCATTGTTTCATTAATGTAATTAATTAAGTAAATATTTTNCCTATGA GACACAATGGAAAAATGGAAACATTCATGGAAAAAACCCCATTTCAATC
192	106 GA ---	---	GTITGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTCTGCACCTCATOC TCCCTGTCCTCCGTCCTCCCAAGCCTATGTTACTGGTATGCTGAGTGGATGGGATGGATTA GCCATGAATATTTTCCATTGTTTCATTAATGTAATTAATTAAGTAAATATTTTNCCTATGA GACACAATGGAAAAATGGAAACATTCATGGAAAAAACCCCATTTCAATC
155	19 GC ---	---	CCATGAACCATGGGCTACA[G/C]ATATTCCTAACTTCAGAGTCCCTCCTTACTGGAGAGGGATCCA CTTTTAAATATGATTCTTGAAGTGGCTGCATATTCCTTCCAAGCACTTAAACTCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
108	194 GA ---	---	CCATGAAGAATGAGTTCCTCCCTCCCTGGGTCACGTCCTAAGAATAGCACACCTTGGAGATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTCAAGACACACCTTTATGCTTTTCAAGCTTT CTGGATTGGGATGAATCTNACATCAATGTGCACCTTCGTGTGGATCCTCTCC[G/A]TGCCCC ATCTCTGGNAGAAGCCACTGGGAAGTCGAAGGAGTGCACCTCAAAATCAGG
105b	131 GA ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTTTCCTTGTGCATCAGTGCACCTTAAAAATTTT GAAAAATGGCAATTTTAAATATCTTTGGAACTTCCTAACACATTACCTATTTTNAACCAAC[G/A] AGGTGATTCTTATGGGAAATATATACAGCAAGAAAAAANANANGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
105	131 GA ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTTTCCTTGTGCATCAGTGCACCTTAAAAATTTT GAAAAATGGCAATTTTAAATATCTTTGGAACTTCCTAACACATTACCTATTTTNAACCAAC[G/A] AGGTGATTCTTATGGGAAATATATACAGCAAGAAAAAANANANGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
164b	177 CT ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAAAAAAGT GAAATCAATGTCTTCCAGTGTATTCACATGGCAGTCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGTTGACTAACGTTAACATGCATGCTGTTC[CT]AACAAAGTGTGTTGGTGTCTC AGTGTCAACATGCTACCTTCTTCAACAAACAAA
164	177 CT ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAAAAAAGT GAAATCAATGTCTTCCAGTGTATTCACATGGCAGTCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGTTGACTAACGTTAACATGCATGCTGTTC[CT]AACAAAGTGTGTTGGTGTCTC AGTGTCAACATGCTACCTTCTTCAACAAACAAA

19	64	A G ---	---	AATGTCCATGCTGTGACTGACCTGTCTAACACCTTTCCCTAGTATTCCTTAGTGGAAGATTCAACAG[AG] AGACCAGTTTGCCTTCACTTAGTAGGGCCCAATGATAGACTTTTAGGTGCTACCACAAGGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTCTGCGCTTGGTC TTCCCTGTTTACCATAITTAATGATGACATGCAACACCTCAGAGCCCTTTTA
74b	133	G C ---	---	ACAGTACACATGGCCCATATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAA ATTTAACTACCAGGGAGTCTTTTATAGTAATTAATAATGTTTATTTAGAAAAATACAAAAATG /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTGGTCAAATGATTGTT AATTCCTAAATTAATGTTTATGTTTATGTTTINATTACTGCCAATCAGCCCAAG
74	133	G C ---	---	ACAGTACACATGGCCCATATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAA ATTTAACTACCAGGGAGTCTTTTATAGTAATTAATAATGTTTATTTAGAAAAATACAAAAATG /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTGGTCAAATGATTGTT AATTCCTAAATTAATGTTTATGTTTINATTACTGCCAATCAGCCCAAG
82	137	G A ---	---	CAATAGACCAATGACTGCCACAAGAGAAATAGTGGATCTACATTTAGAAACCACATGTTTTT AATGGCTCTCTCTCTCTCTCTCTTTTAAATGCTCTCTCAACACCAATTCACATTTATCTTTTCAA TIG/AJAGCAATTTGTCCAATTTAAAGTCAATGAAAAATAATGTACATTTTTCACAACAGTATACATTAA GCCCTGCAAAAGTCTTATATGCTAT
54b	194	G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTGGCCCTTGGGA CAAAGACCAAGGACAACCTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAACTC TGGTTCAAGGAAGGCAAGGGCAGTTATGACCACCTTTACAACCTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
54	194	G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTGGCCCTTGGGA CAAAGACCAAGGACAACCTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAACTC TGGTTCAAGGAAGGCAAGGGCAGTTATGACCACCTTTACAACCTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
39	210	G A ---	---	AGCCAGCCACATCATGTTGAGTCTCTGCTCATCTTCCATCTTATTTCTCTCTACTGCCTTCACCTT CCATTAAAGAACTCTGTGATTACATTGATGTTTGGTGTACACTACAGAAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTAACACCTTAAATCTATTTGCAATCTTTGTCAATACCATAACATATT CATGG[G/A]TTCTGGGATAAGGGTAGACATTTTATGGAGGCATTA
10b	130	T C ---	---	GAAAAATGATGTTTTGATTTCCCTTCCCTATCTTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTGATGAAACTCTGTCTATAATTAACCTTCCCTTCTCTGCTTTATTTGCTT/CJACA GTTTAGGTAAATAAAGATGCCCAAGAAATTCAGTATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAAGGGAGGAGGTGGGGGGTTTCTGGGAAGA

10	93 T ---	---	AGACAGCTGAATGGGGACATCTTTCTATTTCGATTTTAGTTTAACATTTGATAAGAAATTGATGAAA GTTTGTACATTCAGATTATCTTTATAGCAGCAGAAAGTCTGGCAATAATAACAGCACACTGACT TTTCCATGGTAAAGAAGTTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTAAATGGAGGAGATGAATAGTACCTTTGAAATTTTGAATTTATGG
11	118 CT ---	---	GAAATCCATTGAAGTTTTGACCTTGAACCTGATCTCATTAACTTTTNCCTGTAGTGGTTGTATTT CATTTTGACAACAGAACAGAGAAAATTTCCACTTAAATTAATTTCTC/TAAAGTATCTATGAT TTAGCACTGTTAGCACCAAGAACTGTGAAATTTATCTCTAGATATCTTCAGAACTCTAGGATGGAAG AA
71b	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
71	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
89b	156 GA ---	---	AATCGAAACATTGATTTTTTTGTAAGGAACCCACATTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/GA/JTNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
89	156 GA ---	---	AATCGAAACATTGATTTTTTTGTAAGGAACCCACATTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/GA/JTNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
188	31 A G ---	---	GATGACAAATTATTGTGATTGGCATTTTAAAJ/GJTAGCATTCCATTTCTCTGGCTTTCGTGTGT TGTTGTTGAGAAAGTCAGGGTTAGTCGTATTGCTCCTTTCTAGTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCTCAAACTGATCTTTAAGAACAATAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
191	145 GC ---	---	ACCATCAATGATACCTCTAAATTTATTAGATGATTAACTGGCTCTGTTAAAAATAAAAAACCT GTCCTGGACATTGAAATAAAACATTACTATTGGTCATTTCTGCTACTTACAAAGGTACTGCACCTA AACAAAGTTAAG/GC/GJTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCAGTGTC TTTCTTGCCCATAAATAAAATTTTACATGCTCT

84	144	A G ---	TTGGTTGGCATTAGCCTCATAACAACTATTTACAATCAATTTGTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTCTGCTTAGTCGACGAGCAAGATTTGAACCCAGGAATCCATT CACCGGTAC/GJGTGCTACCTGGGTAATAAATGTTTAAATTAATCTATGGCATTAGATTTTCAAGA GTCTAATGTGGTTTGAATAAGGTGTGCTTAAATTTGTTTATCAGTATGC
39	185	CT ---	TTTCTGCATTTGAATGTGATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTTCAATTTCCACCATTTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGCTGTATCC/CJTCATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
127	63	A ---	AAATGAATCCGCTTTAGAGCAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGA/- JGATTAATCAATAAGCATAATTAATTTTATAATATGGAATAATTTAACTAGATAATTAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGAGGAGGTAGTTTCTACTTATAGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCCGATGACATGATGAATGTTCTAAGCAGACAG
390	87	CT ---	GCCTTTGAGAAATGAAAGGGAGCCTGGACCATTCAGGGCTTCTCATCTGATTATTTTGTGTAT TTATTGTTCACTTATTAATTC/JGTCTGTCTCCCTTCTGGTATGCTGTGTCATGAACAATGAATTC CCAGTGCCTGGCCGATTCGTGGCTCTAGAGGTGTCAGAAAAGTTCCGGTGAATAGAAATTG ACGAATGGGTTGAGAAATGAACCTGTGAATCTATGGAAGACAAACGAAT
404b	87	GA ---	CCCTGGCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTAATTTAATTTG/AJAAAGAAACTTGTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCTCAGCAGTTCCATGGTGTGATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGTTTATAGATTATACAA
404	87	GA ---	CCCTGGCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTAATTTAATTTG/AJAAAGAAACTTGTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCTCAGCAGTTCCATGGTGTGATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGTTTATAGATTATACAA
545b	77	A C ---	TAGGAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCCTC/JCJCCAACACCTCTGTTTCTGACAGCCAGTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTCAATTCA
5545	77	A C ---	TAGGAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCCTC/JCJCCAACACCTCTGTTTCTGACAGCCAGTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTCAATTCA

-860b	134 A G ---		---	ACTCAAGTTGGGGATAAATCAGAAAGTTCTATGTACAACCTTAAATTTTGTAAAGATTTTATGT TTCTTTTATATAAATTATGGATTTGTTTACTCCCTAACCAACCTTCTAACTGAGGAACCTACIA/ GJTATACGTGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAATCATCAACTTCTGTAT
-860	134 A G ---		---	ACTCAAGTTGGGGATAAATCAGAAAGTTCTATGTACAACCTTAAATTTTGTAAAGATTTTATGT TTCTTTTATATAAATTATGGATTTGTTTACTCCCTAACCAACCTTCTAACTGAGGAACCTACIA/ GJTATACGTGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAATCATCAACTTCTGTAT
-3106	208 C G ---		---	GCAACAACCTATTATACCTGATCCAAACCCAGGTCTACTAACCTTAATCAACCTAACCAATAC TATATATTGCTCTGTTCTGAATTTATTTTATAGAACTGTAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGTCCAGGAGTCTCAATGTGAAGTATAATCTTTACAGAG TAATT[C/G]ATAGTAGGTCAACCAAGTCTATATTGTATGTGAAGGAAAG
-6109d	129 T C ---		---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C/ AAACCTATATTNCTGTCCTGTGTCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
-6109c	147 T C ---		---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCTATATTNCTGTCCTGTGTCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT TGNAAAATTATCCCTGAAATTTTATACCA
-6109b	147 T C ---		---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C/ AAACCTATATTNCTGTCCTGTGTCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
-6109a	129 T C ---		---	AATGCCTATCACCTCCATCATGCTGCATACTGATTGATTCATATGCTTATTTAGCACCTGTC TTCCAACACATGCTGTTTGTTCATGAT[C/G]GCATATCCCAAGTGCCTTAGACAATGCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTGTTAAATCAATAAATTAATCAACTTGGCATATGCAGG GMC
I-6112	96 T C ---		---	

44	103	T C	TAATTGCACAACATTACATATCAGGGTTCTGATTGAAAGGAAGANAATTCCTTTCTTTAGTGATT GCTTAATATTAAATTCATAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTTTGAAGAAGG AAATTGAGTGTGGGAATTAAAGCAACAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTCTCTTCCCAAGGATGGATACATTCTTAC
68	124	C T	CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCACAAAGATTTCCTCCTAGTAGGGCTTGGGTTGGCACCCTTGGCTCATTCCTCTCTCCCT GGGTCCTATTGACTTTTACGGAGCCTAGAAGAGCTGGACAAACCTGCTTCTTTGCAGAAAGAGTCG GGGTTCCAAAGATTCTGTTACGATTTTATA
136b	234	C T	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGCTGAGAGAGCTCACTCCCCC ATATAATCCCTTTACATGTTTCTTATAAGACATACAGTTTAACTCAATTAACAACTAAACAGCTT ATATACTGGCAATATAATACAGATGGTTTATGTCAGAGTAATAGATCACATGAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTTGGAGGACACTGACAGT
336	234	C T	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGCTGAGAGAGCTCACTCCCCC ATATAATCCCTTTACATGTTTCTTATAAGACATACAGTTTAACTCAATTAACAACTAAACAGCTT ATATACTGGCAATATAATACAGATGGTTTATGTCAGAGTAATAGATCACATGAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTTGGAGGACACTGACAGT
381	92	C A	TTGGATACAAAAATTCAGTTACAAATCAGTAGAGCTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTAAACA[C/A]GTAATTTAAAGCTCAACATTTTAAACAGGCACAAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTACAG
436	198	C G	GGTTGAGGCATTGGAAAGGCAGAAATTTAGGCGAGTAGAAATGGACATTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGCATAATAAGAAGTTAGACTTTGGTGGTTGTAGTAGTTGTAGTAGGAGCGTT[C/A] GATTGGGTGATTCACAGACAAGGTGATGTTCTAAGATTGTATTTATTGT
449	186	C T	GAGGCTCTTTGCTTTCTCAGTCAAGGCTGATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTTGGTGCCTCACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTCTATTCATCTGCATCTCTGATCTTATGCTGGCTCTATTCCTATCCCTATCTCTGA TCTTATGTCAGACCTGAAGTTCCTAATTTTCTGTGGTATTATA
449	186	C T	GAGGCTCTTTGCTTTCTCAGTCAAGGCTGATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTTGGTGCCTCACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTCTATTCATCTGCATCTCTGATCTTATGCTGGCTCTATTCCTATCCCTATCTCTGA TCTTATGTCAGACCTGAAGTTCCTAATTTTCTGTGGTATTATA

63	72	T C	---			GCTGGAGAGAAAGACCTCCAAAAGAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACA[T/C]TGAAAAAATTAAAGTAGAACTCAAAGAGCCAAAAGTCCCAATTTGTGTCATTA TAAGAAATATTTTGAATGGAATCTTAAAGATGATTTTATTGATCAGTTAAATGTTCTCTCTCCTC CAGTCCCATTTATATGACATTCGGCATGCTG
174b	76	C T	---			AAGCAGTAAATCTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTGACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
174	76	C T	---			AAGCAGTAAATCTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTGACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
478b	175	T A	---			GAACCTAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGCTATATGCTTTATTTTGTGA CACTGCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCTTGTGCTGCTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
478	175	T A	---			GAACCTAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGCTATATGCTTTATTTTGTGA CACTGCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCTTGTGCTGCTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
3559	149	G A	---			CACATTTGAATGCAACTGAGAAAATGGTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTT[A/G]TCAAAATTTTAAAGAGAACAGGAATAAGGAAGGCCTAACAGAGGAG TTAAATTAATTGTGCAAACTTATCAGTCTTC
3564b	54	G A	---			TTCTTTATGGTCCCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCTCNCCTATTCCTTTCCAT GCTGCTGCCTCATTNCTCAGAAATGGAAGGCAATTTGATTATNATTTTTTTGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA
6564	54	G A	---			TTCTTTATGGTCCCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCTCNCCTATTCCTTTCCAT GCTGCTGCCTCATTNCTCAGAAATGGAAGGCAATTTGATTATNATTTTTTTGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA

08b	46 C	CTAATCAGTAGCACTGAACATGGCTCTAGTGAAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTCCTCTCTAGTCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAATCCCGACACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACAGAAAAAGGAA AGC	---		
08	46 C	CTAATCAGTAGCACTGAACATGGCTCTAGTGAAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTCCTCTCTAGTCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAATCCCGACACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACAGAAAAAGGAA AGC	---		
166	68 C A	GTTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTCCAAAACGAGGAAACCTCCCC A/C/AJAAATCCCATCAACACAGTCATGCTGGAAGGCATTCTGCTACTCTGTTGGTTTCATGTAA ATGTTGGGTGACTCATTCGCCCTCTCTCTCAAGTCCAGGCTCTTGGGTAGACCCAAACTA ATACACAATGTTAGGCACACAAAGAGA	---		
370b	120 A G	AGATTAAACATAATTACTGGGCCATTGAGGTTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATCTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTAGCCA GCATTGCCATTGAGGGCCGAGTCAAGGTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAACTTAGAAGGGAT AGATTAAACATAATTACTGGGCCATTGAGGTTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATCTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTAGCCA GCATTGCCATTGAGGGCCGAGTCAAGGTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAACTTAGAAGGGAT TTTGAAATAAATTTCATGCCCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG	---		
704c	33 T C	TTTGAAATAAATTTCATGCCCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG	---		
704b	33 T C	TTTGAAATAAATTTCATGCCCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG	---		
1704	28 T C	TTTGAAATAAATTTCATGCCCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG	---		

				CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTAGATAACAGAGGAAGTCCCAGTTATCTACCT ATTCCCTTAAACACATTTTGTGAGGCTGGAATGATCCCGATAGTAAACCTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTTTACTGAGTCGACACAGGATGTCCACAGTGAGCCTC ATCTCAGTCCATGGAGGAGTTGACTTAGACCTTCTCTGGACAGGAAGGTC
10	106	GA	---	AAAACAAATGGTGCATTGCATAATATTGGGTCACAGTATAAACAAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAATAACANGATCCTTCTTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCCAGTCCCCTCTTC
66b	148	GC	---	AAAACAAATGGTGCATTGCATAATATTGGGTCACAGTATAAACAAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAATAACANGATCCTTCTTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCCAGTCCCCTCTTC
66	148	GC	---	ACAGATAAAAGTCTTTATCCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAAATTCAC[G/TTT]TACTGCATAAGATATCTTCATGTACAACGT ATGCTTTGTCTTCTTTGGAGGACGCTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTCAATAGGGCAGAGTAGANTACTACAGGAAAGAGTAAATTCAGGT
787b	97	AG	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCAATTAACATTATAGCAAGTTTCAACACATTCA TCAACAAGGCGCTTCAATCAATCAGTCAACCC[C/G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGTGGCTGTAGGAAGTAGGGTTATGCCCTCTAATCCCGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAGGCAAC
793	105	CG	---	CACAATAATAAATCACTCCCTACCTTGAAACCTTAT[C/J]AGAAAGCAATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTGCTGAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
3810b	37	TC	---	CACAATAATAAATCACTCCCTACCTTGAAACCTTAT[C/J]AGAAAGCAATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTGCTGAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
3810	37	TC	---	GCATGATTAAACAGTGCAGAAAATAACCAAGTACATTGGGTGAACGATGAGCTAGTGTCTAGTA TTTGTCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACAATGATGAGCT GCAGGGTAAC[C/A]TGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAATCTTGGTTCAGGTGCGGCTGTGCAG
6817b	145	CA	---	

[illegible]

[illegible]

[illegible]

WI-7252a	520	T C	CCACAGGATCCAGCCCAAGCGGCCCTCCGGCCCCCTCCACACTCGCAGCAGCGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGCCGCGCTGGCTGGAGGCTGCCCGGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCGAGGTGGAACCTCAGTCATTAGACTCTCTCCCA
WI-7265m	252	T A	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGAATTTGTTTATATTATGTAAATATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTTGCCTTT
WI-7265l	231	T A	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGAATTTGTTTATATTATGTAAATATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTTGCCT
WI-7265k	121	T G	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCCATTCGTGGTTTCATTGTAGTT GTTAAGGAAACCAAGCATATAGATGCAATTAGTGAATTTGTTTATATTATGTAAATATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTTGCCT
WI-7265j	174	T A	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGAATTTGTTTATATTATGTAAATATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTTGCCT
WI-7265i	227	T C	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCCATTCGTGGTTTCATTGTAGTT GTTAAGGAAACCAAGCATATAGATGCAATTAGTGAATTTGTTTATATTATGTAAATATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTTGCCT
WI-7265h	80	T A	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGAATTTGTTTATATTATGTAAATATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTTGCCT
WI-7265g	170	T G	AACTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGAATTTGTTTATATTATGTAAATATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAGATTTGCCT

7265f	231	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
'265e	227	T C ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
'265d	174	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
'265c	170	T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
265b	121	T G --	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
265a	80	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCAATTTTCCACCATCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
281b	183	C ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCAAAGC ATCTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCCTGCGCCCTGCAGGCTCCCATGAAGGCCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTCTGGCAAAAACGGAGTCCGCGAGGCCGAG GTGTGTGAAGACCACTCGTCTGTGGTTGGGGTCTCTGCAAGAAGGCCTCCTC
281	171	C A ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCAAAGC ATCTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCCTGCGCCCTGCAGGCTCCCATGAAGGCCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTCAGACTCTCAGTCTCAGTCTCAGGAGGCCG CAGGTGTTGTGAAGACCACTCGTCTGTGGTTGGGGTCTCTGCAAGAAGGCCT

WI-7301	205	A C ---	---	---	AACTATGCCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGACACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGGAGGATATGATGTTACAAAGAGGAGGAAATTTTGA CGGTAGTAATACTATGGTGGTGGGAACTATAATGATTTTGGAAATACAGTGGACACAGCAATCA AATTACJTGGACACATGAAGGGGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49	G A ---	---	---	CTCTCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA/GA/JTTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCTTTTCAGCAGTGTAAATGAATCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAAACAGCCATGTGGGTCTTCTGTCAGTATGAACGCTTCTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTTGTTTTT
WI-7314b	49	G A ---	---	---	CTCTCTTTTCTTCAGATCTGCTCCTGGGTTTAA/JTJTTGGGAGGTCA/GA/JTTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCTTTTCAGCAGTGTAAATGAATCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAAACAGCCATGTGGGTCTTCTGTCAGTATGAACGCTTCTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTTGTTTTT
WI-7314	36	A G ---	---	---	CTCTCTTTTCTTCAGATCTGCTCCTGGGTTTAA/JTJTTGGGAGGTCA/GA/JTTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCTTTTCAGCAGTGTAAATGAATCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAAACAGCCATGTGGGTCTTCTGTCAGTATGAACGCTTCTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTTGTTTTT
WI-7321b	199	C T ---	---	---	ACTCAGGGAAGGATGCCCATTAAGTGACAAAAGGGTGGGTGGGCAACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATCIC /TJGTTGCTGGGGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199	C T ---	---	---	ACTCAGGGAAGGATGCCCATTAAGTGACAAAAGGGTGGGTGGGCAACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATCIC /TJGTTGCTGGGGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248	A C ---	---	---	AGACATTCTCGCTTCCCTGAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAACCTTGGGCACATGCTCAGGCTACTATAGTCCAGAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATAAAATTCGAAATTTGGGATTTTCAAAAGATAATATTTTACATACACTGTATGT TATAGAACCTTCATGGATCAGATCTGGGGCAGCAACCTATAATCA/AC/CA
WI-7338c	221	A G ---	---	---	CTCTTCTCAGCACATTGATGGGCACTAGAAATACAGAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTCTTACCTTGAGC CAITATTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATCAAGAGCTATCTGCAGCTA GTGTGTTTCTCTTTACACAC/AG/JTATACACACAGACATCAGAAAATTCGTGT

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTTACJCCCTTG AGCCATTATTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTCTTCTCTTTACACACATATACACAGACATCAGAAAAATTCGT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGCTTCTCTTTACACACAGTATACACAGACATCAGAAAAATTCGT
WI-7338	221 A G ---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATCACTTTAAATACCATTAATACATTGTATTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTTAAJAAAAATCTTAATGATTATTTTATTACTACTGTGTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384c	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATCACTTTAAATACCATTAATACATTGTATTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTTAAJAAAAATCTTAATGATTATTTTATTACTACTGTGTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATCACTTTAAATACCATTAATACATTGTATTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTTAAJAAAAATCTTAATGATTATTTTATTACTACTGTGTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145 T A ---	---	TGAAATCCTGGTCTCTGGCTGCTCTAGCTGGTTATTTTACTTTGCCOCCCTCCCACCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACTATTTAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGCTGTGTCAGAACTTTTCCCCCAAGATGTGTATGTTATGG
WI-7388c	106 A T ---	---	TGAAATCCTGGTCTCTGGCTGCTCTAGCTGGTTATTTTACTTTGCCOCCCTCCCACCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACTATTTAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGCTGTGTCAGAACTTTTCCCCCAAGATGTGTATGTTATGG
WI-7388b	106 A T ---	---	CTTGCTGTGTCAGAACTTTTCCCCCAAGATGTGTATGTTATGG

WI-7388	94 T A ---	---	TGAAATCTGGGCTCTTGGCTGTCCTGTAGCTGGTTATTTTACITTTGCCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGTTACCTCTATTTTGGCACAAGCGTCTCGGGATTGTGTTTGA CTTGCTCTGTCCAAAGAACTTTTCCCCAAAGATGTGTATAGTTATGG
WI-7438	64 A G ---	---	TTAGATTTAAATTGGCAACCAGCAACTCACTGCCACCACTTCCACTGCAGATCTNCTATTCTCGG[AVG] GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTTCAAGTTGNCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTCTACTGTCTACTGTAACATAGTTTGTNCTGGTATTGTTA TTGGAAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ---	---	CCATGATCCCTCCTCTTGCCAAATGGAGGAGCCTGTGGATGGTACCAACAACAAAGCCCAAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTTC[TC]GTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGTCTACTTCTCAATGTTTTGACA
WI-7454	152 T C ---	---	CCATGATCCCTCCTCTTGCCAAATGGAGGAGCCTGTGGATGGTACCAACAACAAAGCCCAAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTTC[TC]GTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGTCTACTTCTCAATGTTTTGACA
WI-7464c	177 G C ---	---	AATTTGAAATCTGAAAAAAGTGTCATAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACATGCACATAAATCTATTATAATTTCTCTATGTA CAACAGAGCCACAGCACAAAGGGTGGGCATAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACATCAT GAAAGAAGCCCTACAAATAGGCCCCAGGAGGAGCAACGTTTCCCAACAATTAT
WI-7464b	168 C A ---	---	AATTTGAAATCTGAAAAAAGTGTCATAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACATGTACATGTAATAATTTCTCTATGTA GTACAACAGAGCCACAGCACAAAGGGTGGGCATAGCAGTTGCCAGCCAGAAGAGCTTTCACATCAT GAAAGAAGCCCTACAAATAGGCCCCAGGAGGAGCAACGTTTCCCAACAATTAT
WI-7464a	103 C A ---	---	CAATTCTCAATCCAACTAGTCTGNTGCCTTAACCATTTCCAGACAAACTTCCACTTCGAAGGTTTTTA AATGCAATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCTTTGAATGCTTCAT /GJATAGTCCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGA ACTCTGTACAAAAATCCCTTTGAAAAATAAATTTTGGAAATGAGTGATGA
WI-7499b	134 T G ---	---	

WI-7499a	33 A G ---	---	---	CAATTCTCAATCCAAACCTAGTCTGNTGCCTAAAGJCCATTCCAGACAACTCCACTTCGAAGGTTTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCAGAGGCACATCAGTTCCTTGAATGCTTCATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAACTCTGTACAAAATCCCTTTGAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAATGCATCCAGCAGCAGACCACTTNAAGTAGTCCTGGTCTGATTGCCCTAGC[AC]GGAGAGTTGAGTGCCACAGGTAAGAAATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAGTAATTAATGATGTCAGAGAAAATATTTAAATATGGACCACCTTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAATGCATCCAGCAGCAGACCACTTNAAGTAGTCCTGGTCTGATTGCCCTAGC[AC]GGAGAGTTGAGTGCCACAGGTAAGAAATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAGTAATTAATGATGTCAGAGAAAATATTTAAATATGGACCACCTTTGTTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTATGCTTTGGGGTTCTTGATGTTCCGAGTGTCAACCCAAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATCCCGGTGATAGAAATGCTAAATGTC[GT]GTGAAATAGGTTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAATTCGGAGAGTGTCTGCTAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTATGCTTTGGGGTTCTTGATGTTCCGAGTGTCAACCCAAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATCCCGGTGATAGAAATGCT[CA]AAATGTCGTGAAATAGGTTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAATTCGGAGAGTGTCTGCTAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	---	GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGAACAGTCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTCTT[GA]GGAAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTCCCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	---	GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGAACAGTCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTCTT[GA]GGAAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTCCCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGAGAGGTC[CT]CTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTCGATTCCTGTTAAAGCCACTGGGTCATAAGAAAGGGAAGTAAATAAATGAAGTCTGACTAGAAATTTCTATTGACAGAGCCAAAGTACATTTAGTATGGCAATTGAGTTGGATATAGTTTCTATTGATGTGCAATTTGAATTCAG

WI-7576b	168 A T ---			AATGATGATAATGATGATGACGACGACAAACGATGCTGTGTAACAAGAAAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAATAATTTTGAAGGCGGTACTAGTTCAGACACTTTTGGAGTTTGTGT TCTGTTTGTAAACCTGCATCTGACACAAAAA[A/T]GTTGAAGGCTTATTCTACATTTACCTACCTAC TTTGTAACTGAGAGACAAAGAGCAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCAATC/CAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA TAAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACAC[G/A]TAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA TAAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCAATCAAAATC/G/A]TCTCTCATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTA/C/A]ACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---			AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77 T C ---			AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50 G C ---			AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAATAATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157 G A ---			AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48 A G ---			AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAATAATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84 G A ---			AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93 T C ---			AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154 C A ---			ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577b	117 A G	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCATTAATTTCTCTGAGGGTTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAATTCATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577	107 G A	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCATTAATTTCTCTGAG/GJAGTGTAGTAAACAGTAGGAGTTAAT AAAGAAATTCATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7619q	106 C G	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTGTCATCCCTCCCTAACGAGACTC/GJCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTGTCATCCCTCCCTAACGAGACTCCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCTC/GJCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCCT CGCTTCTTCTTACAGAGAAACAT/GJACATACCGAGAAACCTATTTC
WI-7619n	237 G C	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCCT CGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACAT TGCGAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAAGGCGCAATGGGTGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTCTTCTTACAGAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCG/GCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619j	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT CGCT/GTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619i	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619h	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619g	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATTA/GTACATACCCGAGAAACCTATTTC
WI-7619f	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619e	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC TGGCAGGAAGAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT TCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619d	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACATACCCGAGAAACCTATTTC

WI-7619c	90	C	---	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTAC ATGGCAGGAAGATGGGGCCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCT
WI-7619b	206	T	G	---	---	CTCTGGCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGAATGGGGCCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCTCTCT CGCT[G]TTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189	T	A	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGAATGGGGCCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105	A	G	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGC[NG]TTAAACCCACATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626c	155	C	T	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATCGACCAAAATGTGCCA TACTAATGATGAGCAATTTAG[C]TACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626b	28	T	A	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATCGACCAAAATGTGCCA CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626	144	T	C	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATCGACCAAAATGTGCCA TACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7689c	134	A	G	---	---	TCCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGC TCCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCTCTAAAJA /GJTAAGGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGCCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC

WI-7689b	134	A G ---	---	---	TCCCATACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGAGCGCCACCCAGCAAAAGTTGTTCTCTAAQA /GJTAAGGGCAGAGTACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGTGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---	---	---	TCCCATACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGAGCGCCACCCAGCAAAAGTTGTTCTCTAA AATAAGGGCAGAGTACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGTGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---	---	---	TGGAGAACATTCAATCTGCCGTCACCTATTCATCAATGAAGATTAG/ACACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCACCAAGTTCAGGATGGTAGTGGAAGAGAGGTCOCAGAGTCTGGCCCTTGAT GCCAGCTCAGTCCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGGCCACCAGGAAGCAC AGGTCCAAGGCTGGTCCACACCTTATCAGCAGCAACCACTGTCACTTCATCC
WI-7703b	164	T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTATTTTAAATTTGTTTTCACATTTGGAACAAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGAAGTAAAT/CJGGTCTCTCACTGTTTATTTAACTCTCTAAATCT TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156	T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTATTTTAAATTTGTTTTCACATTTGGAACAAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGAAGTAAAT/CJAGTAAATGGTCTCTCACTGTTTATTTAACTCTCTAAATCT TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---	---	TTAAATGAGTGTGTTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGCCTCATCCGAGGCGAGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	C T ---	---	---	TTAAATGAGTGTGTTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGCCTCATCCGAGGCGAGGTCAGGAG GGGCAAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106	C A ---	---	---	TTAAATGAGTGTGTTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGCCTCATCCGAGGCGAGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC

WI-7743d	275	CT	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GGGAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7743e	106	CA	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	CT	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GGGAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7743c	106	CA	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275	CT	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GGGAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7743	106	CA	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275	CT	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTACCTGGGCTCTGGGCTCGGAGCTCATCCGAGGAGGGTCCAGGAGAG GGGAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7758	144	AG	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGCTTCAGAGACTTCGTAATTAAAGGAACAGAGTACAGACATCATCAAGTG GAGAGAAATCAGTAGTTAAAGTCAATTAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAATGAGTAAATTTGTTTATTTTCCCATTTGGAGTGTAACTGACTGCC

WI-7765b	126 G C ---	---	ACAGGGCCTTTGGAGGTGCAGCCCCCACTGCCTTTGACCTGCCTCCCTTCATGCATGGAATTCCT TCATCTGGMCCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TAGG GAAAGATCCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTG ACTAAACCAAATCACTGACCTTTGCTGAGCCTGTAATAAAAGGTCGGA
WI-7773b	237 C G ---	---	TTAATTAAGTATCCAGCAAGACCAATCATTTGATCATAGATTATTTTAAGTTTATCCGTAATTTT GATAAAGATTTTCTATTCCTTGTTCTGTCAGAGAACCTTAATAAGTGTACTTTGCCATTAAAGGCA GACTAGGTTTCACTGCTTTTACCCCTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTGAGCTTTGACTAGCCATCTCAAGCA[C/G]TTTCGACGTTTGA
WI-7774b	170 T C ---	---	TGCAACCTCTTTTGGTATGGGAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGCGCACCCAGAA CAGATCCAGCTTCGGCATTTGATCAGACCACCAAGTGTCTTCCGGGAGGAACACTTTTAA TTACCCCTTTGCAGGCACCACTTTAATCTGTTT[C/J]ATACCTTGTCTTATTAAATGAGCGACTTAA ATGATTGAAATATGCTGCTCTTAGTAGCAAGTAAATGTGCTTGTCT
WI-7785c	165 G ---	---	GCAGAGCCTTCCAAGGACATATTGCAGGATTCGTATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCAATGGAATAAACTGTCTCCCCCATTCCTATGAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCTTGTATGATTTATTTTGTAAATGTATCTTGGTGTGC
WI-7785b	165 G ---	---	GCAGAGCCTTCCAAGGACATATTGCAGGATTCGTATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCAATGGAATAAACTGTCTCCCCCATTCCTATGAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCA TAATTTATTTGTCCTTGTATGATTTATTTTGTAAATGTATCTTGGTGTGC
WI-7785	156 T ---	---	GCAGAGCCTTCCAAGGACATATTGCAGGATTCGTATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCAATGGAATAAACTGTCTCCCCCATTCCTATGAACTGC ACATTGGTCATTGTAATANN- /NNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCAATAATTTATTTGTCCATTGA TGATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84 G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTTACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCTCTGCTGACTCGGGGCTGTCTCAGACGACTAGGCCAGGACCCATCT
WI-7789b	84 G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTTACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGCTGACTCGGGGCTGTCTCAGACGACTAGGCCAGGACCCATCT

WI-7789	73 GA ---	---	---	<p> TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGACCACATCTACAGAGACTCTCCG TGACG(A)GTGGAATTTAAGTTTAGGGTCCCTAAAGCAATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTACTCGGGGGCTGTCTCAGACCACTAGCCCAAGGACCCCATCT </p>
WI-7790b	190 CT ---	---	---	<p> AATTGTCAGTCACCTTCTCAAAACCTTACAGTCTTCTTCAAGGTTACTCTTCATGAGATTCAATCCATT TACTAATCTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACCTC(A)TTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC </p>
WI-7790	190 CT ---	---	---	<p> AATTGTCAGTCACCTTCTCAAAACCTTACAGTCTTCTTCAAGGTTACTCTTCATGAGATTCAATCCATT TACTAATCTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACCTC(A)TTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC </p>
WI-7795b	81 CA ---	---	---	<p> CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC(A)GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAAATCTCTCTGAGGAAAATGTCCAAA TAAGATGAATCAGTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG </p>
WI-7795	81 CA ---	---	---	<p> CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC(A)GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAAATCTCTCTGAGGAAAATGTCCAAA TAAGATGAATCAGTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG </p>
WI-7814c	41 GA ---	---	---	<p> TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG(A)TTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATATGGGATTTTC TTTCTTTCTCTGGTAAATATGACTTGTATTTTAAAGAAATAACAGAA </p>
WI-7814b	41 GA ---	---	---	<p> TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG(A)TTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATATGGGATTTTC TTTCTTTCTCTGGTAAATATGACTTGTATTTTAAAGAAATAACAGAA </p>
WI-7814	28 GA ---	---	---	<p> TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTCAATTTAGTCATGTGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATATGGGATTTTC TTTCTTTCTCTGGTAAATATGACTTGTATTTTAAAGAAATAACAGAA </p>

WI-7830d	150 C T ---				GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTCGGTGTGGA
WI-7830c	54 G A ---				GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTCGGTGTGGA
WI-7830b	134 G A ---				GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/ATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTCGGTGTGGA
WI-7830	44 A G ---				GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTCGGTGTGGA
WI-7865e	25 C T ---				CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191 C T ---				CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25 C T ---				CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191 C T ---				CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA

WI-7865	25	C T	---	---	CCACCTCCTATCTGATTTTCCAG[C/TAATGAGGCGAGGAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCACTTACCTATACAAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTATAAGATTCAGGGTGCTTCCAACTGAATCTCAATGTTCTCAGTACGAAAAAC CTGAATCACATGCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191	C T	---	---	CCACTTCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCACTTACCTATACAAAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTATAAGATTCAGGGTGCTTCCAACTGAATCTCAATGTTCTCAGTA[C/TA]GAAAAAC CTGAATCACATGCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92	A C	---	---	TTCAACACCTGCTTCCACCTCCACCATCTGTGCAATCACTTACCCCTCAGCCTCACTAGTCCCC CTAACAATTACCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATGGC CTGTTGAGTTTAAATGTTTAAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92	A C	---	---	TTCAACACCTGCTTCCACCTCCACCATCTGTGCAATCACTTACCCCTCAGCCTCACTAGTCCCC CTAACAATTACCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATGGC CTGTTGAGTTTAAATGTTTAAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173	C T	---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[C/TT]AGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATCTAATGCCTAGAT
WI-7868b	173	C T	---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT /C/TTACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCAATTAATATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATCTAATGCCTAGAT
WI-7868	66	T C	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTATTAGAGGG GTGGGTGGCGGGAATCC[C/TA]TTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATGCTGCAAAATGAAATCCAATGAGCAGTAAATTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7870b	85	T C	---	---	

WI-7870	76 C T ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGTGGIC/TGGGAATCCTATTATCAGACTCTGTAAATGAATATAATGTTTTACTCAGAGGAG CTGCAAAATGCTGCAAAATGAATCCAATGAGCACTAGAAATATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	TTAGGTCTCATGCCACTCCGCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTCAGGACTGGCGGGGGCGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCTGGAGAAAGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCTCCCAAGGCTGTCTTCTCCAGAGCACAGAAG
WI-7889b	54 C ---	---	TTAGGTCTCATGCCACTCCGCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTCAGGACTGGCGGGGGCGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCTGGAGAAAGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCTCCCAAGGCTGTCTTCTCCAGAGCACAGAAG
WI-7894c	142 A G ---	---	AGCCACCCCAATATACTGTTATCCAGAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTGTGAATTTATATTTGCGTATAC ATTATC/AGJTATGTAAATTTGCAATTTTTTATTGAAAATTTGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	AGCCACCCCAATATACTGTTATCCAGAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTGTGAATTTATATTTGCGTATAC ATTATC/AGJTATGTAAATTTGCAATTTTTTATTGAAAATTTGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAGTGACCTTCAGAGCAGGT GCCACAACTGGCCATGIC/TJCTGCCATTGAACAGTGATTAGTTTATCAAGCCATGGTGACACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAGTACATTTCTCAGATTTGAACCAAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAGACATTTAAAGAAATC
WI-7900d	128 C T ---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAGTGACCTTCAGAGCAGGT GCCACAACTGGCCATGIC/TJCTGCCATTGAACAGTGATTAGTTTATCAAGCCATGGTGACACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAGTACATTTCTCAGATTTGAACCAAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAGACATTTAAAGAAATC
WI-7900e	84 C T ---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAGTGACCTTCAGAGCAGGT GCCACAACTGGCCATGIC/TJCTGCCATTGAACAGTGATTAGTTTATCAAGCCATGGTGACACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAGTACATTTCTCAGATTTGAACCAAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAGACATTTAAAGAAATC

[illegible]

WI-7901	33 C T	---	---	AGAC TAGGTACAATGCTCCCTTTTATATATAC/TAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCACTTTTATAAACATGGTAAGAC CCTTTTAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGTTATTTGGGCGAGCGCGGTGGTGGT CAC/CAGTCGCTGCTGCTGCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G	---	---	AGACTTAGGTACAATGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCACTTTTATAAACATGGTAAGACCCCT TTTTAAACAACTCCAGGCCCTTGGTTGCGGGTCGCTGGTTATTTGGGCGAGCGCGGTGGTGGTGCAC TCAGTCGCTGCTGCTGCTCTGTCATACAGACAGGTAACCTAGTTCTGTTGTT
WI-7926c	150 C A	---	---	CATTCGGCATCTGTCAACGAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACCTA/C/AJATTTTAACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926b	28 A T	---	---	CATTCGGCATCTGTCAACGAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCTTTC ATTTACAATGCAATACCTA/C/AJATTTTAACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926	150 C A	---	---	CATTCGGCATCTGTCAACGAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACCTA/C/AJATTTTAACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7947b	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCAATAGCAGCCAGCCACACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACAGCCGAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGTCATTTCAATTCAAATCCATAGATTTCGAAGCCACA GA/GT/TCTCTCCCTGGAGCAGACTATGGCAGCCCATGCTGCCACCTG
WI-7947	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCAATAGCAGCCAGCCACACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACAGCCGAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGTCATTTCAATTCAAATCCATAGATTTCGAAGCCACA GA/GT/TCTCTCCCTGGAGCAGACTATGGCAGCCCATGCTGCCACCTG
WI-7963b	145 T C	---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTATTAATAAAAAATGCC ACAAATTCATTTCTCCTCTAGTATTACAAATGGAGTTATTTCTCGCTAAAAAGTGAAGAAAT TGAGTGAATGAT/CJAAATTTTGTAAATTTAGGATAAGATCCAAAGTTATTTCCCAACTCTTTGTTGCC CCATAAGTTAGGCATGAGGAGGAGCAGCTATTAAGGCGAGAGACGGAAAA

[illegible]

WI-8021b	57	CT	---		ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTGTGAATCTCATCTGGAAA[C/T]GATCCC ACGCTTAGAACCTTCAACCAAGGAGTTTCTTGTAGTGATTCTCAAAAGTCTGGTAGGCATTCTGA ACTGGTCTTCACTTTGAGATCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGATTCGAATCGGTGAATTGCCA
WI-8021	57	CT	---		ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTGTGAATCTCATCTGGAAA[C/T]GATCCC ACGCTTAGAACCTTCAACCAAGGAGTTTCTTGTAGTGATTCTCAAAAGTCTGGTAGGCATTCTGA ACTGGTCTTCACTTTGAGATCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A	---		CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTGTCAGTCA GCTTGATTTCAGGAGGACAGGGCAGAGGATCCAGTGGCATTCCCATGGGAAGACAGAAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTATCAACCAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAAGAGC
WI-8024b	206	A	---		CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTGTCAGTCA GCTTGATTTCAGGAGGACAGGGCAGAGGATCCAGTGGCATTCCCATGGGAAGACAGAAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTATCAACCAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAAGAGC
WI-8077	167	A	---		GAATGAGCCTTCTAGCGCGAGGAGCTGCTGCTGTGTGGCTGCATGCAATCTATGGAATGC TTTTTGGCCAAAGCGGGGACCTGAGGACTAAGCTCTGANNNNNNNATCTCGCCCAACTCCTTCT AAGGAGTCTGGGTGTCATGCCCTACAAACQ[A/G]TAAATCTCATCAGATGGATTTTATTAAAGTT GTGATTGTGACTTACTTCCAACTTGACTCTGGCATAACAAGGGAAAA
WI-8118f	114	GC	---		TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTGGAAATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[G/G]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A	---		TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTGGAAATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[G/G]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T	G	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTGGAAATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[G/G]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44	CT	---	---	---	TCTAGGTTTAATCAAAGCAATTGCAANTTTGGATTGGAATGA/TCACCTCCCTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATCCTCCT AAAATCAGACTCATTTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88	TC	---	---	---	TCTAGGTTTAATCAAAGCAATTGCAANTTTGGATTGGAATGACCACCTCCCTGCTAAGGAAGCTAT GTACTTCATGCTGTGAAAC/TCIGGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATCCTCCT AAAATCAGACTCATTTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299	CT	---	---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAATGGCAGCAGGGCCTCGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46	AG	---	---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGMGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46	AG	---	---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298	TC	---	---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAATGGCAGCAGGGCCTCGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85	GC	---	---	---	GAGGGGAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTTAAGGG/CGJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTTTC TGTGATGATGAAAAGATTCTACTCTGACCTATTCATAGGGTTAACCCT
WI-8314	78	CG	---	---	---	GAGGGGAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCT/CGJTAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTTTC TGTGATGATGAAAAGATTCTACTCTGACCTATTCATAGGGTTAACCCT

WI-8321	178	GA	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAGTTAAAAGTTACAAATGTGTCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATCTAGTCTCTGAGAAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATCTTTCTTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	GA	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAGTTAAAAGTTACAAATGTGTCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATCTAGTCTCTGAGAAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATCTTTCTTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123	AC	---	---	TATGACTCACITTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCGAGCTTAGA/CJACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCCCGAGCAATGCTACTGCAGCTACTTAGTAACAACCTAG AGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	AC	---	---	TATGACTCACITTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCGAGCTTAGA/CJACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCCCGAGCAATGCTACTGCAGCTACTTAGTAACAACCTAG AGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	TC	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGAGGGAAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCCAATCACCTNTCACCCAGGCCCTCTCCAAACACGTGGGG
WI-8378	308	TC	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGAGGGAAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCCAATCACCTNTCACCCAGGCCCTCTCCAAACACGTGGGG
WI-8426	184	TG	---	---	TTTAGCACATATTAGCATTAAGCTCAACGATACAGCAATATGTTACATTCCTTGTGAAAAACAG TTGTTGAGACTGTTAANNNNNNNAATGTAACCTCGACTTGTGCTTAATAGGATTTGACCNNTAA GAGGNTCTTTTGTGTGGGNGGGTGTGCTTGTGAACTTCCATCTCTGTG/GCCTTGTAGCTGGTG AGGCTGGAGTATGGANGNCCCGGGCCCTTGGCNATGNATCAGTGAG
WI-8450h	61	CA	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCTTCTACATACACTC/AJCA TCTTCTATCTTAGTCCAAAGTTTGTGTTTCAATCCCAATATACCAATTCATTTGTTATTTAAGA AAAAACCTTCCAGTTATGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATCCATTGTTATTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATCCATTGTTATTC/TCTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATCCATTGTTATTC/TCTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATCCATTGTTATTC/TCTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATCCATTGTTATTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATCCATTGTTATTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTTCOAAGTTTGTAGTTTCAATCCCAATTATACCAATCCATTGTTATTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ---			CAAGGAAAGCTGTGAGTCTTCATAAATTTCAAAAGAGTTACAAAAATACGTTATTTTAAAGCTA CAATTCAAGATTAGCATCCAAACCTACAACATGATGTACATTCGTACACACCATACCACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTATACCTTGTAAGAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCATTTTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGAGTAGACTTAATTTTGATAAAAAAAT TAAAAAGCAT[A/G]ACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATATTCTCCCTTTGTTTGTCTTTTAAAAACATTATTTCTGAAAAA ATCAGAAAAACATGATCGTGGAGAAATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAATCCAGTCTGTCAGCTCAGTACCTGTC/TGTGACACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCCAGAGGCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAATCTGTCAGCTCAGTACCTGTCGTGACACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCCAGAGGCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9446b	75 T C ---	---	---	GAAGGCTTGATTAAGGGAGGNTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAATCTCCTCTAAAGNGACACATGCCCAAATGACCANGNCATAGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGNCCTTACNTTATCACTGTGCTCTGCTTTTGTCTACCTA TGNGAACTGCACACTAICTGTGGCAATATTGT

WI-9446	75 T C ---	---	---	GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGNAACCTTACCATTCCATAGACTATAAAGANCAITTA TAAAAAAAT/CJCCCTCTAAAGNGACACATGCCCCAAATGACCAANGNCATAGCAAAACCTTTTAAAT TACTCATCTTCATATGTGTGTTGNCCTTACTNTATCACTGTGCTCTCTGCTCTTTGCTACCTA TGNGACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185 A ---	---	---	ATTAAAAATGTCAGGTTTCATGTTTACATTTCTTATATCAAGTACAAATGGTATATATACATTTTTTT GAGATAATTAATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACIT GGAATTTCTACATGGAAGGCAACAAATAACTAAACTTGACTAATGAAG
WI-9497	185 A ---	---	---	ATTAAAAATGTCAGGTTTCATGTTTACATTTCTTATATCAAGTACAAATGGTATATATACATTTTTTT GAGATAATTAATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACIT GGAATTTCTACATGGAAGGCAACAAATAACTAAACTTGACTAATGAAG
WI-9523b	193 C A ---	---	---	GTGAAAAAGTTTCTATTCCATCCATACATAAGATTGTGCTAAGGATCATTTTGGAGAATGTG CAGCATTCAGAAGTTGTATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGTTGATTTCCACACATTTGTA/CJAJAGTG AAAGCTCTCAGCTTGGAAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	---	GTGAAAAAGTTTCTATTCCATCCATACATAAGATTGTGCTAAGGATCATTTTGGAGAATGTG GTGCAGCATTCAGAAGTTGTATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGTTGATTTCCACACATTTGTACAGTGA AAGCTCTCAGCTTGGAAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	---	AAAAACAAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGATAGTACTGCCCTTNCITAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCAAGAACACTAGAGTCTACACCCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG GT/CJGCTGGATACCACTAAGAAAGTCTACTGCGCAAGCTTGGTTATGATTTT
WI-9555	97 G A ---	---	---	CCAAAAGCCAAACCATTCATATGATGGATTTCATAAACATTTATTGATCCTTTTGGAGTAAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/CJAJCTTGAAAAATCAATTTCAAGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTTCAG GGNTAAATGGTACAAAAAAGGCTGTAACITCTTTCACATTGATCACA
WI-9625b	172 A/T ---	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAATCAATCATTTT TAAACATAGCTACCATATATTGTATCTNCCTTGGGAAAAACCTTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTGTGGACAAGTCTCTATGTTTACCATTTTATATTGACATAA AGTAGCAGACACTAGTTATTTCATTTAAAAAAACACACTGCACAAATCTTTTC

WI-9625	172 A T ---	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGGAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAAATTTGGAAAAAACAACGCGACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTTCATTTAAAAAACAACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTCTACTATACCTTTTTCATCCTTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATGCTAGACCTAAAAATCCAAGCT TACAACTTC/TGTCTTACCTGATACATTTATCCATTTACTTTTCAATTTTGAATTTTAAAAATGTTA ACTTAATACGTCCTTTTTCAGATGTCCTGCTTTTGTAGTTAATGTGTTT
WI-9676n	114 A G ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCTATGTTGTTT
WI-9676m	184 G T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCTATGTTGTTT
WI-9676l	84 A C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCTATGTTGTTT
WI-9676k	202 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATGAAGG C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCTATGTTGTTT
WI-9676j	92 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCTATGTTGTTT
WI-9676i	173 T C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAAATGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCTATGTTGTTT

WI-9676h	134	C A	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCCCCQ C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGGCTTTCCTGCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40	CA	---	---	TGGACCAACACAGACAGATGTTCTCTGGTGCCTGTGTAIC/AJATTACAACATCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTGCTGTTGTCACCTTGCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCITTTATTTCTGTCCCTTATGTTGGTGGCACATGICITGTTATGCTGTC
WI-9738	40	CA	---	---	TGGACCAACACAGACAGATGTTCTCTGGTGCCTGTGTAIC/AJATTACAACATCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTGCTGTTGTCACCTTGCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCITTTATTTCTGTCCCTTATGTTGGTGGCACATGICITGTTATGCTGTC
WI-9756	47	A	---	---	ACTGAAATGTAAATGGCCAAAGGCACCCAGGACCTTAAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACATAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGCCCTTATCAGCTTTAGTC AGTAAAGATAAGAAAGCCCTGCTGAGTATCCACTCCACAACACACAGAAATATACATTTTGGAAAG ATTCCACTTAACCACTTGATTCTTCACITTTTATGATTTAAACTCTCCGTGG
WI-9758	135	AG	---	---	GATGGTCCCTTAAGGATTTGCATTTGTTAATGGCAGACTGGTGC AAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTC AAAGAAGAAATCTTGTTCGCAAGGCAATTTTATACTATTTA A/A/GJTAAAATAACTCTGTGAGTTCTATAGCAATGCTAAGTAAAGTAACCGCTGGTTCTAAATTT ATTACG
WI-9778	127	GA	---	---	ATTAAATCCAGGCAGCGGGGAAAAATGGATCTTTCATATGCTCTGTACCCCAACTATAAATTTTG GTTCTCATGCACCATTTTCAITTTTGCTTCCTCACTCCCAAGTACCACTGATTTTACCAATTTGAJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCCTCA AAGAAATGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	CA	---	---	TCGCCCTTTGCCCTCTCATGCCACTCCCTCAGCCTGCACAGAGCGTTTCTCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACTGCAGGACTTCTGACAATGCAATTTTC/AJTGATCCCAAGGAGGA CTCAAAAAAAGTGGAAATGGGAGAAAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTGTAAAGTGGACTAAAGTTTGAGGACCAAGCATGGAAGGTTGGCTTTGGC
WI-9841	101	AG	---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC/AJGTGTGTATGTATATATATCTATTAAACATTT AGGATATATACACACAATAAAACGCTGTGAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTTACTTGATATGCTGTTG
WI-9880c	222	GA	---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTTGGCAGTTAAACAATAAATGTTATTAGATC ACTGGTCTCTGTGGGGTTGAGTTTTTATGATAICTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATAAGGCACATGAA AATGGAATGAAATAATGAJG/AJTGACATAGGAATTACCTACATATTTTG

WI-9880b	157 C A ---				GAACATAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGA[C]ATATAAGATCCCTTTTAAAAATTATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108 C T ---				GAACATAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTTGAGTTTTTATGATATCT[C]TCTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCCTTTTAAAAATTATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127 C T ---				ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTAAAAAACAACGCCAGTTATCACAGTTTCTNTTTTGT[C]TJCAACC ATTTCCATAACAAAGAAAGCTACACAAAATTNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109 A G ---				TCCCTCAATGACAGATGAACATAAATTTCTCTGGGTAGAAATACCTTATGTCCTATGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A]GJTGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109 A G ---				TCCCTCAATGACAGATGAACATAAATTTCTCTGGGTAGAAATACCTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A]GJTGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102 C A ---				ACAACGCTGAACCTTCATACAGTCAATGGTACAGTCAAAACATCAGATGTACAGACACACAATTTA GATGAACCTGAAATTTAAGNTAAATAAAATAAAAT[C]A[C]AATTTTCAGNAAACAAAATCAAAC ATTAAGGNTCCCTGNNATATTTCTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCCTATTACCCAGTCTAGGGATTCTG
NIB551	161 C T ---				CGTCCCTTCTCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAACTGACAATGGGTGTCCCC TACTGAGCTTGGGGCCAGGTGTACTTAGGAACCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C]TJTGACCACATACATCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTCC
S72904	51 G T ---				AGCATAGAAAGTGATTTATATTTTAAATGGTTTCAAGTGGAGTTCTTT[G]TAAATTTGTCAGTTC ATTCCTGGAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAACCAAGTGCTGAACCTCTCCCTTTCTGTCAATGGTTGCTGTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTCTTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	---	TATCTTTTATCCTGGGCCACAGTCTTGATTATCCTCTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAAAACACAGAGC/JACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTCAGATTGAGC
ESTC1	33	---	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	---	GCTACTACCACGGCTGCTGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	---	GCCATCAAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCG ACTTGAA
ESTC107	20	---	---	---	---	TGCTGCTCCTCCTCACANGCTGTATTACCTTTGAGAGTGTGAGGCTGTGCT
ESTC109	35	---	---	---	---	AAACCAGGAAGGCCTGCCCGCAGAGGCACATGNACAGGCGAGTGCACAGTGACC
ESTC110	23	---	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	---	GACAATAAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGGAAGTGG
ESTC129	20	---	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTCGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAAACANGAGAAGCTGAAAAAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTTGTCAGGTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTTCTGCTCCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGAGCACGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTTGGTACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATACAATACAGTCTCAATACAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCCATTTCTTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGNGCTTTTITAGCAGCATTTCCG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTGTCTACACAGACACTTAAGTACTGTATCGCTGNATGCAGCGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	TCAGTTCATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCCCATTTTTTCTTTTAAATACMACTACTGGTCTNAAACTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACACAGNTTGCACGAATTATAAGTGGATCAACAAATT ATATTATTGATACAACTCATGAGCAATTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCTGGCTGCTCGGATGGAGCGGGGGGGCTCA CCACCCTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCAACCACAAGGACAGGTT TTTAGCATTTGCTGGTGCAGTGGGGGCTGAGCTGGGNGCAGTGGCAGTGTCACTGGGCGCGTTTG GGACTGGGTGA
ESTC160	38	---	---	---	CTCTCGTCGGTTTGCAGTTCCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG TCATTCTCCATAGAATAATTGGTTTTGTAAACNGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC162	36	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTCTGGATTAGAGGAAAGTGCCGCTGTTTCCATGACTT CACTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC164	31	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAATTTTNCITTTATTTCTATTAAATACCTTTTAT TCTCTTTATTCCTCCATAAAAGGCCAACCAA
ESTC169	22	---	---	---	TCAGACACTGCCGACATCAGCATTTGCTCTGNTGTACAGCTCCCTTCCCTGCAGGGCGCCCTGGGAGAC AACTGGACAAGA
ESTC176	23	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTTAATATATATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC177	42	---	---	---	GCITGACTAGCGAGGCTACATCAAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCTCAGCTTG ATTTTACCTCA
ESTC18	29	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGATATGGCTGG TCTATTACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACATCACTTGCTTCCAT CTTGC
ESTC181	21	---	---	---	AMAGTACATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA TCCTCAAAATACCACCTTCCCTTAACCTATCAGCTAGTAAGCNITTTCAAAGGAGGAAATGGGTTAC CTTCAGGGG
ESTC186	43	---	---	---	ATCTCCAGTGTCTGCTGCCTCTCCNCGCAAAGTCTCCACAAAGCACA AAGATTAGGACAGACCGGTATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGCTGTGGAA CGCTGCTTAGATC
ESTC187	24	---	---	---	TTTGGTGAATCCCAATATATAGTTTTAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG
ESTC188	25	---	---	---	
ESTC189	27	---	---	---	
ESTC196	42	---	---	---	
ESTC197	26	---	---	---	
ESTC20	33	---	---	---	
ESTC200	44	---	---	---	

ESTC201	35	---	---	---	---	TCCTACTTGGGTAGTTAGCAACATTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGGAGGACAGACGNCAGCGGCTGGGTGGCGGCCAGAAAGGCTGGCGTGATGTT
ESTC203	27	---	---	---	---	CGAGATGAGGC
ESTC208	43	---	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC
ESTC210	29	---	---	---	---	AAGACAGTTGCA
ESTC212	27	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC
ESTC214	21	---	---	---	---	CTAAGAGTGAATA
ESTC216	49	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAAGAGTGAGTGACGGTGACCTGTG
ESTC217	28	---	---	---	---	GGGTAACTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGGCTTCAGAGCAGAGGGCTTGGT
ESTC219	32	---	---	---	---	TCAAGTC
ESTC22	41	---	---	---	---	CTCAGAGTCCTCTCTCANACCAGGGCAGGAGGAGTTAGGGAAT
ESTC223	27	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCACAGGTATTNTAGATTGGTCAGAAAA
ESTC224	37	---	---	---	---	CAAAAGACCA
ESTC225	20	---	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAAATCTGCATGATTAAATAACATTAACAAGTTTCAT
ESTC23	27	---	---	---	---	AAACACAGCCCA
ESTC230	43	---	---	---	---	GTACATCTCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG
ESTC231	24	---	---	---	---	GCAAAGGAAGC
						TCATTGAAGAAATTTATGGGTTTTATTCTTATTCTAATTGNGAGATGCTTAATGTCACAGGCTACA
						TAAGGGCC
						CITCTGAAGCCCAAGAGAGGGGGCAGANGTAGTTCTTGATTAAAAAACAGAAAGGGAGGAGGA
						CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACA
						TGCACGTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTCAGAAGGA
						ATGIGTAGGATCG
						TTCTACTTTATTTCATATTCACCACACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT
						TCCTGAAGGG
						GGTCTCTCCAGAAATTTGAAGACATATTGGTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
						CAAAAGGGTAGTCATATTCCTCCANCAACAGCATGATAAATAATTC AAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTCTCTATCCCTATAAAAAAGGAAGCAGAAATCTGC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCCGCCCTCAATTCATATTTATCTTGAGCGCGCTTGGTCAGGTTTGAT
ESTC31	32	---	---	---	ACAGCCCCACAGAACAATTGTAAACAATATTNTCAGTCGGTGATCATTTGTAATATACAATACAAAG
ESTC33	25	---	---	---	AGCACTCCAGCTCCTTGACGTTGTGGACCGGAACCTTCGGAA
ESTC39	26	---	---	---	AAGCAAGGGAACCCACCTGGCTTNGGTACAGAACACAGACCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAATCATTTATGCTGATGGAAGAAACCAATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGAICTTTTAAAAATATTTGACTTGTCCCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTAACNCTCTCATCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGGTGAGCCCTGCCGCTGCCATGGCCAGGGAGCCACTGGTGGGANCCGGGAGATG
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAGNAGTGGAGGGAAGGACACCA
ESTC57	20	---	---	---	AAATGGGCGCTCCAGTCCNCTCTCTGGGCACAGATCCACCAGTCTGCTC
ESTC59	38	---	---	---	GAACACAAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTCAGACTTCAGGAAAAATGATTTCC
ESTC6	27	---	---	---	TCTGCAGCATTTCACTACCAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAAATGCATTATG
ESTC61	57	---	---	---	AGTGATTTTGGCTAGGCGTGGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCNCCTCTCTCC
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGCCACGGGAGGGTGGGGAGACGACACTTTTCCCTGGGAAA
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCACACTTACTTACTGCTCATCCGT
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCCTGAGTTGCANGCACCGATGGAGATTTGGACACT

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGGNTTTGGGGTGACGCCTAAAAAGTGTGACC
ESTC74	49	---	---	---	AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAAATATTCATACNNTTGGGTTGAAAAGTTG GAAGA
ESTC77	40	---	---	---	ATGACTTTCCTGTCCTCCATCGAAACCCAGAGTTTCCCCAGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGTCTGAGATGNTCTCAGGCTGCATCAGCTGCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATATACANCCATTATTTAGAC TTTCACAAACCT
ESTC85	28	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGCTGCTGGTTGGGGAGGCTACAGCCTGACCACATTTC TTTGC
ESTC89	22	---	---	---	ATTGCAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33	---	---	---	CTGGTCTCTTCGCTTGGCAATTCGCTCCTCCTCNGCCAGTGTCCACCCAGTGTCTTCCCGATGAT
ESTC93	29	---	---	---	CTCCCTCTCTCAGTTCACAGTGGAGACTANGGAGATTACAGGGCAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTTGTTCTCTCTCCAGAAAGTTGNAGACGCTATTATTAGTTTGAATATCTGTCG
DWU-100	127	CIT	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTC GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGAATCTTCCCACTGGCCAG ATCTTATCAATGATCTTTCACCTAAGAAACAGCAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGGGATTTTTCACAAAATCAAAGAAAGAAAGGCTTAGCTG
DWU-177	77	AG	---	---	TTCCATCCTAGATATCTACTCAAATAATTGAGACAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGCAGGGCTTTCACAGTAGCCAAACGATGAAACAAACCCCAAGCTATATATTACCA GATGAAAGGATAAAACAAAATGTGGTCCATCCATACAAATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTATCCCTACTACACTGTGGAT
DWU-286	213	A/C	---	---	CAAAATCCTGGACTATCAACCTTGTGTCTTAATCCCTGCAGCATTCAAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCAATCATGCCAGCTTCTGTCAATGATGATGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGCTGCGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGGACITGGGAACCAAGCCCTATCTGAGTCTTCGGCTCCCTCC

DWU-252	94 A G ---	---	---	AGTATACAAACATTTAAGCTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGIGT CAGAAAGGAGCTACAAACCTACCCCTCA/GT/GAGCATGGTACTTTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCCCTGTTGAATGACAAAGTATGTGGTTTGTGTA AT
DWU-330	85 C T ---	---	---	GAACATTCCCTCTGCAGCACTTCACTACCAAAATGAGCAATTAGCTACTTTTCAGAAATTGAAGGAGAAAA TGCAATTATGGGACTGA/C/TCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTTCTTTTGCAA CAAGACAAGCAAGCCACATTTTGCAATTAGACAGATGACGGCTGCTCGAAGAACAATGTCTCAGAAA CTCGATGAATGIGTTGATTTGAGAAATTTTACTGACAGAAAATGCAATCTCCCT
DWU-370	231 A G ---	---	---	GAAAAATGTTAATTGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTTGGTTTTAAAAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAGAAAGGTGAATGTTGAGGGCCCTTCACCTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCCCTA/G/GCATCTATTTCCTCTGTGC
DWU-1537b	89 A G ---	---	---	CTCTTAACCTTCAGTCCCTCATCTATAAGAAATAGGGATTCAGTTGTGATCACAATAGCTCAGGTAATC CAGGACCAAAACCCAGGAGC/GTGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGTAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	---	CTCTTAAGTTTCAAGTTCCCTCATCTATAAGAAATAGGGATTCAGTTGTGATCA/C/TTATAGCTCAGGTA ATCCAGGACCAAGAAACCCAGGAGCTGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGTAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATTCAGGGTCACTGTCTCTCTCCCTGCTCCCTGTGGGAAT CAAGCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGCCCTG/GA/GCACTGAGCTGCAGA CCCGCAGACCAACTCTGAGCTTTCTGGGCTCTGAGTCTTGCTCTC
ESTD-ADAa	184 G A ---	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATTCAGGGTCACTGTCTCTCTCCCTGCTCCCTGTGGGAAT CAAGCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGCCCTG/GA/GCACTGAGCTGCAGA CCCGCAGACCAACTCTGAGCTTTCTGGGCTCTGAGTCTTGCTCTC
ESTD-ANT1	160 T C ---	---	---	TCTCTGTCTACTTCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGCAATTAAACAAATATTCA TGAGCTGCCCAACTGCGAAACAAAGAGGGCGCAGTGGAGCAGGAGATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCT/C/GAGCTCAGATGATCTCTGT
EST10398 2b	168 A G ---	---	---	TGCCTGGGGTGGCAAGGCTGCAAAACAGGAGGCCAACCCAGGAGGCTTTTATGAAGCGGCCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTCAATTTGGGGCTTGACTTTCCAACACGGAGAAG CATTGTTTCTTCGGGCCAAGAAAGGTATCTACC/G/G/ATAGTGTCTATTAGGCATTTG

EST10398 2a	147 C T	---	---	TGCTGGGTGGCAAGGCTGCAAAAGAGGCAACCCAGGAGGCTTTATGAAGGGGCCATGGTA AGATGCTGCCACTCTTATCTACTTGTATGATGTTACATTTGGGGCTTGACTTTCCAAACAGGAGAG CATGTTTCTTCTTGGCCAAAGGATATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14 G C	---	---	ATACTGTGGCTTATGCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-				CTTTCATGCAGATAGGCTTCTCTACTAAACACAGAAATTTGAGAAGAGCAAAACAACTTTCAAGG
D4S95	90 T C	---	---	ATAATGGGGCAATCACTTTCTTTTCTTTAGATCTACCGG
ESTD-				
GPPK2L	38 G A	---	---	AGTCTTCATCTGCGGTGTCAGGTAGATCCCTTTACACGAGJCCGAGAACTGCTCGATATC
ESTD-				CTGGGCTGCGCCGACGAGCTGCTGGACCTGGACGGCGGCCAGGCTCACCTCTATAGTGGGGTCG
HRASb	82 A G	---	---	TATTCGTCCACAAAGTGCATCTGGATCAGCT
ESTD-				CTGGGCTGCGCCGACGAGCTGCTGGACCTGGACGGCTGGGGCCAGGCTACCTCTATAGTGGGG
HRASa	37 C T	---	---	TCGTATTGCTCCACAAATGCATCTGGATCAGCT
ESTD-				GGAGGACGAGGTGGGGAGGGGCTGCTGCTGCTCCAGTCCACAGACCAGAGAGCGGCTCAGTG
NRAMP	81 A G	---	---	TATCCCAACCCCAAGTGTGGGGCTGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18 A G	---	---	GTGACCTTCTACITTAAGJAAACTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC
EST36751				AGATCTGAAATTTAGGATAAAACAGAAAGGAGGATGTAAACA
7	36 C T	---	---	CCAGTCGTTCAATTTAGCTTGCAGGTTTAACTCTGATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
				CACGTGGAAGGAGCTATTTTGGAGGCTTAAAGATAAAGAACTGTCCCAAACTTGTGGCTGAC
				TTTATGGCTAAGAAAGTTTCACTGGATGCATTATAACAAATJAGJTTTTTACCCTTTTGAATAATAA
				ATGAAGGATTTGACCTGCTTCCGCTCTGGAAGAGTATCCGTACCGTCCGTGACGTTTTGAAACAATACA
EST40552	109 A G	---	---	GATGCCCTCCCTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288				GCCTCTATACCCCTGTGGTCCCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA
3				GATTGACAGGTTTCATGACGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGAJCTGGGAGCCAGT
EST18288				GTGGACAGCACCCCTGGCTTCAACACCTACGTCCACTTCCAGGTAAGGCAAAACCTCTCTGCTGGCTC
ESTD-AK-168	121 C T	---	---	TGSCCCTAGGACTTAGTATCC
				GGGAGTGACAGCTAGAGCACCAAGGGGGGCTCTTACAGCTGTGTTCTCATGGAGGACAGGCTTCT
	31 C T	---	---	GCCTATCTGG
				AATCCCAGCACITTAGGAGGCTGAGGCGGCATATCACAGAGGTCAGGATTTGAGACCAGTCTGA
				CCAAATGTTGAAACCCCATCTCTACTATAAAATACAAATAGCCAGGATGGTGGTGCCTGT
ESTD-ALB	180 A G	---	---	AATCCCAGGAGGCTGAGGCGAGAGATCGCTTGAACCTGGGAGGCGJAGGTTGTGGTGAGCCGA GATGCGACCATTGCACTCCAGCTGGGCAACAGAGTAAACTCTGCTTC

EST70523 3	182	G T	---	---	TTCCGCCAGCCCCCATCTTGGCACCTGTGTCCTCCCTCAGGGGCCACCCCGGGCACTCACCGCTCT CGCTCGGTAAACATCCGGCGGGCGCGCTCTGAGCACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCCCTTCTGTCCCGGGCTTCCAGGGGCCAGCCCTGTCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
ESTD- APOA2	101	C T	---	---	CCAGTGTGTGGACGTGCTGTATCCAGCTACTCGGGAGACTAGGCATGAGAATCTTTTGAAC CGGGAGCGGAGGTTGCAGTGAGCTGACATCGCTGGCCACTGCACCTCCAGCTAGGTGACAGAGC AAGACTCC
EST58707 7	112	C T	---	---	CAGTGTATCTGAAAGCCTACAGGACACCAAAATACCTTAATCATCAATTTGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCAGATGAAGGCCAAATCCGAGAGACCTCTAGAAATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTGTACACTACATTTCTGATTGGTGGACTCTGTCTGCTAAGAACCTT
EST74167 6	137	C	---	---	AGACCATGAAGGAGTTGAAGGCTTACAAATCGGAATCGGAACCTGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGCGGGCACGGCTGTCAAGGAGCTGAGGGCGGCGAGGCCCGGCTGGCGCGGACATGGAGGA CGTGC GCGCGCGCTGTGTCAGTACCGGCGGAGGTGAGGCCATGCTGGGCCAGAGCACCCGAGGAGC TGCGGTGGCGCTCGCTCCACCTGGCAAGCTGGCTAAGCGCTCTC
EST43211 8	132	C	---	---	CGCTGTGTGAGTACCGGGGAGGTGAGGCGCATCTGGCCAGAGCACCGAGGAGCTGGGGTGG CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGCTCTCCGCGATCCGATGACCTGCAGAAAGCGCC TGGCAGTACCGAGCGCGCGCGCGAGGGGCGCGAGCGGCTCAGCGCATCCCGGAGCGGCTG GGGCGCTGTGTGAACAGGGCGCGTGGCGGCGCGCTGCTG
ESTD- ARSB	126	A	---	---	GGAAGAAATGGAGCCTGTGGAGGAGGCGTCCGAGGGTGGGCTTTGTGGCAAGCCCTTGTCTGA AGCAGAGGGCGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCCAGAAATGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144	C	---	---	TGTAGCCAAAGTCACCTGCATCATCTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATAGTGGTTCCTGTTTCTCTTCTGATCAT TCTTACAAGTTATAGCTTTATTGGAAGGCCCTAAAGAGGCTTATG
EST26021 1	137	A	---	---	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGTAGTTGAGTGACATGTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATCTCTGCAGCACTTCACTACCAATGA GCATTAGCTACTTTTCAGAATTGAGGAGAAATGCAATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTTGTCAACAAGACAAAGCAAGGCC
ESTD- BA511	29	A G	---	---	GGGCAACATAGTGAACCCCATCTCTACAA/GJAAATACAAAATTAGCCAGGTGTGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGAGGATCCCTTAAGCTGGGAGGTGGAGGCTG CAGTGAGCAAGATGGTGCCACTGCA

ESTD- CB22	119 C T ---			GGCAAGTTTTATTGATAGAGAGAAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACATGGCAGTGGCAACCCATAGGG[C/T]GGATACAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTACCACCAAGCAAGGAGGACCT AGTACATAATTGCTTCATTATGGTCTCTCCGGCCTCTCTCTCACACAC
ESTD- CB23	136 C ---			TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCCGGCTTCTCTCACACATACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAAACAGTGTCTCCACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGATCTCCACACCCCAAA
ESTD- CB24	145 A ---			ACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAA AAACGTGTCCACCCGAGGTGCTGTTGAGCCATCAGAAGGAGATCTCCACACCCCAAAAG GCCACACTGGTATGCTTGGCCACAGGCTTACCCCGACACAGCTGGAGCTGAGCTGGTGGTGATGG GAAGGAGGTGCACAGTGGGTGAGCAGACAGACCCCGCAGCCCTCAAGGAG
ESTD- CB25	146 A G ---			GTTTTCTTCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTTCTCTCTATCTTCGCCGTC TCTGCTCTCGAACCCAGGCGATGGAGAAATCCACGGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGTAG[C]CTACATGCTCTGTTCTTGCAACAGAGTCTTACCAGCAAGGGTCTCTCTGCC ACCATCCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTAGCCGTC
ESTD- CB27	125 C T ---			TTTTCTGTTCCCTGAAGATTGAGTCCCAACCCCAAGTACGAATAGGTAAACCAATAAAAAAT TGTTGTTGGGCTGGTGCATTTAGAGAGTGTCTGTGGAGTCTGCTCATCACTGAC[C/T]TATCTTC TGATTTAGGGAAGCAGCATCCCTGGACATCTGAAGTGACAGCCCTTTCTCTCCACCCCAATGCT GCCTTCCTGTTTCATCCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---			TTTTCTGTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/ATATGTA TTTCTTAAACAATAAATTTGAAAGTCCAAATTTACTCCTTGATCCATGGACTGCAGAAATAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTA TTGCCAATAAGCAGTAATATTTTGAGAGGAATCTTGTTTCAATGCAAGTAG
ESTD- CYP2D6	61 A G ---			CAGCCAGCGGTGTCGAGGTGGTCCACCTCCCGCAGAGAACAGGTACGCCACCCTATG[C]AG[C]A GGTCTCATCTTGAAGCTGCTCAGGGTCCCTTGGCCTGAGCAGGGCCGAGAGCATCTCGG
ESTD- D11S1873	40 A C ---			AAAAAACATTTTAAACCTTTTCAATCATATACACCATA[A/C]ATTTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTACTTGCAATCTAAATATGATTAATGCAAGTTCAACAG ACAACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---			CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTACGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGAAAGGCTCTCTGGGGCGGTG GGGTGTGTGGCTATGTGGTGTCTGTGTAGA[C/T]GGGGCTTTGGTTTCAGTTGCATATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCCTC

ESTD- D17S33a	75 C T	CATCCCCAAGCCCATCTCTAGCCACTGGCATTCTTTGCCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGTAGTCATGGAAAGGCTCCTCTCTGGGGCG GTGGGTGTGTGGCTATGTGGTGTCTGTGTAGACGGGGCTTTGTTTTCAGTTGCACATATTGCGTT ATTGCAGATTGCTTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G	TTTGAGACCAACCTGGCCCAACATGGGGAATCACAICTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGGAGGCTGAGGAGGAGAAATTGCTTGAACCCQA /GJGGAGGCAGAGCTTGAGTGAGCCAAAGATCACACCACCTGCACCTACAGGCTGGGTGACACAGTGG GACTCTGCTCAA
ESTD- D3S11	44 G	AACTGATTAGAACCTGAAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTCATCATTAATAAATCCAATAAAGTACACTGTAATAAAGAAATTTAACAGAAATATCATTTGT TTATCAAACCTATTATCACTTATTATTGTTAGCCACTACTAAATCTAAAGCATGTTCTCTGAAAG TTTA
ESTD- D3S12	37 A G	AGGTTCCACATTATTGCTGATGTTTCTGATGTTTCQJ/GJGGAGCCTTGATGTCATCTGTCATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTTATTATTCAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTCTCTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTTATCCC AGAAGTGAACATACCTGCTCTCTAGAACCCAGAGTCATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTATTGGAAGGATGCTGCTGGT
ESTD- D3S2a	248 G	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTCTCTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTTATCCC AGAAGTGAACATACCTGCTCTCTAGAACCCAGAGTCATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTATTGGAAGGATGCTGCTGGT
ESTD- D7S399	83 A G	TGAATCTTAATTGCTATCTCTACAAAATGTATAATCTGAACTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJ/GJGCTCTCTCTACATCATCTTTTCAAAAACATTTTTCATCCATGGACTCCATAC TAGAATTTTGAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGCTGGGACCTCAGTGTCCCTGGGAGAGGAGGAGGAGTGGGAGGAGACA GAATGCTGATTJGJCTGTTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAAG ACCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAT
ESTD-DMa	66 C G	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCTCCACJG GJTTCCATGGGTGTGGGCTGGGACCTCAGTGTCCCTGGGAGAGGAGGAGGAGTGGGAGGAGAGA CAGAATGCTGATTATCTGGTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAAG CCTCCTGATTGAGGAAGGGAGCAGCAGAGCGMAGAGAACAGAT

ESTD- DRD1	154 C T	---	---	TCCCAGCCCTATCGGTCTATTGGACTATGACACTGACGTCTCTCTGGAGAGATCCACCCATCAC ACAAACGGTACGACCCCAACCTCGCATGAACTCGCATGAACTCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGC/TTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C	---	---	TCTGCCCTTTGGTCAGGAGGCTGCCGGCAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCGGACCCG TCCCACACGGTCTCCACAGACTCCCGACAGCCCGCCCAACCCAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T	---	---	AAGACGATGGCCAGGATAGCGCGCAGTAGGAGAGGGCATAGTAGGCGATGTGGCGGGCTGGCTGG CACTGTGGAGTTCTCTGCCACAGGTGTAGTTCAAGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGGGAGGTGGTGATGCCAAGGGGCTTCTGTGAGGAGA
ESTD- EP882	93 C T	---	---	TCTTTAGGATCCGATCTGGCCTGGTTGGGCATCGCTCCGCTAGGTGTAGCGGCTCCACAGCTGG GGTGAGGGGGTGGTGGGTCAAGTGC/TGGGGGCGGGTGCAGACCCACCGGGGCTGGGAGGACTTCA CCCGCCTCACCTCCGTTTCTCGAGCAGTCTCCGCATCGTGACT
ESTD- ETS2	43 A G	---	---	ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGACAC/CAGGAGCCGCTCTGGCGCTG GCAGTCCGTGGAGCGGATGTTCTGGCTGTTGAGATCTCAAGAGCGAGCATGCTGTGGACACA CAGAGACTATTTTAGATTTCTTTGCCCTTTGCAACGAGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAGGAAACCAACATGTCATTTCAGAGTTAGTTTG
ESTD-F9	111 A G	---	---	AGATCTGTAGTATTTTCTCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTTGTAGTTAATTTGTGTAAGTATGATGTTTAA/GJGTCAAACCTTCATTTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A	---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA AGAAATCAAGCACITTTTCAAAACATTGAAGTTGTTTTGAACCTTGGTGTCAACCTTTAATACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GDDH	200 C G	---	---	CCGAGACCGGTACGTGGGGTGGGAGTGTGGAGGGAAGGAGGAACTGGGGGTTAGGGACT TTCCGGGGTGACTTTCCGTTCTGTCTTGCAGAGAAAGGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTGGACCGTGTCTGTCTGCTGCCCTGTTCAGCTGTCTGTCTGCCGCACTC/ GIGACTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	88 A/G	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAAGCCCTGCTGAGCCCACTCTGTTCAACCATGAC AACCACAGGCCCTCTCAGGA/GJACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCAGGCGGCTGAGCCCGAGGAGGAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAGCTGTCCCGAGGTACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAAAGGGCCAGGGTATAAAAGGGGGCCACAAGAGACCGGCTC[A/T] AGGATCCCAAGGCCCAACTCCCGCAACCACTCAGGGTCCTGTGGACAGCTCACTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACACAC[A/G]GGCATCA TTGAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTCATGGTTCCCTAGG
ESTD-HT2	154 G ---	---	GGGCTAAATTTCCGAGCACTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGTCAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTGCTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149 C ---	---	AACACAAAGCCGAGGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGCTTAACCCCT GAGCTATGGAGCCCTGCTGCTGTTGTTTTCTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTCTACAAATGAAA ACATTTTCGTGCTGTAAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGACCTCCACCCCTCTTCTCTCCCTTGGGA CTTTGAGTCAAAATTGGCCTGGACTTGAGTCCCTGAACCAAGAGAAAGAAAGG[A/G]CCCCAGA AATCACAGGTGGCAGCTGCGCTACCGCCATCTCCCTTCTACGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCATTCACCGGCTTGGCAGGAGTG[C/T]CTGGGAGAGAAAGGAAGATG TTCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGFBP1	43 C T ---	---	TTTACTATTTCAATGGATACAGAAATTGGGGAGTCACTATATCTTATGAACAAATAATTCAGATTT CAGTGTAAAGTAATGTGCTTACATTGTGTGAGTGACGGGGCAGTGGTGGATCCGAGAGTGGTGGG TGCAGGGACATAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGATACGAACGAAAGT ATGTAATACTTCACAAATACTAATAAACGGAGTTGAATATAAACCCCA
ESTD- IGHV4-6	120 C ---	---	CAAAGTAAGCACCCAAATAATGTTAGCTATTACTATCATTTATTTATTTATTTATTTTGTG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGACGTGGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCCTCTGGGTTGATGCCATTCTCTGCTCAGCCCTCCGAGTAGCTGGGAATACAGGCAACCCGCC ACTGTTCCCGGCTAAITTTTGTATTTTAGTAGAGACGGAGTTCAACCTG
ESTD-IL1A	110 A G ---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCAATAGCCCTCCCTGTCGTATTGAGGGTGT GGGTCTCTACCTTGGTGGTGTCTCTGCTC[A/G]GAGGCTCTCTGTCATTTGCAGG
ESTD-IL1B	99 A G ---	---	TCCAGGGTGGCTGGACCCAGGCCOCCAGCTCTGCAGCAGGAGGAGCGTGGCTGGCTGGTGAAGCATG TGGGGGTGAGCCAGGGGGCCCAAGGACGGCACTGGCCCTCAGCCCTCCCTCAGCCCTGCTGTCA/ TCCAGATCACTGCTCTCTGCAATGGCCCTGTGGATGGCCCTGCTGGCCCTGCTGGGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGCG
EST74082	134 A T ---	---	

EST45311 0	151 C T	---	---	GGCCTCCTCTCTCCAAATCTGTCCCTATAGTTTTCCCTCTATTAAGTGAACATGACATGTCATCTTTTAGT GGATAGATGCACACAAACACAAAGCCATTATGGGGAAGATCCACGTGTGTGGCCATATTGTAACA CATTTTTCTGCAAATC/TACCTCTTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G	---	---	TGCCCCATCAGCGGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTCCAGCCCTCAAAATGACAGCCATGGCCGCGGGTGCTTCTGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGAGGGCTTGAGGTTGGT GAGGTTAGGTGGGTGTTCTGTGCAAGTCAGGACATCAGTCTGATTA
EST38216 3	26 A T	---	---	ATGCAGGATGAAGGTGGACAGGAGGATGAGGGCCAACTGTCTATCCAGGGCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149 G T	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTCTCCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTC/TAGTGCCAGTATCCAGAGTTTGGTTTTTGAAGTAGCAATGCOCTGTGAA AAAGAACTGAATACCTAAGATTCTGTCTGGGTTTTTGGTGCAATGCA
ESTD- KRT10b	183 C T	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTAACTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCT/TGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTAACTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTTTTAAATAGTCT TCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T	---	---	ACCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCATCTCTCCCGTCTCAGGTTTACCACT/TGTCAACATTGACACA
ESTD- KRT8a	21 C T	---	---	ACCTCACCCCTCCCTTAGCCCTAGCCCTGAGGGAAGCAGGAAATCTCTCCAAATCCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATTA GGCTGCCATCTCTCCCGTCTCAGGTTTACCACTGCAACATTGACACA
EST75099 6	82 C T	---	---	CACCTGTGTGTCTAGATCTCCTCAGTGGCGCCCTCTACTGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCCTGGCCGCTCTTGAGGTGTTGG

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAATTTGAACCGTAGCAAACTGCAATTTGGTATTTAGA AAATAAAAAATTTCCAATATGATGCTGTGTTATACCTGCTGCTGCCATGCAGCATCATAGCCTGT GGGAACCTGAGGGGCTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCGGGCAATCTGACACGTGTGCACCCAGCTGTACCAATTAAGTGAACATGGCTTCGAG AGAGTTGACACAGATTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCTGGATGA
ESTD-LMP2	35 C G ---	---	A TACACACTTTCCTTACCCATTCACTGAAACGACTTCG/GCAAACTGGAGCCTTGTAGGMAATGGAGT TGACCTTCCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCCATGCA AGGGTTTGTCTTAATCTCAATTCATGTCTCTTCATCTTTAGCTGTGGGGTTTGTGTTG TCTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATTATAAAGAGATGTATCTAAACAAAAATAG AGATTGTTATCAGAAGTTCACAACTTTATTAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTCTGATGCTGCCCTCCCGAGCTCTGCTCCCTAGCTG/GAACTTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGTTGGTCTAAGTGTGCTGATTACCTG/GGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGTTCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAACCTAGTACCAGATCCACAGACTGATATGGCTGGT AACATGGACTGTATATTGTACAAAAAAAGTTTATTTTCTAAAAAAAGAAAAAGAGAAAA AAATTTAAAGGTGACTTATATCCACACTGCACACTGCCTAG/GCCCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATCT GAGAAAACTTCTTTTAACTCACCCTTGTGGGGTTTTGGAGAGGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCTTAGGCCCCAGCCCTGCTTGCTCCTCCCTGGCTGTATCTTCTG/GTACTGCAAGAGAGAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGAACACAGTGACCATAATTTCTTCTGCGAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATCTTTTGTGATATATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTTG CTJATTCCTGTGGTTTTTAATAAAAAAT
ESTD-NRAS	202 C T ---	---	GCCACCACACCCACCCAGCACACCTCCACCTCAGCCAGACAGGTTGTTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGGGAG/GTACCGCTGTATCATCGAGCGCGCCGGG CACATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCCAAGTCTCTAGACAGACAAAAACC TAGACAATCACGTGGCTGGCT
ESTD-PAH	100 A G ---	---	

ESTD-TAT	224 C ---	---	---	AAATGGTCAGGACCTGATCCACAAGAAGTGGTACCATTTTCATCAGGCGCATCAGTTCATTGAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTACCTAGAACGTTTGTACAACTTTTCTCCAGTATGGATGGGATATGATGGGGGG GAGAAACAAATTTAAATAGGACCATGAGACACATCA
ESTD- THPB	125 A C ---	---	---	TGGGCTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTGATTTCCAAAGAGAAAGTCCCCAAG CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCAGACAGGATCAGCTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCCAGCAGGACTCAACGGTCCCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTCAGCTTCTGGATTCTTGTCCCAACCAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGCAAAATCAATGTCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAAATATGCATCCAGACAAGAGGTCAATAATATTGATGTCGTTAA CATGGGTGTGATCCATTTTTCATTGGCCATAGGTCCCTATGGGATGACA
ESTD-TYR	122 G T ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAAATCAGTCTGGTCTAAACAATGCCCTACTCTCTTATGCATTAGTATCACA AACCCTGGTGAATATAATAGATTGAGTTAATTAAGTATTTCTTACCTTTATTACCTTCTTTCT AATACAAGCATATGTTAGTACATTAAGTTCTAGGCATACCT
ESTD- TYRP1	222 A C ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAAATCAGTCTGGTCTAAACAATGCCCTACTCTCTTATGCATTAGTATCACA AACCCTGGTGAATATAATAGATTGAGTTAATTAAGTATTTCTTACCTTTATTACCTTCTTTCT AATACAAGCATATGTTAGTACATTAAGTTCTAGGCATACCT
ESTD- TYRP1	222 A C ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGCCCAAGACAAGGTACAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCACTTCAGACTGAGAACCCGTTATATGTAAGTGTGATCGACAAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGCCCAAGACAAGGTACAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCACTTCAGACTGAGAACCCGTTATATGTAAGTGTGATCGACAAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGCCCAAGACAAGGTACAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCACTTCAGACTGAGAACCCGTTATATGTAAGTGTGATCGACAAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGCCCAAGACAAGGTACAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCACTTCAGACTGAGAACCCGTTATATGTAAGTGTGATCGACAAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCAC[AV]GTGGCGGGGATGGCGGGGAGTTC TGGTTGGGCCACGGCTGTGGCCTCGTTGTGAACGGTAGCCTTTCGGTTGCGATGCGCTAAACCTTTGT TTCTTGGCCAAAGGAGGGGCGGGTGCATGCCTGAGATGTAGATGGGOC
ESTD-VWF	36 G ---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTCCACACTGTCTCTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTACGTCAAGCCTCAGCACCCAGATGCTTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGAGCACAGAGATTATTTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGAGTACCAG[C/G]TGTGGTGA AGGAGTGGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
ESTD- TNFα	152 A G ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACCAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCTCACACAAATCAGTCAGTG GCCCAGAAGACCCCTC[AV]GTAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATG CTTGTTGCCCAACTTCCAAATCCCCGCCGCCCGGATGG
ESTD- TNFα	88 A ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACCAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCTCACACAAATCAGTCAGTG GCCCAGAAGACCCCTC[AV]GTAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGCCCAACTTCCAAATCCCCGCCGCCCGGATGG
EST52418 6	113 A G ---	---	CAATTACAGGGTCACTGCTATGATGTGTTTGGAGCCCAGTACCCCTTGGTGGCTACAAGATGTG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGAGGCATACACT[AV]AGTGAAACTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACCTATTGGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTTCACATTGCCAGGA CCAGTGAGCAGCAACAGGGC[AV]GGGCTGGCTTATCAGCCCTCCAGCCCCAGACCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCO CCGGTCACTC
EST51976 7	123 A T ---	---	AGCGAAGAACTGGGCCCCCATGCGGGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG[AT]CTCTCTC CTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGGAGCAGCAGGAGGTGCAGATGCTG GCCCTTTGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTGGTAGTCCAGTGTGACTCATCCAAATGATTTCCAGTGCATCTGTTCTCGAGTTTT CTCTGCCATGTGCTATTGACGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCC[AV]TTAAACAATCTATGAGCCAGGAGAGATACGTATTCCTGCAAGCCGGGCTATGTG TCCCAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	---	AGACCTCAGTTTCCTCTTCTGTAAAAAGGGAAGTTTGTTCCTGGATCTCCATGGGCCAGCCTTAGCA CTGGTCCCTGTAGTCTGTATCAGGTAGAGGAGATGGGACAGGTGGAGAGGAATTTTGAAGGGCA TTGGAAATCAGAGCAAGAGACAGATATTAAAGAGCTGGGGAATGTGG
EST39852 8	106 C G ---	---	---	CGGCTTCCTTCCAGGTATTGTGCAGAAAGGCCGAGATGAOCTCTATGTCTCAGATGCATTCOATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTA/C/GJGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAGGCTGTTTCCAGTGTAAAGGCATGCAAAAGGCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	---	ACCTGGTGTGCTGGTGGTGAACCTGCTCTTGGCATTGCCGGCCCTCTGGGGCCCGTGG TCCTCTGGTGTGGTAGTCTGAGTCAACGGTCTCTTA/GJGTGAAGCTGGTCTGATGGCA ACCCTGGGAACGATGGTCCCAAGGTGCGATGGTCAACCCGGACACAAGGGAGAGCGCGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	---	AGTGACTTCCAAGGAATGGCTACCCAACTTGCCTTCATGGCCCTGCTGGCCAACCTATGCCTCTCAGA ACATCAOCTACCAGTCAAGAACAGCAATTGCATACATGGATGAGGAGACTGG[AVC]AACCTGAAAA AGGCTGTCAATCTACAGGCTCTAATGATGTGAACCTTGTCTGAGGCAACAGCAGGTTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAGACAAATGAATGGGGAAGACAA
ESTD- COL2A1cd	112 A G ---	---	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGTAGACAACA GTGGTACATAGCTGTATTTATGCTCTCTTCTCTGCTCACTTCA/GJGGGTTCAGGTGGAATA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAAGTCAACTCAAGCATATACATACTGCCT TTGGTACGCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	---	TGAGAGAACACCTAGTCTCCATCCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACA/C/JTGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATATTTATTTGACCAACACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGGAGAAGGCCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCTTCTCATCATGAAAAAC TGGGAGGCCGGCATTA/GJGTGCTCATGCCTGTAAATCCAGCATTTTGAAGGCTGAGGCGGGTGGAT CACTTGAGGTGAGGATTTGAGACCAACCTGGCCCAACAT
EST12274 0	135 A G ---	---	---	CCCCAGTTGACAGCCACTGCTTAGACTAAGTTCTTGTCTCCAATAGAGCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCCTCATGACCAATAATTTCTTCCCTCCTTAGGATGAGGTG A/GJTAGTAATGACCGATGGGTGAGAACTGTCTGTCACTGAGGATGAGGATGAGGATGAGGATGAGGAT TAAATCAAGCCACAGAGCTTGCAGATC
EST76807	91 G ---	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGCTCTATCTCCAGGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCCGAGGCTCGGAGGACTCAACACTGCCCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG

ESTD-SSA1	111 CT	---	---	TTCACTTTGTGGATTGTTCTTTTGTGCTGCGAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAGTTTGTCTTGGCTGCCTGTGCTTGGGATATTTGAAGAGATC/TJTTTGGCAGTCCAAATGCTCTAGAGAGTTTCCCAATGTTTCTTGTAAAGTTTCAATAGTTTGAGGCCCTAGATTIAGTCTTTAATCCATTTGAATTGATTCTGTGA
ESTD-FYR1	109 A G	---	---	CTTCGTGACGGGAGGTCAGTCCCTCGGCTCTTTTCATGGACATATGGATGGATGTCTGACCAATTTCCCCTGTGACAGTGATGACACGCGCAGACTTGTCTACTATAGAG/GJGGGAGCTGTGTGCACTCATGCCCGCTCCCTCTGGAGGCTGAGCCACTGAGANTCAGCTGGAGTGGGAGCCACCTGGCTGGGGCCAGGCCACTCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCGTGCAGGATGTGCG/GJCGTGTGCTGGAGTAGCCCCGACTCTTGTAACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST4438 7	100 C 62 CT	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCTGCACCAATGGCTCCAAAGCCGTAGGGGAAGCTGGGGGATCTAGGGGATGGGTGAGGAATGGGCCAGCCAGTCCCGGGTGGTGGTCCCAACAGAGAGGCCGTGGAGGAGAGACAGGAGATGGGCTGGATGAG
ESTD-PBDA	103 A G	---	---	GCAGCCAGGAGCGCTGCACCATGCCCGCATAGATCGGACCTCAAGCTCAAGGATTCAGGA/CJTGTCCTGTCCGACCTAAGCGAGCGCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G	---	---	CCITCTCATGCCCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAA/GJCTCTACCCGAGCTTGCTCGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G	---	---	TGCAAAACACACAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCTCCTAACATCTATGTACTGTGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/GJCAAGTCCAAGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACITGAATGTTATTCAACTGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACITTAGCTTAG
ESTD-ACE	96 CT	---	---	ATGGCTTGCCTTGGATTTACGGGGCACAAAGGCTCAGCTGAACCTGGCT/GJCCAGGAOCTGGCCCTGCACCTCCTGTTTTTCTCTCTTCATCCCTGTCTTCTGCAAGGAATGCAGTGGCCCCAGCCTGGCTGTGGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAGCCAC
EST54419 8	88 A G	---	---	GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCAGTACAAAGGATCTGCC/JTGTCTCCCTGCGTGGGGGGCCAAACCCGGCTTCCA TGAGGCCATTGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGCAACATCTGCACAAATCGGCTGCTCTCTGCTAAITTTGAATGATATTGTGCTGTGGGACCTGAGCACITTTATGGCACAAATGATCACTATTTTCTTGACCCCTACTTAC/GJATCCTGGGAGATGATTTGGGTTTAGCGTGGTCTGATGTTGTCTACTATAGTCCAAAGTGAA

ESTD-PS-1	99 A G ---	---	---	GGGGAGTAAACTTGGATTGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACAAACCATTAGCCTAGTTCGTAGCCATTAATTTGGTTTGTGCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTGTAT
ESTD- B3AR	104 C T ---	---	---	GGCTGCCAGGGTTCCGTGGAGGGGGCCCTAGCCGGGGCCCTGCTGGCGCTGGCGGTCTGGOCACC GTGGAGGCAACCTGCTGGTCACTGGGCCATCGGCCTGGACTCCGAGACTCCAGACCATGACCAA CGTGTCTGTGACTTCGCTGGCCGACGCCGACTGGTGTAGTGGGACTCCTGGTGGTGGCGCGGGGCCA CCTGGGGC
WI-567b	48 A G ---	---	---	TCTCACACTGACCCCTACCTTCATCCTCACCTCTGCTGCCCTGGTTCAGGCCCTCATCTCTTTTA CAGGATCCGCCACAGATCCCAACTGATCTGGCCTTAGGCTCTCTCCAAATCCATCTTCAAAAG GCTGCCACTGTGATCTCCCAAAGGTGATCTGATGCTACCATCTTCTTCAAGCC
WI-801c	58 G T ---	---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCCCTTCTGTJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGATTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCCCTTCTGTJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGATTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	---	GAAATTCACCTATACAAGAACTATTTCTCTAAATTTACATTAGTCTCATTTCTGAAATATTAT TTTTTACAAGTACCCCTTTGATTATTTTGTATTCATTTGTAAAGAGAGATTACAATCAGTAACGC TGTTCAATTGATAGTGTATCACAATGTCTAAATACITTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTA
WI-2529	71 C T ---	---	---	AGGAAATGGCTGATCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAACCTTCTTAACTGCTGCCCTTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAAGATCATTCTTATAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	---	TAGGGCTGTCTTCCCCAGAGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCTATGAGGTAACTTGAAGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATATGACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGGCTGAGCAGAGAGCAGCAAGGAGGAAAGGAAGT

WI-2625	98 G A ---	---	---	GGCAGTCTGGCTGTAGGTAGACAGCACTGAAGGATGGAGGAGAGAGAAAGACAGGAGAA GCACTGTGGTAGTTAACAGGCTTATTTAGGA[G/A]CAAAATTGATGACTCCCTGAGGACTCGCAG AAATTACCAGCAGTGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54 G A TAGG	TGACCTTCCTA GTCTTCCTTA	GCCTTAAGTGT AATCACAGGG	TCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCTCTAGTCTTCTTTATAGG[G/A]ACCCTGTGATT ACACTTAGGCGCTACCTGGATTATTTAGAACAATC
WI-2939	72 G T GTGCC:TTT	GGCTTGCTCA	CTTGTTGAGGG AAGGCTCTG	CCATTGTTGAGTTGGTGGGTGCACCTGTGCATCCCTCGCACCTCAACAAAGTGGCTGTCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAAATGCTTTCCATGCTCCCGTGTCTTTGAAAATTCGACT TTATCCTGAAAACCTCAGCTGCAGTGTATCTCCGGTATAAGCCACTCCTG
WI-3203	99 G A AGACGAG	GGTTATGCGGC	TCAAGTATTGC CTTGTGTGG	CTTGTAACCATGCATTTACAGCATACAACCTCAGTGAATGCCGTAAACCCCATTAATAAACAT CTTGCCATCGAAGGGTTATGCCGACAGAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA GAATAAGATTTTGGATGGATGAAAGCAGAGAGGAGATGCTAAAGTGA
WI-3473	101 A G GCGCTAGGGA	AAGCATTTTA	CCTGATGTCAC CAACATTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTTGGGAGATAGTTGGTATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[G/T]AGAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCAATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTCTTGGCTCCCC
WI-1796b	29 A G ---	---	---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCAATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCCC
WI-1796	29 A G ---	---	---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGAAAGATGGGTGAGT AGTCACATTAGGATTTTCCAAATAA[C/T]AAAAATGCCTCTGAAAAATATCTCTCCCAIGTCCCTGTC TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTCC	GAGAGATATT TTCAGAGGCAT TTT	GCTGAGCTTTGTGGCAGAGCCAGGACAAATTCAGCTGCCGGATTTTAAATAGATTCTGCAGCACTGCAA CAGGAACCAAAATCAGT[C/T]GGGTAACTGAGAGTGGTTTTTACACCCCAA
WI-1959b	87 C T ---	---	---	GTTGTGCTGTAGCAGACACAGAGGCA[G/A]GAGGAAAAAGCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTAAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G ---	---	---	CTTGAGTATCGTGGATTTTGGTATACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAATGTATCTGTTCTACAATTATACAGTAGGAGACATATGTTCCATGACAAATGGTAAT TTTTAA[C/T]GACAGTTTTTAAATGAGTGAAATACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTCCTATAAATAGC
WI-1980b	140 C T ---	---	---	

WI-2015b	190 A G ---	---	---	TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCGACAAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGTGCTTTTCCAACTA/GjCATACTTT CTAATACCATAGAG
WI-754b	49 C T ---	---	---	GAAGGCACAGGAGAGATGGCTGTCTATCCAGCCAGGGAGAGAGGCjCjACATTTATTGGTAA TCCTATAAGTGCATCTTTAAAATTTGTATTACTTTAGA
WI-754	22 T C ---	---	---	GAAGGCACAGGAGAGATGGCTGTCTATCCAGCCAGGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAGTGCATCTTTAAAATTTGTATTACTTTAGA
WIR-1b	56 A G ---	---	---	AGGCAATCAGACCTACAGAGGAAACCCCAATAAAACTCTGTATGCTGATCGTACATCCjA/GjTGCCTG GAGGTGATGCTCTCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-1	56 A G ---	---	---	AGGCAATCAGACCTACAGAGGAAACCCCAATAAAACTCTGTATGCTGATCGTACATCCjA/GjTGCCTG GAGGTGATGCTCTCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-3b	72 A G ---	---	---	TAATTTAAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTTAAAGGCTAAATAAGAA GAAGTjA/GjTCTAAAAGTTATTAGTCTCAGAGCCTCACACATTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---	---	---	TAATTTAAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTTAAAGGCTAAATAAGAA GAjATjGTATCTAAAAGTTATTAGTCTCAGAGCCTCACACATTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---	---	---	GAGCCTTTCTAAAATAGGATTTGACTAGCAACCTCTCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209 C ---	---	---	CGGGACAGAGACAGACAGAGAGATTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACAACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5f	196 C ---	---	---	CGGGACAGAGACAGACAGAGAGATTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACAACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5e	194 C ---	---	---	CGGGACAGAGACAGACAGAGAGATTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACAACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGTAGG TTTGAAGGGAAGGCAAGGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5c	177 C	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGTAGG TTTGAAGGGAAGGCAAGGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGTAGG TTTGAAGGGAAGGCAAGGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5a	37 A	G	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGT AGGTTTGAAGGGAAGGCAAGGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC AGGTTTACGTCCAG
WIR-6	63 A	C	---	TAACCTGAAACTTGTCTCTCATCTCAGGGGAGAACACAGACTTCATGTTAAGACCCAGAA[WC] CCAGCTCTGGGTTGGGCGAG
WIR-7	12 C	T	---	TTCTGACTATTCTAAGCATCTGTAGAATATTGAATACATAGCTTGAGATTGATC
WIR-8	46 C	T	---	GGGCTCTATGACTATCTCTGTCATTGATTGACTAATGATTCCTGCTGCTGGCCTTG
WIR-2	56 C	G	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAGTTGTCAGAAAGAGGTATGA[CG]CTGAAG AAAGAAATTACTCTCTTTGACCAATAAATAACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WI-7059	93 G	A	---	TGTCCTTGCTTATGCCTGCCTCTTTCCGCTTGGCAGGATGATGCTGTCATTAGTATTTACAAGAAAGTA GCTTCAGAGGGTAACTTAACAGAGTGAJTCAGATCTATCTGTCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGAAGTACATTAGCAGCATCTTTAACACAGCGGTGTGTTCAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-18694	41 A	T	---	GGTCATTCCTTTTATCTGTGAGGAGCCAGCTCTGACTTATCTCTCTGTTCTGTCATCTCTCCC CCACATACCAACTTCTTCCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A	G	TGC	CCTATATTCA AGTTTGGAAA TTGTATTGCTG CTTGCAAAT
				CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[AG]JATTTCAGCAGCAATACAAAAGTA TTTATGAAGAAATGCATAATCTCTGAAAATTATGAAAACATCCCT

WI-18517	87	C	CAGGAATCAG GTGCAACA	TGTTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTGTCAACTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGAC/CTTGTTCACCTTGCCAAACACAACTG/CTGC
WI-18668	76	C	GGCGAAAAAC TAGGCAAAAA GC	GCTAAATTAAC CTGCACCTTTT GC	CGATTGACAACCTTTATTTTCAACTTAGTAACAGTCCAAATCAGGTAGATTGGCGAAAACT AGGCAAAAAAC/TAAGCAAAAAAGTGCAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTCCCTCTACT
WI-18680	75	T	AGCATCTGGA TCAACGGAGC	CCTCCTGAATA TCAACGGAGC	TAAACATAGGAGTACTGTACACGCAAGCATGCAATCCCTGAGTCTGAGTCTGAGGCTGTCACTCTAGC ATCTGGAAT/CTGCTCGTGTATATTCAGGAGGGGA
WI-18704	99	A	GGGTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTGTGCGAGCACACACCAAGAGCGAGTTGGGCTTGAAGGAGCC CTTGAGGAACACAGGGTCTCCAGGGGTAC/CTCAGCAGGGCTTCAGCTTAAAGTGG
WI-18673	29	A	---	---	TGTGGCAAACTTGTATTTAATTGCAAAAC/AGTCTTAAATTAAGCACATTCAATAATGAACCAAC AGGAGATTGCTGACTTTGTAACATATGAATATATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGATACAAGGAAG
WI-18640	121	T	GTGCTGGGTG GCGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCAATGTTTATTTGAGGGTAAATTCCTATTAGGATATGAAGGATTACGAACGATTGAGATT GTGCTCTCAGGAGGGCTCGGGCCAAAGTCTGGGGTGGGGGTGCAGAGT/CTGTGCTCTTC
WI-18533b	91	T	---	---	AGTGGTATTTGCGGACC
WI-18533a	59	T	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCAATTTTAAACTCCCGAGATTTCCTCTTTATT TATATTTCAATTTTCTCTCTAA/CTTAC/AGGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A	TCATCTGATAC CTTGTCAGAT ATTT	AACCAGGATA AGGCTACAAC ATTT	GGGAGAGGAGGTAGATTGCCAAATGAGGCAATTTTAAACTCCCGAGATTTCCTCTTTATT TTTATATTTTCAATTTTCTCTCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D49493	159	A	CCTGAAGGAA TCTGGGAAT	ACTTTCAGGCC AGGC	GAGCATATGCTGCATGAGGACCTTCTATCTTACATTATGGCTGGGAATCTTACTCTTCTCTGATA CCTTGTTGAGATTCTCA/CAATAGTTGTAGCCTTATCTCTGTTTACAGATGTGAACCTTT
EST10030	98	T	CAATTTGTTC TCTCAAGTCCC	GCAGTGTGGT ATGGATGA	CAGEACTTGTGGTGCAGCTGCAGACACAGACAGCAGTCTATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCGAGTGCATCATAGGGGTCTTTTCAATTGCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAAT/AT/AGCCTGGCCTGAAAGTGGCCCATCATCATACCCACTGTT
EST10052	24	G	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	CT TATTTTATAGAGGAGACCTAGGAGGAGGTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCC/CT/CTCATCCATACCACCTGCTGATTG
					TATTTGGCTCACTCTGAGGCTG/CA/AGAGTCTAAGATTGAGGTTCCACATCTTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGGTGGGAAGTCAATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGGAA

EST10605	118	C G				CTCTCAAGTAG	GCTAAATTTTC	CTTGCCTAAATCACAGTTCTGTAATTCATACAAAAACCTTTGTTTTCTCTGACAAAACGTACACATAGA
2						ATAAGAGGCA	AGAAAGAATT	AACAAATTTCCAAATGGACAGAACTTAAATTTGTGGAGATGCCCATGTCTGTTGTGAGAGACTTAA
EST11048	61	T G				TAATCT	TTGTTT	AAAAAGAAAAAGATCCC
0								
EST11260	101	G T						CATGTGTCATCCCATGATTGAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTTTGJAA
8								ACAAATTTCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAAAACCAGAGAGGAGCAC
EST11349	109	C T						TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGTCTGAAAGAAATGAAGTGTCAACACAAVA
9								TTCTATATCCAGCTAAATATCATTTAAGAATGAAGTGTGGAAATGAAGGCAATATCAGATAAA
Wl.								TTTGATGGAGAAATCCGAGGCTGCCAGCATGCCACACAGTAGATTTCTTTGGACGAAGAAATCCT
16632a	71	A G				CGAGCOCT	T	CTGTGGAATTCAGCTTTACCGCCTTTCCTCATCTGCTGGTGTC/TJTTCTCTCAGAGCTTTAATGTCCGT
EST11772	74	A G				CAACCTACTT	CTAAAACTCC	CCCTGCTCTCGAGTCCAG
6								GAATCTGGGTATTAAATAGOGGGTGCCACAGGACACATAGGAAGAGCATCCAACCTACTTTGGAG
EST11795	82	G A						CCCTT/GJAGGAGTTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA
3								AAGGGAGGAAGGAGTGGGA
Wl-16644	42	G A				CAATAAGCAG	ACTTCATGAAT	CCAGGAATAAAGAAAAAGAGTCAGAGGAAACAGCTTTTGATGTTATGAGGCTGAGACACTACTCT
EST12005	56	A G				CTCATTTTGAT	TTTACTTCATG	TTCTTCA/GJG/GACTATTTCTGACTATAAGTGAAATAATACATTGAAGACTTCAGGAGCTCA
9						TAC	TATACC	CTTGCTCATTTATTTTGTGCATGTGTTCTTAAAGGCTGTGTGAAAGATAACTTGGAAATGTGGGAAC
EST12055	32	T C				TTGTATAATA	GGCTGGTCACT	ACATAGATCCCAGA/GJATTTAAAGGGGCTGGAAAAGT/AGCCTTAAGAC
1b						ACACTCAGTA	TTCTGGAT	AGAGCAATGGTCGATCTCAATAAGCAGCTCATTTTGATAC/GJAGGTATACATGAAGTAAATTC
EST12492	95	A G				CAAAGTCTGT		ATGAAGTAAATTCATTATACAAAAGCCTCCACAGAACTTCATGCACCTTGAGCTATGTGAAC
4								TGAAAAGTAACAGTGGGAT
EST12492	25	A G						GCCTAGTAATTCCTAAAAGGAACATGTTTGTAATAAACACTCAGTACAAAAGTCTGT/GJATCCAGG
1b								AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTCCTCATAGTTTTTGAATC
4								GTGGAATAATTTTATCTGTTACGCTTTCC/TJATTAATTATCTGTCCTTGATTTAGCACCC
EST12492	95	A G						CACCCGATTTGCAGGCAGTGTCTTCTAAACTGTGCCCTGTGAGCTGTAAAAAGTCTCT
1b								CCCTTAGCAATAGACTTGGAGTTGTGTCCAAATACCAGTTACATACTGTGGCCAAAATTAAGCTCTC
4								TTCCCGAGAGGCATTAACGTGAGATTAT/GJGGAAACGACAGCAAAATTGACGATGCAGCTTTTAA
EST12492	95	A G						CCTTTTTA
1b								ATCTTGAGGTTTTCTGGCCCTGTGAG/GJ/VGTAATCTTTTACTTACACAGGTCAGGAACCCCTAT
4								AAAGAAACTGTGTAGAAAAGATATCAGGTCAGACTTTTTTAAAGGGCTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAAACCAAACTGGAGGCAAGTCCACAGGTACACTTGTCAC[G/C]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAATGCTCACGGGGAAATGACCAATTTTAAAGGGCCATGTG GTCGTCAGGCGATTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTATTATCCAAATGACAGTGTCCCTGAGAT[C/G]GATGATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTTCATTATTCATTGTTCAAAACACTGTGTAGTACCACATTGTCACCCGGG[C/A] /GTTGAGAAATACAATATTGAAGAAGAGTCACTGCCTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGGTCTCCAGGATTCAG[C/A]CTGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTTCTGGGAGTGACCGGATGGGAATCCATGTTGCTTGGCTACTCCATCAGGTCAATTGCG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA[A/C]AACAGGCCAGTTATTTACCAGAAATTTGTTTGGGTTTCA ATGTAGTGTTAGCTTTAATACACTGCACTTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGTCTC	AGGATTTCTATGAGGCTTTAATCATAACCTAATACTGTTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATCTCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTGTTTTCTTAATGAAGCATATAAAGAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAGCTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAAGCAGCTTCCCACCCCAAG CACCTCTGAAT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTTTAAAAATTTAATCGCTTTATACAAATTGACACCAATAAATGCAC[A] /GTTATTTAAAGTTTACAATTTGAGAAAGCTGACACGTTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTCATAGCTGCTTAGGTTTGTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTCCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCAATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT[T/G]GACTAACCCAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAACAAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAATTTACAACCAACTTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGGTACTGTCTTCAATCCTTTGTCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT G	AACAGAGGTTT TGACAAAAGA	ACAAGAGGTTT TGACAAAAGA	AAAGATATAAAAAACACTCCCATCAGTAGCAATACAAGGTTATACATTTTAAACCAGATTTTCTCAGG CCCTT[C/T]TTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTTGATATAACCA

EST13278 2a	51 A G G	CTTACCGAA CAATATTTAG G	CATATCTGG GTGGTGAGAA	TTGCGAAGACGTTTACAAGCTCCAAACCTTTACCGAACAATATTTTAGG[A/G]ATTTGAAATATAT TTCTGTAGTCTACCAACCCCAAGATATGACAGCTTG
EST13282 0	99 A T	CCACACATTT AGTCCAAGA	GATGGAAATTT TGAGGAAGGTT	GCTCACTAGATGAGCAATTGACCAAAATATTTAGATAATACCTGTGGGAAAGTGTGTAATTACTAGCC TGCCTGAGAATCCACACATTTACGTCCAAG[A/T]AACCTTCCCTCAAATTTTCCATCTCCCATCAGA CG
EST13290 9		CAATTTTAGA AGTTGGGTTT	AAATCACTTCA TGGAAATTTCA	AGCTCATCTGCAAGCAATTTTAGAAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTCTGTGCTTAACCTTCAGTTTACTTAAGACCTAAAGACAAAGTGGTATCATCATCATATTTTGT ATGTGGGGCTTTTGG
EST13518 2	45 C G		---	GAACATCCTCCAGTAGTATTGAGGTAAATGATTCAGCATTTA[C/G]ACTTTAAAAATTTACCTCA ATGTTCCCTCGGAGTGTCCATAGTTTAAATGACTTCGACCTTCCTTATAACCTTGTATG
EST13522 8a	66 A G		---	CAGGTTGGTGATTCTCAACTAGGAGCTATTTGCCCCCATCCCCACCGGAGTGTCTGGAGAC[A/ G]GTTTGAATGTCACTCACTGCGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C		---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AAT[C/G]CACACAAAGGAATAAGGAGAGGAGGTTCCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAATGGT
EST13785 0	101 C G		---	AAGATTACGGACCATAGAAGCTGCCCCCGACCCATACACACACAATTTATAGCAGGTAAACCAA CTGAAAGGAACAAAGTAATGACTTTCTTGAAACAA[C/G]TGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G		---	CCCTAACCATCTGTAACCCGAGCC[A/G]CAGTGACCGGGACTTGCTGCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G		---	CAATGGTGTCCTATGTGAACATAT[A/G]ACCTATTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGAOCGAAACAGGAGGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGACAAGTC AAAATATTTT AAAAGA	AATATCAATGCATCTTGTTGGCATGCTAGACAGAGGCAAT[A/T/C]TTTTGAAGATCTTTTAAAAAT ATTTGACTTGTTCCCTTCACACTCATTTTAAATGT
EST14812 2	50 A G A T	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTAC TTAAATCCCAT TAATGACT	TTACATAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATTTCTGAATA[A/G]AGTACATAATGGG AATTAAGTAAATCTTTAGAAAGTCCCGAGTTTGCCCTTTTCTAACATTTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATCACCCACC ATACTGGTT	CGGGAANAACA GTACCCGAA	TTTGCTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCGCTCTCCCTGACTGAACCAAGTAAT TCACAGACAATGGCGCACCACTTAAATAAACTTGCCCGTCAACCCCATCTACTGGTT[A/T]TTC GGTACTGTTTCCCGTA

EST15420 6	109 C A	GGATAGCTGA	TTTAAACCCCAAGACTGTAGATGTCAGGACCTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTCATCATATAATCATATAGCCAAAGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	...	AGACAACAGAA AACAGAGATA TTATTCTC	GTCACCAGCACATTTTATTAGACGTGAAAGACAAAGACAAACAGAGGA[G/C]AGCAGAGAAATAATA TCCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	...	GGTTTGCCAT CTATAA	AAGGATTGAAACATACCTAGATCATATAAATTTGTGAAGGTTTGGCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCCAAGGT
WI-16782	96 C T CACTGTAAGG TC	...	GGTGGAGTCT CTGTTCTCTCA	CTCTTCTCTCCTAGACGTGGAATACACACGAGATACAGTATCTGGAGATGTAGCAGTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGG[C/T]GATGGAGGAACAGAAAGATAGAAGATTTGGGGT GCTGATGAAATGTGGGG
WI-16783	64 A G G	G	TCCTGAGATGT CATTACCTGA	AAAAATGTAACCTTAGAGGTGCCCTCTTTGTGTCAGCTTTTCTGAGATGCTTTTACCTGAG[G/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACCTCGAGT
EST15948 2	58 T C	CAGGACTTAAGGTCAATTTTGGCTGGAAGACTTTAACTAAAGGTCAGGGCAACATAGGAT[C/T]GTGA CAGCACCACTCGGACCAGGAAGTCTGAAATCGTCACACTAGCGTGGCCAGCCCTTTTCTCTGGC TGCTCTGCTCCAGAGC
EST16088 8	89 G C	GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATTCATTTTGAAGCTGTTTGTGACGC TTTCCAGAAAAGCCGCT[C/G]GGGTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T	CGTCTGAAGTTTCTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[C/T]AAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G	ATCCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTCACATTCCTCA GGGGTCCAAATAATGCAACATTTTTCACCTGCTCCATGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTGGCTC
EST16104 9a	83 A G	TTCTTTTAAATAACCCACAGACACCCCATGACACTTCCAATTTACAGAGCAAAAAGTGAATTTGCAG CTGGTTCTCCAGGGA[G/T]TGGCCCCGAGCTGGCTCAGTTCACTCCAGGACCTCAGTC
EST16118 0b	119 T C	ATGGTATAACAAAATCAGTCCAGGTTTTTTT[C/G]GTAAACAAATGATCCTTTGGCTTTCCCGTGGC CTCCTAAACAACTAAACAAACCCCTCTACGTTCTAATCAGTCACTAACGATATCGAGTGGCAAGT CITTCACA
EST16118 0a	32 C G	ATGGTATAACAAAATCAGTCCAGGTTTTTTT[C/G]GTAAACAAATGATCCTTTGGCTTTCCCGTGGC ATGCTCCTAAACAACTAAACAAACCCCTCTACGTTCTAATCAGTCACTAACGATATCGAGTGGCAAGT CITTCACA

EST16151 2	53	CT	---			AGCCAAITCAAACGAACTCTATCAAAACACACAAAAGGCCTAGAGGAGATTATC/TAATGAACGCT AAATAATCAAGGCAATTTTIGATCTAAAGCATTTTGTCTAGCTCTACAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54	GA	---			CATTGGTGGGTAGGGAAGATAGTAGTGTGCAAAATAAAATGGTAAACAGCAG[G/A]AAATGCAAA TTATAGCTTCTTTTTCATATAGGGAATGAAATTTATTTACTAGGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59	A	G	---		GCAGGTAAACTGTGGTTCACAACGTAATTGCTTTTCATAAAGAAAGAAATATCTAGTTG/G/GGTAG AGGAAGGCACGTCTTCTCGGCCCTTCTTCGTTTCATATTTTATGTCACTGTCTCAACGTGGGCCGCTGT GCAAGAGATCTTTGAGA
EST16198 4a	28	GA	---			AAATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAAGAGCTTTAAGTATTTTCGCATTT CCCAGAGGAAAAGTCAGCATCATAAACACATGGGTACACATGCTCACGCACATGGTGTC
EST16229 2c	52	T	C	---		TGTGAACCTCGAATTCGTTGTCCAACTCCTGAGTCAACAGTTTCATTTTGGAGTT/CJCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACTCCACTAGCTGATTCAGACAGGAGAGGCTGCA
EST16229 2b	45	T	C	---		TGTGAACCTCGAATTCGTTGTCCAACTCCTGAGTCAACAGTTTCATTT/CJTTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACTCCACTAGCTGATTCAGACAGGAGAGGCTGCA
WI-16816	124	A	G		GGAGCCATTGT GTTCAGGACAG	CAGACTTTTCTCACACCTCATTTGGCTGGAACCTGGTCCACATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGGTATCAAAATTTGCTTAAGGCCAAGCAGGAGGCCATTGTTGGGGTTA/GJAGTCTGCC TGAACAAATCTAGGCTC
EST16269 5b	49	G	A	---		GCACCTCTCTGTGGCTGTCTCTGTCCAGCTGCTGCCAGTGTCCAGTGCCACAG/GATJGGTCTAGCCTCATGG CAGAAGCATTTAGCCAACTCTGCTGTCTGCCACTCTCTCTCTTCCGCCGCTGGGGCTCACCACC TCTCTCTCTCAATC
WI-16824b	83	GA	---			GTCACCCACGCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTGTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTCTGCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47	T	C		CAGCTTCTGAC TTCCTTCATAAG AA	GTCACCCACGCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTT/CJGTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGCTTACACCTTTAGCACGGATAGTTTCTCTGGTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96	T	C	---		TTGCTTTTATTATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTTCATTACAAA AATGGCTTCCAAACCATTAAAAATGAACCTT/CJGGAATAAGGCATAAACGGAACAGTAACATCA
WI-16857	47	G	A	A	CAAATAAGCA GCTAATGGCA	TATAATCCATCTCTCAACACACACACAAAATAAGCAGCTAATGGCAATJG/AJTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAAATGTTTTCTTGATAATGTGGAGAAATCTGCTCTTTATGTA

WI-16879	79 C T	GATACAGGCC T A T A T T C C C A	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACAACTCTAGGGATAAAGATATAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCACCCAG
WI-16882	99 A G	GAATATGCCA G C G T C T C T G A C	GACACATGTC GGTAAATGCC	ACATGAATGGCAACCTCTAGGTGGGAGAGACAATCTCCCCCTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAATGAATGCCACGCTCTGAC/N/G/GCGATTACCTGACATGTCATCTCCCT
WI-16888	70 G A	GCTAATCTTGG G C A G G T T C	AATGTTCTGAA TTGACCAAAT TAA	GTAGTAAATGTTTCATCACTACCGGGGAGAGCAAGAACAACCTAGTAACCTTTGGGCAGG TTC/GA/TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C T	ACTTGGCCTGT G T T G T T C A	GTCTATCTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTTGCCCTCCCAACATCAGACATAGTTCCATGAAACAGGAACCTTTGGCCTGTG TTGTTCA/C/TCCCACTGCTAGAGAGTATAGACA
WI-16910	74 G A A	AAGAGTAAAG A T G G C G T A G	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGAGGTTATATTCGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA/GA/GTATCTGTTATAGAAACGATACCTTCTTTGGGCTGAACCCAGTGAAGGT
WI-16918	93 C T	CAGGCATTAA C A C C A G C A C	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAATACACCACTTCTCTGCTACCAACAGAGCCTAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACAGCAC/C/TGATGCCACTTCTGTATCAGGAACCTTAACCGTGACAACC ATGAAAGTCTCTCTGAAG
WI-16947b	127 A C	GGAAAGCAGA C O C T G G G	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTTTAGAGGTCTCATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGAGACCTGGGG[AVC/JCA CGGGCAATCACATGAGATG
WI-16947a	58 C G	CATGGAATA G G C C T G G A G	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTTTAGAGGTCTCATGGAATAGGCCTGGAG[C/GJACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGAAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAC T A C A T A A C A A	TGCAAGTTATC AGTATAAATA CTCATATT	CATTTGTTTACTTTTAAATGCACACTACATAACAACCTAATAT/CJCTTAACTTGGTCCAATATTT AGTATAACTAATAAGATGATTTTATCTACTGATAACTTGCATGCCATTAA
WI-16995	55 T C	GAGCAGTAGA G A C T G A G G T A	CATGTTGATT CCAGCCT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATTT/CJACGGCTGG AAATCAACATGCCTCTCTCTGTGGAAGTTGTCAGCATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60 T G	AATAGTATT ---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTGAGAT/G/GGTG TAGGACTGTAAAGGAATGTTTGGGGGTTAGGAA
WI-16992a	46 G A T C	MGCACCCAG A A G T A C A C T G	CACATTCCTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTGAGATGAGATGATG TAGGACTGTAAAGGAATGTTTGGGGGTTAGGAA

WI-17010	23	T C	T T C A C A G G A	A A T A A T A C G G T	A T G T T C A C A G G A A A G C C A T G T C J A T G A C A T T C A A A A C A C C G T A T T A T T A G A A G C T C A T T T A A T
EST17127			A A A G C C A T G	G T T T T G A A T G T	T G T T T A A T G C A G A C A A A A A T C A A G G C T A A C T A A A A G C A G A T C C A A T G A C C C A G T A G A T C A A C C T A G A
9b	74	C T	C A C T G G C A C	G G G A G G C A G G	G G T T C C A C G
			A G A C A G A T	G G T G	A T T C C G T C T C C A A A C A G C A T C C A G G C C G G C A T C T C C C C A C G A T T T A T A A T A C A C T C G G C A C A G A
			A A T T C T C T T A T	G G A C T A T G G C T	C A G A G T C J T J G G G A G C A T G G G G C A C C C C T G C C T C C C A G G C T C C T A A G T A A C A A C T
WI-17040	94	T C	C A T C T C A A G C C	T A T T C A G T G A T	C A C G G T T C A T A A A T T G T A C A A A G C A T G A A C A C T C A G G A C A G A T T G G C A C A A T A C A T G C A G T T C
			G	G	G A G A A T T C T C T T A T C A T C T C A A G C C A G T C J A T C A C T A G A A T A A G C C A T A G T C C C A G T C T C G T T T T C C
			G C C A A G G G A T		A A A T C T T C T C A T A T T G T
WI-17044	47	G T	T A A C G T A T A G	G G G A T O C C C T	T T G T T T G T T T T T C T C T C T C C C A A G G G A T T A A C G T A T A G G T G J T J C T T A A C A A G G G G A T C
			T G G	T G T T A A G A	C C C C A C T T A T A G C T G A C A G C A G C T G C A A C C A C T G A C T C T C C T G C A G A T G G C A G G A A T C G A A T
WI-17021	62	T A	A C T C	T G G C A G C T G C	C A A A A G A A A A G C A A G T G
			T G G A C T T G T C A		G C A T G T T G G A G C A G A T C C C A T G G T A A G C C A A A G T G G A C T T G T C A G C C T A T A A C T A C T Q T J A G
			G C C T A T A C T	I G T A G A G T T A G	C A G C T G C C A C T A A C T C T A C A G G C A C A G T A A C T A C A C T T T A T A C A G G A C C A T G C C A A A G T G C C T G G
WI-17065	90	T C	C C T T	A A T G A A A T C C T	G A G G T G C C A A T A A A A T C A A
			T G T A C A G C C A	G A G A T G T T G A A	
WI-17066	32	A C T	A C A T C A C T G T T	A A T G T T C T G G A	T T C A T A A G G T T G T A C A G C C A A C A C A C T G T T J A C J A T T C C A G A A C A T T T T C A A C A C T C T C A A A A A G A
				A	A A C T C G A C C C A T T A G C A G T C A T C C C T G T A G C T C C C T A T A G G C A A T G G C A A C T G C T G A T C
WI-17074	86	T G			
WI-17104b	108	T C			
WI-17114a	37	T C	T T T C A T C A A G	A T A G C A G A G T G	T G C T G A C T G T C A T G A C T T A G T A A G G C C A C A G A G T T G C C A G A A C A T C T A C T A A C T G T T C C A A G C A T
			G A C T T T G T T T	A A G A G A C	A A C C T C C T A C A C A G G C C J T J G J C T A C A T A G G A G T A T T T G G C C A A G A C T C A C C A C T A G A A G T G A T T
			G A T G A A A T T C	T T C T C A G A A T C	C A G A T G A A C T A C T A T G C T G G C T C A T C T G C A A G C T T C C T G A T G C T T T C C A G A C G G C T J C J T C T C T T T A A G A A A T T A
WI-17150	76	T G	A G A T A G T C T T C	C T G G A A G A T A T	A G G T C C A A C A G A G A T G T T C C A T C A A G G A C T T T G T T J C J G T C T C T T C A C T G T C T A T T T A T A T A C
			C T C T T	G	A A G C T A C C T C C A A G G C C A G A T G C T A A G T G C T A A A A G A A G A C T G C A G C C A C A A T C A G A G T T A C A T
			C A T T C T T T G T		G G G A
WI-17163	43	A G	A A A T A A C A A	C A G A A T C T G C	C G T G G C T G A C T A A G T G C T C T T C C A T G T G G A C A C A T C C C A C T G A A C A G G A T G A A A T C A G A T A G T C
			T A A C G T T	T T T G C C T T	T T C C T C T T J G J C A T A T C T C C A G G A T T C T G A A A G G C C T C C T T T G T C T G C T A A T T T
					G A A A T C G A A T A C G T C C A T T C T T G T A A A A T A A C A A T A A C G T T J A G A A G G C A A A G C A A G A A T T C T G
					T A A C C A A C A T T G A A A G G G G A C A C A G G G A G G G G C A G A G G G A A G G G C C A G A T T T T C A A C G G T T T
					C C T C C A C A T C T G C A G A C A A A

WI-17178	127 T C	GGACTCCCTCA	CCCTCAATTTT	AGCAATGTCCTCCCTCCAAATTCATTAGCTATGATGGAGTATCAGTTCATTTCAGAGCGCAATTA
WI-17180b	81 C G	CTGAGGAGC	CAACTGCTTC	GGCAGGGGGTTTAAATATCTGATGGTTTAAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA
WI-17180a	47 T C	TCGCA	---	GCAGTTGAAATTTGAGGG
WI-17156	54 G C	TCCTCTAAA	CAAGAAATAT	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACCTTC/JCCCCAAGTCTCGTCGCA
WI-17149b	79 T C	CTTAGATATC	ATATTTGATTC	CAGGCTTCAACAATTTACCAACATCTTGCCCATTTGTTTCATTATCCGCCACCCACACTGACAGATGAG
WI-17149a	48 C G	AGGAGGAACA	CATGA	GGAGTC
WI-17197	67 G A	CTGGGCTAC	GCATACC	TGAGGTAGCAGGGGCATCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATTC/JTTCCACAGA
WI-17198	38 A C	CCTAGTTT	GGTGAGTGGT	ATCAATATATATTTCTTGTTGGAAATTTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT
EST18753	27 C T	GGTCTCAT	GCCTGA	TAATATCTTG
WI-17108b	74 C T	CA	CC	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATTC/JTTCATGCACGTGGTG
EST19067	41 A G	---	---	ACCCAAATTTGTCATGTGTGATGAACACTACAAAGGATGGGAAAGAACACATTTCCCTCACA
EST19067	40 A C	TTC	CCA	ATTTGCTATGTTGCCCTGGGCTGGACTCCAGCAATCCCTCTGCCTCAGCAGAAAGTAGTGGGGCTACG
EST19125	28 A G	---	---	A/JGGTATGCACCACTCACCTGCTTATCAGTTTCGTTTAAATAGAATATTTGAC.TTTTAGATGCGCA
				TGTAATTCAGTACTTTTCTCCCTCTGCTCCCTGCTCCCTAGTTT/JC/JTAAATTCAGTGGACAAATGGACAA
				ACCATCTCTGTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
				TTC
				TCCCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATGGATCCCTCCCTGCTGCGAGTGGCTGG
				GATAAGACAACTGOCACAGGCCCTGCCCTAGGAGTAGTCTTAAATGCCTGATGGTGGG
				TTATTTTAAACATAACCAGATGCACCTTGGTTTACATTCCTGTTGCCATTGCAAGTCTCAAAGT
				AAACACATCTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACTTACAGAGT
				ACACAAATTTACCATCGTGACCAATTAAGGGTATAGTTCA/JG/JTGCGCATTAAGTACATTCAACT
				TTTTGAGCAACCCGCCATCACCATTTCATCTCCGTT
				ACACAAAAATTTACCATCGTGACCAATTAAGGGTATAGTTCA/JAGTGGCATTAAGTACATTCAACT
				TTTTGAGCAACCCGCCATCACCATTTCATCTCCGTT
				CTGTTTCTCAGAGATGACACTGCCAACA/JG/JTCACAGATTTGCATACAATACAGTTATGATTGGC
				TATTCACAAATTTACAGTAGTGTCTTCTCTGAAAAA

EST20824 8	115 T	AGTCGGGAGT GCTGATG	AAGATTTTATC TGGACCGA	GTGTGGAAGCCGGAGTTTATTATTCAAAATCAGTCTCTCTGAAACTCAGGGGATTGAGGTTTTTA AGGATAACTTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTCTGATTGTCGGGGTCCAAAGATAAA ATCTTAGG
WI-17347	50 A	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCTCAGAACTTCTCAGCCCTGAGTAGCACAAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGAGTGGGACCA
EST21904 b	128 GA	TTCAATGGCC ATTTTAATAA GTG	GGCAGGTGTT AGAAAGCAT	TGATTGTGGGCTCTGGGAGCAGGTGGGCAGTTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAATGTACTAGGCTTTTCATATGGCCATTTTAAATAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T	GAAGATCTGT CTGGCATTCTT	TGGAATAACA GCCCCAC	CAAAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTCTTTTTCGGGGCTGTTTTCAGGGCACA
EST22197 2	78 T	AATTATTCTGC TATTCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCAGTCAACCAAAATCCACAGGAGAAATCTTAAATGTTTACAAGCACCAATTTATCTGCT ATTCTCTGCCATTCACCGCATCTTCATGGTAGAGTATCACAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATACATAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATACATAAAATCCAGTAAATCCAGTGTAAA CAGTAGCATTCATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T	GGATTAGATC ATCTTTTATT	TGAATGCTAC TGTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATTCACATAAAATCCACCACCTGTAAA CAGTAGCATTCATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A	---	---	TCGAGGAGCTCTGAGGAGCAGCACCACCAAGGACGTGTCTCCAGGGGCAACCGTGCAGGCAAGTGTG GTCCAACTCCTTCTCTCCCTTTACAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCCTTTTAACTGT
EST22433 c	103 A	AAGACATGTT CACCAAGTGA GAA	CAGGTTACGCT TAACTGACAGA	GATGTTAATGACTTCTTTGAGATATGATGGAATAATTCAGGTACACATGGAAGACATGTT CACCAAGTGAACCAATCTAACCAAGGTTTACCAGTGTCTGAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A	AAATGGATCC TATCTGCACA	AGTTTCAGTT GCATGAATTT	TATCCATTTCAAGAAAAAATGACTTAAAAATACAAATCTATCCAGAAATGGATCCTTATCTG CACAGTCCATTTGAAGAAAAAATTCATGCAAACTGAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTTGT	TTGCCTGTTAA	TTTGACTGTAA	GCCTTTTATGTCTCCTTTAACATCAAAATGTTTTATAACACACCTTGATCCTTTTGTCTACCCCCA ATT/C/CATTACAGTCAAAATTACAGGCAATATAATAGTCTAACAGAAATGCTTGCAATTT
EST23021 0	108 T A	TTATTTCTCAGCTTACCATTGTGTTACTTATATCTCTGTACAAAGGTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTAATCTTTGCCCTTTTATGTTTGTGACAGTTTGTGCTTTCT
WI-17387	55 C G	CCTTTCAGAT	GCCTTTGCCTA	AGATTAATAGT	ACAGAAATTTAACATGCAAGTTTCATTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101 A C	AATGTAAGCT	CCTTCCCTCC	TGTAAGC	TTTTTGGCTTGTCTGCAGATAGATGAAAAGAGAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAGCTCCAGAGGCAG/CAGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23733 9	31 T G	GGCTGTTAGTT	TGCACCTTAAA	TCCCATCAAT	AAAGGCTGTAGTTTGTGTTTTTCTTTTCCCTTT/GJTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGGCTCAGAGATTTCTAGAGCGGCGC TGAAGAAATACCCACCTAAA
WI-17470	83 A G	GTCCGTOOOG	CCAGTGACGAG	GOOGA	CTGACAGTCCCTGTGTGCGGGGTGTCCATGTGGCGTGTGTGAGTGAGACTTTTTTACTCGCTCCC GTCCCGCCAGCCCTTJAGJTGCGCCTCGTCACTGGCCTTGGTCACTTTGTGATTTCTGTCTGTTGGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTCTAGC	AATTATTATT	TGCAGGCAATA	TTTTAACGAAATCTCACTACTGCAATGCATTTGTCTCTAGCTAATGAATGCAT/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAACTTAGAACAGTACATGGTGCATAG
EST25356 3b	95 C G	TCCTTGATACAGGTAACCAGTTTGTAAACATTTATTCAGAACTTCACGTATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	TCCTTGATACAGGTAACCAGTTTGTJACJACATTTATTCAGAACTTCACGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	GGGTGACGCTCCAGATGGGAGACAAGCCAAATTTGGAGAGAGATTGGATCCAGCTTCATTCAACATT ACTACAGTTATTTGATAATGATAGAACCCTAA/C/JTAGGCGCAATTTACATTGACGGTCAATGC
WI-17581b	86 T C	ATTCAACATT	CGTCAATGTAA	ATTGCGCCT	GGGTGACGCTCCAGATGGGAGACAAGCCAAATTTGGAGAGAGATTGGATCCAGCTTCATTCAACATT ACTACAGTTATTTGATAAT/C/GATAGAACCCCACTAGGCGCAATTTACATTGACGGTCAATGC
WI-17596	86 A G C	ACTTCTTGTG	CAATCTTATAG	CTAGAAATCGA	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAAGGCTACT TCCCTGTGTAAACACTCC/CJAGJATATTGTGCTTCTAGCTATAAGAAATGGGCGCACTAAGTGGGCTC

WI-17623	46	T C TGTGGTTTTAATTTCCCATATAATTAATGTTGGGCACATT/CJGCAITGCTTACTGGGTC ATTCATATATCTTTTGGAAGCATCTGCTCCAATCTTTGCCCTGACTTTGGAGTTTTTTGGT
EST26419 1b	46	T C ATTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGAT/CJGGCAGTCCAACTTCT TGGGAGGAAGTAATTCATGTAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35	C A AG	ATCAAAGGC AATATGTGC	CAAGAAGTTG GACTGCC	... ATTCATACAGAGATACAAAGGCAACTATGTGCAG/CJAAACAATCTGATGGGCAGTCCAACTTCT TGGGAGGAAGTAATTCATGTAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69	G C TCAGCTTTAATTTAAGGGACATGTAAATAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG/CJAGGTAGACCAGTAACAACAACCAAGAAAGCAAAAGTCTGTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39	A G TACTTCAGTTTAAGGCAATCCACACAGAGACTGTCT/CJGAGACGGGCACAGAAACCAGACACC GTAGAAACACCACCAOCATGCATGACGGGAAGCAGAG
EST27152 1	101	C T CAAAGGATTTTATTTGTTCCCTAAAGTAATAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCT/CJTTACATGGGTACTCTTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 0a	33	G A ATTT	GCACTTGCAA CAATTTAATA	GCTGGTGTGAT GCTACTGTAAT G	... TTTTGACATTTGCAACAATTAATAATTTAT/CJACATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTTCTGTTACACATTTCTGTTAAACAAGAACCCATACATT GGTAAATTCATTCT
EST27662 4	51	C T CTCCAGTCTG	CACATTCGT CTCCAGTCTG	TTATGGAATG GCTTATGTAAC C	... ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTGCTAGGTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTTAGGAATGTTT
EST27788 3	100	A G ATTTATTAGGCGGTACAATCCAAAGTGGTAAGGTGAAGGAAAGGCGAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACCTTTACATTCAGGAG/CJGGCTTCCAGACAGCCATGTAGAACCCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58	G A AGAATTC	GGAGATCATC AGAATTC	GTGCAGAGAGG TACTCCAAGTA C	... TCTTCTAAACCTTCTCTGTTGGATCCCGAGTGCAGTGGGAAGTCATCAGAACCCAC/CJAGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58	G A ACATC	AATAAATTC AATCTGTAC	TCAAAGAAGGC TTATCCATTT	... TAAAAATTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACACAAT/CJAAATG GATAAGGCCCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTAT/CJAAAAAAGTAATCAATCTGTGCCTCT AAGTCAATGGAATGAAGAGCTGTGCCAGGGACACACCACCGCGTCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG
EST28036 4	37	T C TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAA	TTCTGCGATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTTCTTCTTTAAAT/AJATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACAACAGACGAAGACATGAGTTGTTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C	TGGGCOCTCC TGTC	TGGGTTGGCAG TGTC	AGAAATGGTCTAGTATCGTTCAGGATTCGGGTGATGGGCCCTCCCTGTC/T/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACCACAGAGAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTATGTGCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAGTGAAGTGCTATT/A/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTATGTGCA
EST29041 5b	53 G A	GGAACAAACA CATTANGCAT CA	GGTATTGTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAACACATTAAGCATATTGTCACT/G/AJGCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTAGAAGGACACCAGTCTGTTGGGCTTAGGGCTACCCCTATTCCAGCAGGTGCC/A/GJTTATTT TCACITGGTTACGTCGTGAAGGACCGTTCCAAATGAGGTTACAGTACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T	CTGCCAGCTT ACAGGCT	GCGTAAAGTGC TCATTCTCTG T	ATTTATAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAVAGAAAGAAACATTTCTGCCAGCTTACAGGCT/C/ACAGAGAATGAGACACTTACGCGATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGATAA/A/G/CJAGCTCAGTA CTGGAATCATGCTTCTCTG
EST30223 2	99 A G	---	---	AAATAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTAATAATCC/A/GJGGATTAAATTCCTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCAGA GTTTCAATAATAGGTAGC/G/AJATAACCAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCAGA AGAGTTTCAACAATATAGGTAGCGATAACCAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATAATTGTGCTTCTG/AJGCGCTGTTTCTTATACCCCAATATCATAGAATT GTTGTGCTTCTATAATGTTTCAGCTTCAAAATCTTTTGTCTTAAICAAATCCAAATGAATTACCTGAATT TTCTCCTCTGTGTTCAAAA

EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAACATTTTCACTCTTTTAGCAATGACA TCGGTTGTCCAGCCCAACAC/TGGAGGTGATTTGGTGGGAATCTTATCACAAATTATCT
EST31968 8b	95 T G	---	---	CGAATTTGCTCTCTTATTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCT/TGAACTGCCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGTACTGCTCCC
EST31968 8a	75 T C T	GGGGTTACTA TAAGTGCATTT	TGTAAGAATCA GTGGCAGTT	CGAATTTGCTCTCTTATTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTT/TGTAATGGGATTTTCTGCTTAACCTGCCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGTACTGCTCCC
EST32063 2	103 C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGCTGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTGTAGT/C/TGTTACAGGCCCATTTGAAATAGCAAAAGGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	---	---	AAGGCTTTCCAAGCATTCAAAGGCACTTGGGTGTGCTTAAGTTTCTGGTCACTGCAGCCCCC[AVG TTCTGATTAGGGAGCACCCCAAGCCCACTACAATATGGTCTTGCAG
WI-17800	29 C G	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GAAGACTGGGATTAATTGTAGGAAATATTTACAG TTTCCACAAGTCAGAAAGAGCTAATCCCAACCCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCTCTAAAGTCTGGGATGACTTTCCT/T/GATTCATCATCAAGTAGAACCTTAAGCCAAT TCAGAATCAGAACTCTTTTGTCCATCAAAATCCAGCTAACTCCAAGCTGAATTTAAATGTTCAATCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAAACAAAATCTTTA TAGTGTCCAAAGATAAATTAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAATAT/T/ACCGACTGAC TGCCTCTTAGTCTGTGATC
WI-17860	121 T A	TTTGGCAGCA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTTTTTGTATAGCCTACTTCTCAAAATGTT/T/TTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCAGATCAGAGTAACTACCA
WI-17866	43 A T	TTTATAGCCT ACTTCTCAAA	CCGTTGTCACT AATCACACAA A	GAAAAAAAAGTCAAAATGTGTCTCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCATGATC AATCGCCACGAGAG/G/AJACTGGATGCCAAAGAGATGG
EST33301 4c	80 G A	---	---	GAAAAAAAAGTCAAAATGTGTCTCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCAT[G/A] ATCAATGCCACGAGAGACTGGATGCCAAAGATATGG
EST33301 4b	63 G A	---	---	---
EST33460 1	44 G A C A	ACGGTGGTTTT CAACTACTAAA	CTGTATTTATT GTTAAATATTT GCATTGTT	CTATCCAAAAGATATTATTGCAGCGTGGTTTCAATACTAAACA[G/A]GTAAACAATGCAAAATATT TAACAATAAATACAGTGATTAAATAAGCCCATGGCATATCCAGTTGATGTAATACTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACACIAGTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCGAGTTAAACAACAACACAAAATGA GTTTTCTTTGAGTGACACAAGCTTGTTCATTTTGGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TJAGTGAATTTTATTAGTTGTCTCGTAGTAGTTTGGTATTTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG AGAACAATA ATAAAATC	TGGGAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJTACAAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
EST34343 8	95 C A	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTTATG TGATAATAACT CCTTCC	GGTACACAAATTTAATGGAAGGAACCAACAGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATATACTCCTAAAGC/TJGGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTCATCA
WI-17982	98 C T			CTCAGTAACCTCGGTGTATAATCTGCCATTTATTGATTATTTATGATAAAACAACCTCTCATTTGTGA AAACAGCTAAGGTGACATCTCCAGACCCCACTGCTCCCTGTATGTAATGTA/CJCTGCTGAGAGTCC ACAATTTGGAAATCCAAT
WI-17993	118 A C			CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAACAACATCTCCCAGGCTCGCAGT AGAGCGAAGGGAACAG/AGJGCTGCCCATGTGCCTGTCTCTAAAGAGCCACCCCTCAGGTTGATGT CACTGTGGGAGACGGGT
WI-17996	84 A G	GTAGAGCGGA AGGAACAG	AGGCACATGGG CAGC	ATTCTTTATAAAACACCATGTCCCTAAAATGT/CJGATTCACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-17136	33 C G			GCCACTGAAAAAAGGTGCTTCC/CJGJGTTTCTAACTCCCTGGACTCCCTCATTTGGAAGTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
WI-18041	24 A C			TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCAGACGCCCTGCCCC/CJGJCTTGA GATTCAGATCCAGAGGGTGTCTAGTCCCTTGGTTAGGTGCTTCTGTGACATTTCTCTTTG
EST35164 8a	57 A G	CACAGCCCTGC CACC	CCCTCTGGATT CTGAATCTCAA	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGGTTACACATCTAGI A/GJACAGCAGAGTGCCTGAGGGAGGGTGTGTTTAAATGCTGATGCATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052b	67 A G			AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGGTTACACATCTT AGAACAAGCAGAGTGCCTGAGGGAGGGTGTGTTTAAATGCTGATGCATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	ATC	CTCAGGCAGCT CTGCTGT	CTGTTGTGCTGAGAACAGAGGGGTCAAGGAGTGGGGAGTAAAA/GAJTGGAAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAGACGGGTGATTTTGTCTCAGGTTTGTAGCAACAGAGGTAATG
WI-18054	46 G A	GAGTAAAA	CGTCAACCTGC TTCCA	

WI-18064	54	GA	AGTGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGTGCCAAATCATCTCTCAAAACCCTGTGGTAGCTGCTAAGCTGTATTTCAGAG(A)GAATGTCAC AATCATACCCTGGGAGAAAGAGTAAGCAGAGTGCTATTAGGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	TCAA	GCATAAAATT TTCCAGTTGGT	COCTCGGCAOC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGTGGAATTTTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGTCAGCAGGTGCCGAGGCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	AC	GTGTAT	AACTCACTAC TTACTCAGAGT GGTTTTT	AAACCCACTACTTACTCAGAGTGTGTATACIATATTAAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGTATAATTTCTGTACTCAGAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	CT	---	---	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCGTG TTTGACITTTATCTCTTATGTAAATGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65	GA	---	---	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCGTG ATGTTTGACTTTTATCTCTTATGTAAATGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41	TCA	AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTCTTTGTAAATTAATACTACTATGCCGTG CGTGTGACITTTATCTCTTATGTAAATGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18086	63	GA	---	---	GTGGCATCCTATAAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATACTTCTTG(A) TGGCTTTGTACACGGGTTTCTTCAAGAGGAAAGATGACTAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18115b	71	CT	---	---	AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGACCTTTGGTATCCCG TTCTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115a	70	CT	TT	AGAGGCTGTC TTTCATACCAA A	AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGACCTTTGGTATCCCG TTCTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG TCAGT
WI-18136	78	AIG	---	---	TTTTGAGAAAGCACTCTGTAAGGCAAGGATGCATTCAAAATGGCTTTGAGGATTATCTTCTTTA GGTAAATTTG(A)GTAAGAACAAATAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAAGCAGCCATCTTCCGGAAGCTC(A)GTTGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGGA
WI-18169	115	AG	GAAGCTC	CCATCTTCCG GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAAGCAGCCATCTTCCGGAAGCTC(A)GTTGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGGA
WI-18190b	26	GA	---	---	TGAAAGAAGTCGACACAGCGGACACTG(A)TCATAAGTGGAAACAAGGATGAAGCTAATCATGGAG GCAAGTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGACATTAATCTCTGCCGA

WI-18190	62 G A	TGAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAAACAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGACAAAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100 A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACAACATTGAAACACAATACAAACAACATTAGGAACAAGAAATGTGTAATCCAA TGTGTGAAAATATATACAAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA TGTGTTCTTGAAAC
WI-18215	78 G A	AGCAGAGTTC CTGCOCTC	CCTCCCTCTCT CCCC	ATTACATAAGCATTCTCCTGAGTACAACACTAGGGGACAGGTATTTACAAAAACAATAGAGCAGA GTTCTGCCCTC[G/A]GTGTGGGGGGAGAGAGGGGATTCAGCAATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A	TGGTGTGATT GTGATACACTT AA	AAATAAAGGT TTTCAGGGGTT C	CATTTCGGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGTATACACTTAAGT[A/G]AA CCCCGAAAACCTTTATTTGNAATTGAAGTTTTTGTCTCAGAAACTGGGCGAGAACTTTTCACATTCTG AC
WI-17892	76 T C	GGAAAACCTG AGTTTGAGATC ACA	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[C/T]CTGCTCACTAGTCTATTACATCTCTGTGGGCATTTCCGGCAGAAAGTGGC
WI-18242	30 G A	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAACAG CTTTC	AATATCCCAAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTTAGCAAAAAT TGGATGCCACAACCTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGMATGTTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T	GCATCAGACATCACCACCTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	GCATCAGACATCACCACCTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATC[C/T]GAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	AAATAGGAAA TATGGACTATC TTCAAA	TTTCATGCATCA TTTGTCGA	GCATCAGACATCACCACCTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATC[C/T]GAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G	GCTGTCAGCTA TTGTTATTTC GAA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTGGATATGTGGTTAGTGTATCATTAATTTTGGAAAGCTGCAGCTATTGTTATTTC AAAT[A/G]TATCTTCTGCTCCCTTTTCTCCTTTTCTGGGATTCATCTTCGATGTGTTATA
WI-18330b	66 A G	AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGG[G] A/GTATGTAGGCAGTGAAGTGCAGGACTATGCAAAAACCATAAAATAAGAACATAATTTTGTGTTGAT TCACA

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WI-18330a	49	G A A A G A	TCCTGTAA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGCCATCCTGTAAAGAAATCAGGGATAAGA[G]A[CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAATAAGAACATAATTTTTTTTGTGAT TCACA
EST37564 5	85	T C A G A	AAATTCAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAAAATTC AAGCCATCTACAAAAGATT[C]TCTCATTTAGGGCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTATTACCTACAACAAGTAAGGAGACAGCTGGGCAGTTTCCAAAGCAGTACCTC CCAAACAATGGTGAAACAGCTTCGTTAGGCTAGTT[G]A[IGCTGAGCCATTGTATGGGAGGCAGA GT
EST37624 6b	102	G A ---	---	---	GTGGCAAGCAGCAGCTAAACACACTCAITTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTGGCTCTCTGGACGGTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCAATTCC
EST37624 6a	58	C T ---	---	---	GTGGCAAGCAGCAGCTAAACACACTCAITTTGCATGAACCTCCAAATACGAACAGTGCAC[CTGCTGA TGGCTGCAGTCTCTGCCGTGCTGGCTCTCTGGACGGTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCAATTCC
WI-18357	89	C G C A T C A A	CCAGCCCTTA GCATCAA	AAGACTCAA AGACTGAAGAT GA	AATGTTTTAAAAAGTCTACCGTGTGAGGTGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCAA[C]GTCATCTCAGTCTTGAGTCTTCCAGCCCCAGGTCCAAGCTT GTGGACCAAGAGACAAGCC
WI-18012g	117	A G ---	---	---	TTTTATCTGGGTGAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---	---	---	TTTTATCTGGGTGAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T T	GCCACTTTTC CCCTT	TCAGCGTGTAT CAGGAACA	TTTTATCTGGGTGAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---	---	---	TTTTATCTGGGTGAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA ACTTAA	GCTAAAGTCAG CTGATTAAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATTCCTCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGTA[G]A[TTAAGTTTATTATCAGCTGACITTAGCATTTGGGAGATTATCTGGAT

EST38512	91 T	TGACGATGCC G AATACTTCG	CACTGCACICT GGGAAGC	TAATAAAACTGACCCAAATTGGTAAACTGTGCTGGACTGAGAGAAACAATGAAAAATCTGTAAT ACCTGATGACGATGCCAAATCTCGTGGCTCCAGAGTGCAGTGAATACTGTTATAGCC CCTGCACCTCTAAAGATCTTTTCCTCCCCAAGTCTTAACAGATGGTATATCTCTCTGGAAAA AGATGAACGTCATCAATGGATTGCTGCTCTGCTTTAGCTTTGATTTTTTTGCTCTTGAGAACCTTG TCCTCCCTGCTGATT
EST38519	24 C T	T	TCTGTTAGGAC TTGGGGA	AGTGGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTAA T/C/TCTCTTATGTGTTACTACTACCTTCCCTTCTCTTCTATACACATAGATTTTCTCTAATTGCAGC CCA
EST38575	66 T	C A A	AGGAAGGTA GTATAACACAT AAGAGA	OCATCTAGGCAGGCTACCTGAGCTCTGTGTCCACAGAGTGGTGCCCTCAGCGCCCGGGGCGGCTGG AGTCTCGGGGGCCCGCCCTGCTCGCCCTTCGCGCCACCATCCTCCTCCAGGGG
EST38616	101 C	G C T C	GAGGAATGGAT GGTGGC	TATAGTAGGTACTTCTTGTCTGCAGCAGGAATTATTCAAGTCTGAAGTGGCATTTCAA/T/CJGCGTG GTATTTTTTCTTTTCATTTTGGCAAGTAAAAAATCAT
EST38652	59 T	C C A T T C A A	TTGCAAAAATG AAAGGAAAAA	CTCAAGCTGAGAAATGGTCAATTTAATATATCAAGTTTACATA/T/CJAGATAGAAGATTAAAGGACCAT CACTGAGGTACATAGCTCAGAGGCGAGATTAAAGATTGGACCCAGGAGTTGGTTCCAGCATATA GGATCCTCACTCACCTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTCCCCGAGAGGCCAGCGGGATGTGTGCCCTCCTCCTCCCAACTCATCTTTTCAGGAACACGAGG ATCTTGCTTCTGGAAA
EST38707	75 A	G ---	---	TGAOCTTGATTTCTTCACTAGAGGGGAGAAGAAATCAOCTACCTACCTTTTGGATGCCCTCCCACTCTACTTGT CTCCTGAGGTGATGG/A/GJCTTAAAGTCCACGATGGTGACCTAAACTCAGTTTAAATTTCTTGCC TAGCAGCAC
EST38759	86 A	G G G T A T A T G G	TCACCATCGTG GACTTAAGG	GACTCTCAACCAAGAGAAAATCAATAGGAGAGGATTGGCT/AJTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTAGGATCTCCTAAGTGGTAC AAACAACCAACATGGTGG
EST38775	40 T	A C	GGCTTTGCTCT GAATTCAAA	CACCCCATATTTGACCAAGGAGTAAAGCCTAGCATGCTCTTTCACITATGTGTGTTCAATCAACAAG TGTTTATGAGAACCCATTACAC/A/CJ/AAAGCATGTGCCAGTCAGCAGATTTCTGTAATAA
EST38815	91 C	A C A	GCTGACTGGCA CATGCTTT	TCCTTACTGTGCTTACAACCTTCTCCCAAGTTTGGGGTTCCTCATATGTTATGTTATGTTATTA TTCAACACAGGTAAGAAAGAACTCATGAC/C/JTCTCCTTGGACTCGCTCCTCCTCCCAATCTCGAT ACCGACTGCACCTGTG
EST38858	98 C	T G A C	GGAGGAGTGC AAGGAGAA	CCCTAATGGATTTACAGCTCATCTGAGTCTCTGCTGTGTTCTGAGGAGCTGTAGAATTTGTGTG ATGCT/CJCTGTGCTCCGTCCTTCCCCAAATGAGCACATATGAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA
EST38865	72 T	C T G T G C G A T G C	GGAGGACGG AGGACACAG	

EST38878 9	47 T	AAACATCAT ACTAGCCTAG CAATCCTAA	CCTTCAATAA TCTCATGTCT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAATTC/TGAGGACATGAGATT ATTGAAGGGAATCCCTCAATTAATATGAACATTTCTTGAGAAATGGGAATTTGAAACATTCCC TTATTCATGTGTCATCTACACATTCCTTTATTTATTTATTTGTTTTCACCTTTCTCAAATATCGGATTGTGC TCATGAGAATAATGCTGAGGGAGCTGGCAGCGCAGTCTTCTCA/GC/GCTCCCTGGATAGCTAAAT
EST38882 6b	113 GC	---	---	TTA TTATTCATGTGTCATCTACACATTCCTTTATTTATTTATTC/TGTTTTCACCTTTCTCAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT
EST38882 6a	35 T	CTTTT	CAA	TA GACTAAACTAACTTTCACTTTGGATTGCACAGCATGGCTAAACG/A/GTAAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACCTGCTGGAGGGAATATAAAAT
EST38909 5	47 A	GCATAACG	T	AACTGAATGGCAGTGAAGACATACACATCAAACTTAGGGAATGTGGTTAGTGTGGTACGTTGAG GGAACCTTATAACCTCACTA/G/GCTTTGTTTACAAAACACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A	CAC	GAAACAAGCG	TAACATTTCCCATTTGAAATCCCTTGGTGGG/GC/GGGGGGGGTGAGATTGCAGTGCCTCAAGATAA TATCACAAATATATAAAACCTTCAAAATGTCTATGCTATGCATTCACACACTGACATGAGCCACAAACAT CCCTTACAGGCACTGTAC
EST38955 5	30 GC	GGTGGG	CACGCCCC	CCCTGTATGATGCTCGGCAGATCCGGACCTTCGGTGAC/GA/CAGGCTCCCTGCCAGGCTTGG CCCTGACCGGGCTCCCGCTCGGCTGCTGAGGAGCTGAAATAGCTGACATCCGCAACCT
EST39002 0	42 GA	AGACC	CCCTG	C CAGTGGCCCCAAGTTCCGGGCTTCTCAGTCTGGATGGCTGTGTGGAAGCTGTGGTGGTAAG GCCTAAGGAATTTGAGGGGCGAGGGGGGATGCCGCCAGCGAGATGGTCTGTAAAGCTGTGGTGC
EST39004 8	79 T	CTAAGGAAT	CGC	AAAGCCTAATCTCTGGA AAAGATAATGTGTCATCAACGCAACATATAGAAACATAAAGATAAAGTATCCACCCCTAAAT CCCTATTATTCATGATATTTTCA/T/CJAGCACTAGTATATATCAATATATTTTTCACAAACCAT
WI-16398	90 T	CTA	TTGATAT	TCAGTTACAC
WI-16403	69 T	CTA	AAAG	GGTGTCTTCATGTTATTTCTCATTTCCCTATCAGGTTTCTGGTCTTTGTCTCAATTTTAAACAT T/CCTTTTATATAGGAATAGCCCTTAACCTGTGGTACATGCTGCCAAAATTTCTCCACGTT
WI-16406	24 CT	AGG	AA	GCCTTAATGGCTACAGAAAGAGG/C/GGGTTTATTTCTTTTAAACACATCTGGTCTGGCAGC AAGTTATATTGCAATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCCTTTTATTCATGATTTGTTTCATCTGAGAAATAAATCTCTGTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACTATATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTAATTGTGCTGAGCCAGCAACCTCGAGTTACCGGCCCTTTACCCACAGGCC AGCTCTGCTTGCTGCAT
EST39366 2	72 T C		---	AGAAACACATTCGTCTGATCAGAGGAAGATGTATGTAGAAATCAGAAATCTGACTGAATTCCTAAA ATCTAT[C/J]ACACTGAGAGGAAAATGGAAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCICA GAGGGGTTTCTAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGAGG	TGATTTGAGAC ATTTACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTGTAAATTCCTCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[G/J]AAAAATGTGAAATGTCTCAAAATCAATGCTTCTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177 23 A G			---	ACAAAGTGACATATCCAAACCACAC[C/J]TCCATCCCCACCTGTGCCCTATCTTTCTTGTTCTTT AGAGCCTTTTCAGCTATTTCTGTGAAGCAAACTGCACGAAGGCTCCCGCTACTCCTCCCTGGAA G
EST39428 8	31 C T	GCTCCACACA ATTTTGATT	GGTCCCTTAG AAGCCACC	AGGTTCCCTGGTTGCTCCCAATTTTGATTC[J/T]GGTGGCTTCATAAGGGACCCAGGATTTCTGCATT TTCTGGGTGGGCTAGGTAATTCGTGTGGCTTTGGTCCACAGACAAATTAAGAAAGATCAGGTCT GGCTGTGC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTCCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/J]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCACAGGCTCCGGTGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA	TCCTGGAAAC TGACATAAAC	AAAGCCTGTAACTGAAGCTAGACAACGTCACCTTTGGAAAGAAAATAACAGGAACCTATTTATAT ACGTAATCACCTTTATACCTGCCTACTGACATAGGACTTCAGAGTAAT[C/J]GGTTTATGTCAGT TTCCAGGATTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGCC	CAATCTCGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACCTGAACAGAA TGCAGGAGGGTGG[C/J]AGAGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGAAGACCAG
EST39501 0	81 A G	AAAGATTCCCT GTAGACATCT	CACCTGCAATT CTGAAGGCT	TGCTTACAAACCCATAACCATAGGCCATGTTCAGACATCTTGACCAAGCCTAAAGATTCCTGTAG ACATCTAACATTAG[G/J]TAGCCTTCAGAAATGCAAGTGCAAGTTCAAGTCAACCAATTC
WI-18387b	84 A C		---	CACAAATGGGACTGCTGAAGAGTGAGAGTTGGACCTTACTTTTGGTGACCCCATACATTTGTGGTCA CATGCTTAGCCATAG[C/J]CATGGTAACATTGACTATGGAGTCTTTGTGAAAGTGTAAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCCTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACIAGJTITGTG GTACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGGGATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GCGTGGAAOCT GAAACAC	TTCTTGGGA AAGCGTC	TCCAGGATGGTTTATTCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGTGACTCGCGTGGA ACCTGAAACACIAGIACGCCCTTCTCCAAAGAAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTCAGGAT AGGT	GCACACCCCTC ACACTGTTA	TCCATTCAAGTGATCACATCTTCAGGATAGGTAGIATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGG TCA	AAAAC TGATT GTTAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTGGACAIC/TGTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA CCTTTGAACATCAAAAGAAATACAAATATATTTTCAAAATTTCTCATCAGTGTAAATTC
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTT C	AAATCTCAGC ATTGCTATAAG C	AGAGAGACAAACAGAAAGATAAGGGAAMTGGGAAGAACAGAGTGAATTAAGCAATCTTGGA TTCAGATTCCATTAAACAGGAAGTTTCTCNAAAAAATCAA/T/C/GCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGA AAATGGGAAG AA	CCAAGATTG TTTAATTTAC TC	AGAGAGACAAACAGAAAGATAAGGGAAMTGGGAAGAACAGAGTGAATTAAGCAATCTTGGA GGATTCAAGATTCCATTAAACAGGAAGTTTCTCAAAAAATCAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CACCTGTCT AGACAGATT C	---	AGCTGATCAGCTGTCTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCAI/C/ITGCACACAAACAGGAGGTGGGGTCAACGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	CACCTGTCT AGACAGATT C	CCTCCTGTGT TGTGCA	AGCTGATCAGCTGTCTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCAI/C/ITGCACACAAACAGGAGGTGGGGTCAACGGCGGAGAGCCAAAGAC TAGGGC
WI-18449	129 C T	CTTTGGCTCT AAGTGGGACT C	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGMACTATAAAAAGGAAAGGAAGAGTAATCAAGGGAGGCCAAAGTG GGAAAGCTGATTGCTGATTAACGTGCTTCCAGTCTCTTTGGCTCTAAGTGGGACTA/C/TTC TGGATACGTACGGGGAG
WI-18457	120 T C	---	---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGTGCCCCCAAGACATTATTTTATCTT AAATGTCCAATATCTGCCCTGATGCTGTGTGTGCACATTGGGGCCACAGT/C/AAATAGGCTAAA AGGCACTCCCACTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA C	TTTAGGCTTG AGATGGTTCT	GGTGCTATAGCTGCTGTACACCACAAATGGCAGAGGTAGIAGTAGAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGTCTCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60 C T	GCTGGGGTGC GAGG	GCACGATGGGA GTGAOC	TGAGGAGGTGTGACAAGCTCCAGAGGGGTGGGGCCGGGCTGAGGGTGGGGTGGGAGGCTTGGT CACTCCCATCGTGGCCCTGGCCGCTCCCTCCACTCACCCACACTGGCCAGTCCACGTTGAGGT

WI-18491	109	GA	AACAAATGGT AGGTGGTATT AATACTATT	CGTGTGCATT TCTTGTATCC	CATAAGATGAATACATGAAGGGCGTTTAGCACAGTCCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAATGACACA GGT
EST50757	79	CT	GAGCTGAGG CTCTCTCT	ACCCTTCAACC GGCC	AGCCCCCTCCACTCCACTCTGCTCCACAAAGTGGCTCCGAGAGCTCGAGGCTGCTCTCTTTTATAT GTGACGGCC[C/T]GGGCGGGTGAAGGTCAGAGA
WI-17875	103	TC	GGACATTTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAACTAAACATCTTCCACAGGTGCTGAAGAAAGTGTCTTCGTTTAAAT TGCCAAGCAGGAGTGGACATTTGGATGGTGACTT[C/C]CCTGGTGGTTCCTCCATAGATTCAACCAT TGCTCTAATGGTGCTA
WI-16543	67	GT	AGATAAACTA CATTTGGGTT	GATTCATCAT ACAGGGACTT	GATCCATTACCTAGGGTAAATCTCCTGAATGTCAAAACAAAGAGATAAACTACATTTGGTTTGGT G/TAAAGTCCCTGTATGATGAATCAAGAAATCCTCAAGTCTGCTTGCACCCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	CG	GCCAAAAGG TTGGGGA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCAAAACCATCTCCCTGACCCCCAGTCCATGGAAAAATTTGTC TTCCACAAAACCGGTCCTGCTGCCAAAAAGTTGGGAA[C/G]TCTGGTGGTACAAAAAGTAATT G
WI-17690b	79	AG	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATTT GGCTCCCTATGAGATTACAGACCCATAACTCTTGTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	GA	AGGCAATTTTC TAGCTGTGTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTT[G/A] TTTGCTTCCCTATAGATTCAGGACCCATAACTCTTGTTCACACTCTGCTATGCTGCTG
EST51717	128	CT	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCCAGATTATTTCTGAAGTGAACCCACCTCCGACCCCA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCCCTCAA
EST51717	39	CT	GATCCAATCTCAGTGTCTAACTCATCCAGATTATTTCTGAAGTGAACCCACCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCCTCAA
EST53012	97	CT	TGGTCACTTTG GGCC	GGCTCTGCCA GGCC	TTCCAGGTTGACAGGTTTATCCACCCCTTCCATCCCATGGCCACCCAGGAGGAGGAGACAG GTGTCTGGAGTGTGTCACCTTGGGGCC[C/T]GGGTTGGGCGAGAGCCACTGGGTTTACATTTCTGT GGGAGGTTGGGACAC
EST53349	96	AG	TGTTGAAAGC AGTCACAATG AGTAC	CATCTGGATAT CTTGTACAT TT	AAACTGCAATAACAAAACAAACAGAAAGTCCAAAGGCTAAAGCTAAGCTAATAATACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAATGTGACAAGATATCCAGATGTTTAA TTTCGAAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATGTTAGAAAGGGCAAGTCTTACACTCAATAGGTTTAAACATGAAC ACATTAAGGGGAGATGGCC
EST53389	74	AG	CA	C	

[illegible]

EST98276	61 A C	---	GAGTCTTGCTATGTTCCAGGATGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTCCTACGAGC
EST98276	22 A C	TTTCCAGG	CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98800	53 A T	---	GAGTCTTGCTATGTTCCAGGAGCCTAACAGGAGCT
J02931	138 G A	G TAA	CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
L41680	88 G A	A	GCCTCCAGCTGCATGACTCCTAAGCCATCATTTGGAAGATTTGGCTAATTTGATAGTCTTACAA
M15795a	84 C	A T A T A G T A G A	AGGAGTCTAGTTTACCAGGCAAGAGGGGGTTGTGTTGGAAAGCGCTGCTATCTTTGTTTCAAAC
M20472	103 C T	C	TGTAAGCAAGATTCTC
M32315b	129 T C	C A T G G	AGAGGATAGAATACATGGAACGCAATGAGTATTTCCGAGCATGAAGACCTGGAGTTCAAAAA
M33875a	131 C T	G A G T G T G T	CTCTTGATATGACCTGTTATACCATTAGCATCTGGTTTGACATCAGCATTAGTCACATTTGAAATG
TIGR- A003M18	29 A	G C T	TAAC[G/A]AATGGTACTACAACCAATCCAAAGTTTTAATTTTAAACACCATGGCACCTTTTGCACAT
			AACATGCTTTAG
			GGATCCAAAAACACGGCTGGGTTTCAGCATCCACCAATGAACTGAAAGGTGAATAAAGGACGTTCAIG
			AGAAATCGACTACCAGCTGAT[G/A]AAATACCTGCAAAAGTGCCTCTAAAATTAATATTTTGACTTT
			AAGGTCCTAGTAAGTGCCACTTCCACTAAGAATACAGTTTGAATGATATAATCAGTAGTGTTTACAA
			GATCCAAACAGTGCACCTCA
			CTTTCTGTCCACCAATTTGACCTTAAGTACATATGATATATGTTTCTGTAAATAACCTATTTT
			TTTTCTCTATCTCTC/GICAAATTTGTTTAAAGAAATAAGTCCAAAGTCGATCTGGTCTAGTTAAC
			CTAGAAGTATTTTTGCTCTTAGAAATACCTGTGATTTTTATAATACAAAGGGCTCTGACTCTAAAT
			GCAGTTT
			AGAGCCACCTGTGGAACACATACATCTGCAATATCTAATCCTACTCAGTGAAGCTCTTCACAGTC
			ATTGGATTAAATTATGTTGAGTCTTTTGGACCACCAAC[C/TT]TTTTGCTTTAGAGTTGTTCAATTGTTT
			TGATGTCATGTTTCCCTTCTCAACTGTGTTCTCCCTGGCATTCAGAGAGGGAGAGGAGGAAGA
			CCCTCTGACCTGCAGGCCAAGACAGCAGGAGGAGGAGTTGGGAAAGCCCTGCTGCCATGGT[C/G]T
			GTCCCTCTCGGAAGGCTGGCTGGGCATGGACGTTGGGGCATGCTGGGGCAAGTCCCTGACTCTCTGT
			G
			TTCCAGGAGCAGCAAAAGGGCCCTGCTGAGCTCTGGTTAGGTTACAGCTGGAGGTGTGTATATATACA
			CACACACACGTGTATACACATATATATGTGTATATATATATATATATATATATATATATATATATATAT
			AATAACCCACCTAAATTTTAAACAAAGGTTCCCTTAAGTGGTAGAACCTTGGGGTGGTATTTTACCTTC
			CTTCT
			TGCTTTTTTTGTAGAGATGAGGTTTTTCTT[AG]TGTGGCCAGGATGGTCTCGAACTCCTGACTTCAA
			GTGATCCGCTCGCTGGCTTGGCTCCCAAGAGTCTGGGATTATAG

TGR- A003P30	117 C G ---	---	---	ACAAAGTTCAAAGGAGAACITTCCTTTGTTTAAATGCAGCTGTGCTCAGAAGCCCTGTGATTTCTCCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA(C/G)ACTGGCTGCCTGAA GGTACCCITGGAGATACT
TGR- A004S34	156 C T A	TTAAA	---	GCTTGCTTTTATGTTTAGTTCGGGGGAAAGGAGGGGCTGACAAACCGCAGACATCTGGACACACAGC AAGGTCACAGGGGAGGTTTGCAGAACTCTTTGCTCTGGCTAACAGTCTGTCATGTGACAATAGCCA AACCTCCTCATTCCTCTATAAA(C/T)CTTAAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97 A C ---	---	---	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT(C/G)AAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TGR- A004T44a	69 G A TGA	GCAAGATAAA CCAAAATGAT	GCCATGCAAAA TTCTTTATCA	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAATGAT TGA(G/A)TATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TGR- A004V08	60 T C GGCATTCTCT	TCCTTCCCACA AAAGGC	---	CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAACAGGCATTCCTTAT(C/G)GCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACCTTAGGGGACAAATTTGGGCAGTAGCTGCAAAATTC AGTAGCTGTCAAATTTCAA
TGR- A004V26	125 A G ---	---	---	TCTAGCTATAAGACCAGATTTTAAATATTCTAGATATAGAATTATCCAGAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACCGGTAAATATATGCATTATCTTCACATGA(A/G)AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TGR- A004V28 a	29 A G CGATCTC	TGTTGGGGTG OGGAGGTGCA GTGAGC	OGGAGGTGCA GTGAGC	CCAGGCTATAATGTTGGGGTGGATCT(C/G)GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCCTCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCACCTAACTAATTTTG TATTTTATAGTAGACATTTGATTTTTTAGTAGACACAGG
TGR- A004X20	25 T C GA	AAGTTTCCCTT CTCTCTGTAG	TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTCCCTCTCTCTGTAGGAT(C/G)CTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACCTGGGCTTCGCTTCAGAGGAGTTTGATATTTGGAAAGTGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTCTCTTCATTTCTTCAAGGCTTCCTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCT
TGR- A004X30	26 T C CCAC	TTTGAATCTT AGAGTAGAAC	TTCTTTATGGA AGTGTTTAAAA CTATTTT	TTTTGAATCTTAGAGTAGAACCCAC(T/C)ACTCTAGTAATACCTTGTAAATAAAATTAATAGTTTT AAACACTTCCATAAAGAAATTAGGGGTGCCAGCTCCTTGATTTTCCCTAGGGATAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TGR- A004Z04	102 T G ATGCAAAACT	TTCAATTTGGGT AAATTTTCATGA AAGCAA	CTTATAATTAG AAATTTTCATGA AAGCAA	CACGGTATATGCCTTATATAGGTATATACAGATCGTACACATAATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT(T/G)TTGCTTTTCATGAAATTTCTAATTATAAGG ACTGTTGCTTCTTCATATTCATTTGAGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTCTTCTCCGATGACCATCTTTTGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGCTGCCG GTCC	GTCITAGCAGAGGAGATAACTTTGAGGGACAGCCCCCAAGGGCCAGGTAGCCTTCAGGGCGGGCA GGGTGGGGAGGTAGGAGACTCTGGACCGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGCTTC
TIGR- A005D17 c	81 T C		---	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTATAGACTGAGAGGG AAACCCAGCAAGGCTGCTGTAGATCTCTGGCCTCTGTGAGGATCTCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGCCAA GAAGATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTATAGACTGAGAGGG AAACCCAGCAAGGCTGCTGTAGATCTCTGGCCTCTGTGAGGATCTCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTACATTATT GAACCTAAAA CTGTACAC	TTGTCTATTAT TTAAGCCCAAC AAAA	CATCAGTAACATATACACAATTGGTCATCACTGAACCTTGGCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTAAAACTGTACACTGTTTGTGGCTTAAATATAGACAATGATTTTGT TCTATTACTTAGTGATAGACAAGTACTTGTGTAGACAAAGTACTTTGTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATACCAAGCCCTCTGAGCTCACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCCTGCCATGGGATAGTACTCTTGGCTGCTTGGCCCTACAAAGCCACCTCTAT TTCATACCAATACCTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAAAACTTTGTTTAGGGAAAAAATAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGAGACAGATGACCCCTGGGCTCCTTATTTTCTTTCAACAGGACC CCACAGATAATTTGGCGTATGTCATGAGGACTGGGGATGCTCTCTATTTG/CJGGATGCTCTCTATTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAGGTACTGCACCTTACAGAG/GJCTCAATTTCCCTGATTAGGA AGCGATGCTAATGGGTATTCATAGGTAAAGTATAAAATGTTGTATTTAAGAGAATCCACAAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGTAATGT	ATGACAAATGATAGTATTAGCTTACCCTTGTAGCACTACTGCGTATCAGGCACTGACTCGG TGCTTTAC/GJATACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTGACAAATGGTCAATTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJGCTTAGGGTGTCTCCACACAGCAGACATCTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCTGCTTACGAGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTCTCTTGATATTTGTAAAAATTTCCCCAAGAGCCGCATATGAATCTGCC

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X57830	106	G C C T	AGTGGAAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC	A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTACCTATCTCGAAAAAATAATAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAAGCATATCTG/CJATGCCTCATTTTATCTGTCAAT GAAAAGCGGGGTTCAATGCTACAAAATGTGCTTGGAAAATGTTCTGACAGCATTTACAGCTGTGAG CCTTC
X74070b	72	T G TGGATC	CTTTTAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC	TA	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATC/TG/GATAAAATCTAGATCTCTAATATTTTAAAGCCAAAGCCCCCTGGACACTGCAGCTCTTTT CAGTTTTTGTCTTATACACAATTCATTTCTTGCAGCTAATTAAGCCGAAGAAGCCCTGGGAATCAAGTTT GAA
Z48804	44	C T	---	---	---	ACTGCCGAAGTGTAGCGGGCCCCCAACCTTGTCTCATCACAG/C/TJAGAGCTTCTCCCGAAGGG CCTTAGGATAGGAGAAAGGTTTCATGCACACAGCTGTGAGAAATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTAGCCTTAGTGGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAAG TCCA
D28513b	133	A C	---	---	---	ATGACCAAAAGCCACCACATTTAGAACTTTGGCTGCCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGCIW GJTGCGGTGAAGCATGAACCTTTGTTTAAATCAAGAGGCTTACATAATTTTAAACAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G	---	---	---	CCACTCCATCCTGATGCCCAAGTATCCACAGCCTCCTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAA/VGJTTCTCCAAGTATCCTACCTCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G	---	---	---	CCACTCCATCCTGATGCCCA/VGJTTATCCACAGCCTCCTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAAGTATCCTACCTCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A	---	---	---	CTCCCTGCCTCCTCCTCCTGCTGCTGATGCTCGTCTCAACAGCGGAACCTGTCTTGGAAATGGGG GAGGGGGGCTTQ/GA/CJTTTCTTCTTCTTGGCTTCTTATTTCTCCACAAACCAATCTCAATAAA GCCAAAATCTTCTCTTCTTCTCCCTCAGGCCACCTCCTGCTCCTACTCCTGCTGCTGCTGGCTTTT CTGGA
D37931	64	T C	---	---	---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG/T/CJ CCCAGGCTCTGCTCCTCAGCTCAITTCCTACTCTTTTCTCTATATAACTCATTCTATAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTAAAGCTTCC TTT

D63807	101 C T ---	---	CAGCGAGGACTTCAGTGCAGTATCCCTGCCCTCAGTCTCTTTAGAAATCACAATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTTCTGTGTTCCAC/C/AGAAAGGACTTTTTGTTTCAAAATGGATCAG AATGCAGAGGAGTCTGTTCTCCCTCCCGCTGCTCGGTCTCGGTGCTGGAGGGTGACCTGTCCCAGATGAC
D90145	21 T C ---	---	TGGGAACATGGGTGAGACCTC/CJACAGCTACCCTCTCTATGGACTGGTTATGGCCAAACAGCCACA CTGTGGGACTCTTCTAACTTAAATTTTAAATTTATTTATATACTATTTAGTTTTTATAATTTATTTTTGAT TTCACAGTGTGTTTGATTTGCTCTGAGAGTCCCTCTGCTCCCTGCTCCCTCCACCTCCCTCCACAGTGTG TCTGGTG
EST14035	59 T C ---	---	ATTACTCTCAAAAATTTTGGTGTGTGTTTAAGTACTTTCTATTATGAGCCCTC/CJGAGGA CCAGACATGTTATTATCAAGCCCTTATATACCATTAAT
EST16668	71 C T ---	---	GCATTTAAAAATTCACATTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATTT ATG/C/JGTAGATTTTCAGATGTAGGTGCTCAACTACTGAGCACTTATCT
EST16904	57 C T ---	---	ACAGACTATCGCCAACTTATAATGCTTAACTTTATGATCAATAGTAATMAATTACA/C/JGAGATA TTCACACTTTATATAAATAGGTTTGTTGAAGATGATTTTTCCCAACTGTAGGTTAACAT
EST21863	49 A G ---	---	TTTTTAAGTACCAGAGGCAC/TGCTGGAAACAGGATGAAACTGATACACCI/AGJGTTACTACTTACTC TTCACCTTCAAACTGATTCCTCCCTAAAGACTTCTACTTAGCMAA
EST21885	80 G A ---	---	GGGTGAAGTAGAATCAAAAGTTAAGAACATTTTATGACACTTATTCACAAACATTTACTGAGCATA CTAGGTGCTGGGAG/JGTGACAGTGAAGCAAAACACAA
EST22623	26 A G ---	---	ATTTAGTGCAATGACAAAGCCCAI/AGJAGAACAGAGGATCAAAATGAAGATTGAAATGTATTACC TTCATAGTATACGAAGTTTAACACAAAGTATGGGAGT
EST22644	98 A G ---	---	AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTTAAATGATTATCCATTTATTACAGI/AGJAAATGTGAAAAGATGGCTTTTAAACCC
EST23587	31 T A ---	---	CCTCATTTATTTAAAAGACGGACATAAAA/JTATACAAACAAAACCCCAAGTCACATTTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST24246	106 T C ---	---	AAAGATCTGGCATTTATTCACATCATCTCTAAATATTTTGTAATTAATCTTTTCCATGAGTATTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACCT/CJGAATAACCCATAGTTACAGAAATGG GTCTGTGTAACCTCAATT
EST24308	45 A G ---	---	TAGTTTAAATTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT/AGJATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435	73 G A ---	---	CTTGAACCTCTGGTCTCAAGTGGTACGTCCGCTCAACCTCCCAAAATGATCGGATTACAGGCATAAG CAGCC/GI/JGCCTGAACCCAGATTTCTTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST25089	25 T C ---	---	TATGTTGCAATTATCAAAATGGTTAT/CJAGTTTTCAATTAACAACTGTAATGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTGTTAGTTAATGCTACATTT

[illegible]

EST33508 1a	36 A G ---	---	---	AAAAATGCTATTGAACAAACTTTTTTATAAGA[A/G]TAAGTTGACTGAAAGGAGGAGTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	---	ACAACATAGGACTGGTTATCTTGTTTGAATAATATGTTGCCACTTCCTATTGTTTAAAAATGA TCATTTAA[C/G]CTTTGAACACAGCCGAATCCCCC
EST34739 3	97 T A ---	---	---	GAAATATCTTCCAGTGGCAGGAACAGACTCCAGATCAACAGGTTGACCTTTTCGTTGATGA GCTGATAGCTTAGGCTGGGGAACTCT[A/G]GGTGCCTTACAACCTCACTGCGAGAAATTTCT TGTTGTCCTCATAAACA
EST34792 6b	104 A G ---	---	---	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATCTTAGTCTATTACA AAGATTTTGTGCTG
EST34835 9b	93 T G ---	---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGT[G/G]GGCCTTAAAGAAACAGACAAATTTGTCTAAAGAT
EST34835 9a	82 G A ---	---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTG[A/G]GCTTTCTGGTGGCCTTAAAGAAACAGACAAATTTGTCTAAAGAT
EST35230 0	93 G T ---	---	---	CACAAAGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCT[G/G]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	---	TCCTTTCAAATTTTGTATGAGGCATTTAATG[C/G]TATAAATTCCTGCTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTTGTTCCATTTTACTTAGTTTCAAGACTTTTCAATTTTCATCT
EST35708 9	32 C T ---	---	---	CTGCCCCAAATTAAGTTTAGGCAATGGAA[C/G]TAGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTATATGCAGCGTGTGCTTCCCTCTCTGAGGTTGGCACCTTTCCCTGTTG ATGTGCAAAGTGTGGCT
EST35747 9	51 C G ---	---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTCCAGTAGGTTGAGATT G
EST35751 9	89 C A ---	---	---	TGTTCCATTATATAAACTGAGGGAACAAACGGTGTGACATGGCAGACATTTTTCATGGAGA AGTTCCCTCCCATGAACCAAGA[C/A]CTTGTCTCATATAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAGGCCTGTGA
EST36301 4	93 C T ---	---	---	CACCTGTTCAATGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCAAGCTACAGC AGTCAGGAGGAGCCATGGCCCTG[C/G]GCTGATGGAGCTTGTAAATTAGCCCCCAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---	---	---	GCCATCAGCCCCACAAGACATGACTACCAACGC[G/G]GGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTCTAGTGT

EST36620 6	50 GA ---	---	---	GACTTTATTAGATAAGGGTTTCGGCTACCTCAAAGCTCTCAGGACTGG[G]A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGAATAAAATACAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 CG ---	---	---	CCGTGATGTGCATGGGTCCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTTCAGGA AAGGAAGTCCTGGGATTCTT[C/G]AGGGGACATATCACACATATTTAAGTCACTGTGTGACTCGG CTTGAGCAAGICATTICA
EST36729 9	62 CT ---	---	---	GAGACAGAACCCATCAGTTAAATGAGGTTAGGCCCTCTCCCTCAATATACTGATTGACAAT[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 AT ---	---	---	ACTGCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGTCTATTCAAGCAACAATTT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 CG ---	---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTAACAATGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 TC ---	---	---	GGTCTCACTCTCTGCCAGGACGGTTTGAACCTCTGAGCTCAAGTACCTCCACCTCCACCTGGCTTCC GAAAGTCTAGGATTACAGGTT[C/G]GTAGCCACCCACACCTGGTCTTGGTTTAAAGTAACCACCTGAA C
EST37269 3b	105 TG ---	---	---	AATAGTCTATGGCTACGGGCGCGTGGGATGTTAAAAATGGGATTTTAAATTAAGATTGTGAACATG CAAAACAGCAAAATTTCTCAGCTTATATTTTGAAAGT[C/T]G]CAGGAGAAAAATGGGGTCC
EST37284 2	93 GT ---	---	---	AAAAGACCTTTCTCAGCAGTAACCTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGAA GCTCTGGATAATGTCACTCTAGGA[A/G/T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGTTCAGGAATA
EST37315 2a	90 AG ---	---	---	AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACATAAGATATCCTCTGCCTCAGCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATC[T/G]CCCTGCCCTGTAGAACCTCAAGTTTGATGGGCAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 CT ---	---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTACATAGCCAAACACATTTTCAAGGCACCTCTAGCTACTACA GGA
EST37376 8b	101 GC ---	---	---	GTGACATCATGCTCTCAATGCCCTTTCAATTAAATAGTAGTTGAGCGCTGGGGGCTGAAGTCAGACT CTCTGGGTCAAATCACAGTGTGTCTCTGC[A/G]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T/C ---	---	---	GTGACATCATGCTCTCAATGCCCTTTCAATTAAATAGTAGT[C/T]GAGGGCTGGGGGCTGAAGTCAG ACTCTCTGGGTCAAATCACAGTGTGTCTCTGCAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATACCTCAATTCTGTGAAAAAC[T/G JAACATGCCTCAAAAAAGAGGGGAAAAAACITTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAATCTGCAATGAATCAGTTATGAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGCTGGAAGCTAGCCTATCGCAITTTTAAACACCCCTTAAATCAATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTACAGTCATTTATTACCTAG[G/G]GTCAATGATTAATAAAACACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCAAAATCACCTGCGTTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---			TTATTGAGTAGCTACACTGTGCCAGAACTAAGCTTTACATGTTTATATCACITAT[G/J]TATCTCA ACAATCTTGAAGGTGGTATTATTTCCCGTCTTAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAAGTCCACAAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA[C/T]CGCATGG AAGMCGCTCTCTTTAATTCCTTAACCTCTCTTCTTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCCTCTTTCAATACCAAAACAAACAAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCTGCTGACTGAGT[C/G]GTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATCTCTCTCTCTCA
EST38950 5	25 T C ---			TTTATTTGCAAAAGTAAGCAGCGGT[C/G]TGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCTCTG CTGAAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGGAACAAAGCTT ACAAACAAGAGCAGCCA
EST39053 6	90 T C ---			TTTTTTGTTACTCTGTAGCCAGTCAATTAATCTGAAGGTTTAAATATATCATTTTATTTGGGATGAGATCA TAGCTTTTACACAAATGCTATG[T/C]AAACAAAGTTACTGAATATTTTACCCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCCTCTGCTCTCTAGCAGTCAAGCACCACCAAGAAAGCCCTGGAAGACCCATGGAAGGAAAGTA TGC[G/C]GTGTTTAGGGAGAGCTGGCACCTGCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCCTTGGATACATCACT
EST40544 7	31 C A ---			GTCAACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCCTGTGACAGGGAACCTAAGCTCT[C/T]CAAAATAACTGAACTAAATCTGT AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTT AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTCTAGAGAACCCCTGTGTATACACTACCGATGCACA[G/J]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTGTTACCACCATTTCTCATTGAACTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACITTTGGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGGAGTTTACAGAATTTTCTTCTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA[A/C]GGACTTGGAGACAGCGATTAAATACGGAACAAGGCTCTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGGTTGTAGGAATTTGGGAAGAAATTTATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC A[A/G]TCTGTACTCCCAATATCCTATGTTTAAAGCT

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EST51340	51 G A ---	---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAAGACTCAGAGCCAGATCCTTTATCCAACCTCTCGA T/CJTITTCCTTGGTCTCCAGTGGGAAGGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGAAGT AGCTG
K01506	63 T C ---	---	---	CTGAVCTCCAGTGGCCCTACAACTCCATCTCAGCTTTTCTCTCACTTCATGTGAAAACCTAQT/CJC CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAGCAGTCAATCCT TAGTAAAGTTTCCAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCCTTC ATTGAGCCCTTTATCCT
L18877	69 T C ---	---	---	TGAGTCTGACACAGATTGCAGCCAGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC CT/CJATCCATTAGTTTCCACTGCCTCGTGTGACATGAGGCCCATCTTCACCTCTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTTCTGTCTATTGGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	---	GGTATTTTACATATCCCAAGCCCTTTAGGGCTACAGT/CJCTCTTGTCTGACCCCTGTAGGGTGCCA TTTGAGTTTACAGCCCTAGAAAGAAAGGCTTTGGCCCTGTGTGGTGGCATAAGCCCTGTAATCGT AGCGCTTTGAGAGGCTGAGGCGAGGAGGAGATAGCTTGAGCTCAGGAAGTTCGAGACAACCTGGGCAAT GT
L38517	137 G C ---	---	---	GGGTCCAGAACCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGGCAACACCCAGCGTCCCCCAG CC[G/C]GTCGTGGTGTAGTCTATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTTGAG
L39059	123 T G ---	---	---	ACTTGAGAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATAGCCAAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTATTTCTTTGTATTTGTATATTTGJGSCCTGA AGATCATCCCGAAGGAGGCTGGAGGTGCCGGTGGCCCTGTGTCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	---	CAAAGTTGTCTCTGCCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACCTGGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGCGCTGAGTCTGCAT CTTAGGGCATGGCTCTTCTCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111	T C	---	---	AAGTGAACAGAAAGCAAGATGGATTGTTGCTCTATAAAAGCACATAGTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTTGGTTTACTTTTCAGAAAT/C/GAAGAAGCTTATTCAGAAAG CAGAAATATCANTGAGCGATTTTAGCCCAATGCTCCAAAACATCATCTGTACCTGGAGATCCA
M18079	52	G A	---	---	GTC GCGACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGACCAAGCTG/A/JTTTATTTCACC CCATCAAGTATAAGGTTACTGATTTGTTGCTTTTATAAACATTGGTATATTCCATTTCATGCCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113	T C	---	---	TAGGGATCTGTGCCAGGCCATTGCGACACGCCACCCACTCCACCCCTGTAGTGTCCACCC TGACTGGTGGCCCCACCCCTGGGGAGGCCCTCCCATGTGCTGT/C/GCCAAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTTGTGCTCAGCAGGGCGCTCCGCCCTCCCTCTCTCTCTCTCTAATA GC
M21539	114	T G	---	---	TCAGCTGTTCCACAGCTCCACCTGCATCTCTCATCAAAAGCCATCCAGGATACACAGGGAGCTTCT TTCCCCCTTAGCCTGTGATCTGCCCCATGATGATCCCCGACAGCAAAAT/G/JTTTCTCTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCTTTTCAGAGCT TCTCTTGGGTGC
M26041c	173	A G	---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTTCCCTGACTTC CTGATTTTCTTTTCTCAAGTGTACCTACTM/G/JGATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A G	---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTTCCCTGACTTC CTGATTTTCTTTTCTCAAGTGTACCTACTM/G/JGATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C G	---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTTCCCTGACTTC TCTGATTTTCTTTTCTCAAGTGTACCTACTM/G/JGATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G C	---	---	TAAGGCAGCTGTGAGGGAGGCCAGTCACAGTCCAGCAATTCACACACCCTTGAC/G/CJAATGCT TGCCAAGCTGTTTAAAGCCAAGAACACCCCTTTCTTTGTTCCAAATTAACCTTAGAAGAAACCCCA CAAAATAAGCAATCAATC
M81695	34	G A	---	---	ACTTACTTACCCTCAGCTGTAGGCTGACGGGA/G/JAACCCTGCACCACCGAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAACGCTGTGCTGGGAGGGGCTTTGCTTGTCAAGGTTTC CAACTGGAAACCCCTAGGACAGGGTCCCTGCTGTGTTCCCAAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166	C T	---	CTCCTCCTTTATTTACGATGGAGGGTTAAATGGAGGATCTCCTTTCTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTAAAAAGATCTTTTCACAACTTACCTTGTAAAGACAAATTT TATTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAAATATTCTATGTCAATGATTTTAAAGCTA TGAATACAAATGGGGGA
U09607	39	T C	---	GAGGCTTATAGGGTCTCTACTTACAGAACACCCCAAT/CAGACATTGCATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTCGAATTTGTAAAGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTTGGCCCAAGAGCAAGCAACCAAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T C	---	GAGCAAGGCAAGAGCGGAAGATGAGTTTGAGCGTTGTATCCAAAGGCTCATCTGGAGCCTC GGGAAAGTCTGGTCC/T/CACATCTGCCGCCCTTCCAGCCCTTCCCCAGCCCCCTCCTCTTGTTCCTTC ATTCAATCAACAAATTTGGC
U10694	20	C G	---	GTGACATGAGGCCCATCTT/C/GJCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGGTTCCCTTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTGGAAITGTTCAAAATGTTCTTTAATGGTCAGTTAATGAACCTTCAACATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C	---	AAAAGGACTCTGGTTCAATCCAGTTCATTTGCTATCTTTTGACCTTGACAAAGTTGTTTAAAC CTCTTTGTTGAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCMAGAGAT/C/TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187	T C	---	TTCTGTCCACTTTCACCTGGTTTAAAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG/C/TGGTCTCATAG CTCATATGCAGGATTCATCA
U17077	122	T C	---	TCCAATTATTGGTCCCAAGAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAAACAGAACGTCCTTGACAGACTGAGCGATGACACCACATCTCTTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTGCGGAAAACAACTGTCTCTTGG AATTA
U18543	58	T C	---	GCACATGCAGAAATAGACTCAGCCTATGTCCTGATTCAGCTGGGTAGTCTAGAACTT/CJAGAAG CTCCATCTTTAATGTTTATTGTTATGTCCTCCCTCCCGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATAGGCACCTCC AAGGCTTAGTAGAGAGGCC

U25975b	164 C A	<p>TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAGCCCTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGCTGCATAACCTGAATGAAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGAC/C/AJAGATATGACTTTTATATGAACCCCTCTTTAGG GTCCAGAAGGAATTGTGGACTGA</p>
U25975a	143 C G	<p>TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAGCCCTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGCTGCATAACCTGAATGAAAGCAATGACTATTCTCTG AAGACAAC/C/GJAAGAGAAAATTGCAAAAAGACAAATGACTTTTATATGAACCCCTCTTTAGG GTCAGAAGGAATTGTGGACTGA</p>
U25997	61 A G	<p>CAGGAGAGGTTATTACAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA[A/G]TT TTGAGTGTACTGTGCTGGTTTGATTTTAAAGTAGTCTCTATTTCTATCCCTTAAAGAAAATT GCATGAACTAGGCTTCTGTAAATCAATATCCCAACATCTGCAATGGCAGCATCCCAACCAACAAA TOC</p>
U28413	29 C T	<p>ATTCTGACAGCTAAATTAGCCCTAAATG/C/ΠGGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTAGTCAAAATGTGTTCTTGATCC CAGATGTTGTGGCCTGGAAAGCCCTCATTTGCTACAGTACAAAGTACACAAGTCGTTGTACCTCAGTT G</p>
U30884c	89 A G	<p>TAGGGGTAGCATTTAAGATTACAGAGTCATTAGCAGTGATGATTTTGGACCTGCCGTATATCTGTT CTTCTATCCACAGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTTGTGATATCTGTGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA</p>
U30884a	34 A G	<p>TAGGGGTAGCATTTAAGATTACAGAGTCATTAGCAGTGATGATTTTGGACCTGCCGTATATCT GTTCTTCTATTCACAGTTAGCCAATGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTTGTGATATCTGTGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA</p>
U31216b	78 A G	<p>GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATTGAGACGGCTGCAACCAACA GCCGTATCAA[A/G]CCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTAGCCCGCC TGGTAGCCCTTCCAT</p>
U31216a	70 G A	<p>GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATTGAGACGGCTGCAACCAACA GCC[G/A]TCATCAAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTAGCCCGCC TGGTAGCCCTTCCAT</p>

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U31416c	76 G A	---			AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGGAGAGTCTCATCTTAGGGCATCGCTC CTCCTCAQ[G]CCACAAATCTGGTGCCTCTCTCTGCTTACAAATGTCTAGGTCCTCCACTGCCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCACITGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T	---			AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGGAGAGTCTCATCTTAGGGCATCGCTC [C/T]TCTCACGCCACAAATCTGGTGCCTCTCTCTGCTTACAAATGTCTAGGTCCTCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCACITGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T	---			ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCAACTCACATTGTTCTCC AGACCGCAGG[C/T]TCCCCAGCCTCAGTTGCTGGAGCTGTACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTCTCTATCTGGGGACGCTGCTGAGAGAGGCCGAGAGGCCGCGCAGAAC ATGCCAGGTGTCC
U37690	54 A G	---			GACCACGCTGAAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCTAGJCCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGGTATGCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C	---			TGAACCGTTTCAACATGGAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCTATACCCACGCTAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACCTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T	---			TCAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTTAAATATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAATTTGGATTCATCTCTGTTTTTTCATGTCTCTCTT GTAACCTGAGATCATCAG
X52011b	148 C T	---			AGGAAGATCCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAATTTGCG AAATCTGTTGTGCA[C/T]GCTCMAATGAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCT
X52011a	118 A C	---			AGGAAGATCCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAATTCGCGAAATTT GCGAAATCTGTTGTGACGCTCAATGAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCT

X54741	24 A G ---				CAGGCCACCTGTCTTCTCTCCAC A G TGCACAGCTTCCTGAGTCACCCCTCTCTGCAGCCAGCTCCT GCACAAATGGAATCCOAGGGCCTCAGGACTGGGCTGCCAGCTTGCAATAGCAWGGCCAGGGCACAGCTGGAGACGATCTTCTGGCAGGGCCTGGCCTTGTCOCAGGCCACCTGGCCCCCTTCTCCAGCAAGCAGTGC
X54869	99 A G ---				AAGCATTTGGGTTACAGTGCATCAGATACATTTTATTTCTTAAATAGAAATATTTATGATTGCAT AAATCTGAAAATGAATTATGTTATTTGCTCT A G ATACAAAATCTAAATCAATATTGAAATAGGATGCACACAATTACTAAAGTACAGACATCTAGCATTTGTGCGGGCTCATTTTGTCTCAACATGGTATGCCGTGCTGCACACCTCCAGAACGCAGGTGCTGGGCGCGTCTGCTGGGACCCCGGAACCTCTCTGCCGGAAGCCGAGCGCAGGATGGGCCCAACTTCGCCCTGCCACTTGACTTCACCAAAATCCCTTCCTGGAGACT G A AACCTGGTCTCAGGACGAAGACTGTGAACTTGTGGCTGAAGAGCCAGA
X6924	147 G A ---				GAAATGTGAAGATGTGACAAAGCCTTTAAGCGTTGTACACTTGTCACATTGATTGTATATAAGATAAT T G T CATACTGGAGAAAACCTCCAGAAAGTGTGACAAATGTGACAAAACATTTAATTAATTTCTCATACCTTATGACAGGAAAGCATTTATACTTGAGAAAATTTGTATAAAGATGGAAAAAGTCATTAATATCTGCTCATATCTTAACATCAGCGATT
X78932	62 T G ---				CTCAACCCATAACCTCAACCACATCT C T ATCTCTCCACCCACATCCACACATCCACCTCCATCCCCAAACCCATCCTCATCCCAACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAACTCATCTCATCCCCAACTGCAGCCCCAAACCCAGGGCCATCCCCAAACCCATCCCCCAAGGCCAAACTCAACACCATCC
X80026	25 T C ---				ACCCCACTCAAGTCCAGGCCGCCAGGCATCTTCTGCCCCGCTGCTTGTGGCCCCATCCAGTCCAGGCGCTGAGCAAGTGTCTCAGTACTTCTCTCT G C ACTTTGAAGACCCCTCCCACTCCTGGCCCTCACTTCTCTGTGTGATCCCCCACTCTGGGCTCTGACACCCACAGTGGAAAGGCCACCCCTAGAAAGACCCCACTCAAGTCCAGGCCGCCAGG A G TCTTCTGCCCTGGCTTGTGGCCCATCCAGTCCAGGGGCTGGAGCAAGTGTCTCAGTACTTCTCTCTGCACTTTGAAAGACCCCTCCCACTCCTGGCCCTCACTTCTCTGTGATCCCCCACTCTGGGCTCTGCCACCCACAGTGGAAAGGCCACCCCTAGAAAGGGCACCCAGAGTGAOCACAAGTCCAGCAGGGAGGGCGGCCGCTGCGGTGTGCGTGTCTTCTTTTCAGCCCCGAGAGGTCCTGACCTGGGGCTTCTCAAGCCTCACTGGGCCACGCTCCCCCGCCGCTCTCTTTCTCCCAAGC G A AAACCAAATGCCGCCCTTCACTCGCGTGCCTGCGAGGCCGGGGCTTTCTTCAGAGC
X80197a	28 A G ---				ACCAACAGCCATGGTCTAAGGACATGGATCGGGTGCCCCCAGACGTGTGCACAGGGGACCTCTGGCCCACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCT G G GGCATGGCAGGAGGCCATCGGGTACTACGCAGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC
X85106	150 G A ---				GGGA
X87160	128 T G ---				

[illegible]

1282	130 C T	---	GTGGGATCACCACCTACAGTCTAAATTTTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTGTACCCATTAGCAATATTCTCTATCTGCCCTACCCCGAGGCCCTACTCTTATCGCTATAGATTTGCC[C]/ACTTGACATATCATACATGGAGCCATACATATGTGTGCCCTTCATGATGGCTTCTTCACTGAGAATAATGTTTTCAAGGT
6810	68 C T	---	AGTATCACACATACATTAATATATTAGATATACACAATAATAAATCACTCCCTACCTTGAAACATTTA/C/TAAGAAGCATTTTTTAATTTACAACACAAGCTCAACGAACTACAAATAGTCTAGTGTCTGTTACGTGGCAAGGATAAGGCTGAACATAAATTAACCCCTTTAAAAATGTCTATGAACAAGTACAAATTTCTTTTTGAGTCTGCAGAGCAATGACCACCTAAGAAATATTTTTAAAGGC
6817	118 A C	---	CCAAGTACATTGGGTGAACGATGAGCTAGTGTCTAGTATTTTGTATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGAGGGTAAC/A/C/TTGTGGATACCCCTGTGTCTACTGGCCTCCAAGGCATTGAGGGGATCATCAAGATGTGGACACCTTGTGTCAAATCTTGTTTCAGGTGCGGCTGTGCAGATCGGCTTTTGGTTTGGTGTCTTAG
6819b	212 C	---	CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCCCTCAACAGTTT[G]/TCATATACAAAATTTCTGCTATTTTGTCTTAGCAAA CAGCAATACTTTTGTCTTCTATATGACACCTAATATCCA
6819a	166 G T	---	CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCCCTCAACAGTTT[G]/TCATATACAAAATTTCTGCTATTTTGTCTTAGC AAACAGCAATACTTTTGTCTTCTATATGACACCTAATATCCA
681xx	39 A G	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[G]/TTACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCCAGCAATGTCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGT TTAACAAAAGAAATGAACGTCTAGG
6972b	149 G T	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAACTATTGATTATGC CACAATTCAGAG[G]/TCCTGTTATTGGTCTATTCAGAGATTCAACTTCTCTCTGGTTAGTCTTGGGA GAGTGTATGTCTCGAGGAAT
6972a	122 A G	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA[G]/G/CTATTGATTAT TGGCACAAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTCTGGTTAGTCTTGGGA GAGTGTATGTCTCGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTCCCT CAATGCAG[AC]
7598j	208 A T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTCCCT CAATGC[AT]GA
7598i	192 G T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTCCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[CT]ATTAATGTGAGAGATTTCCCTGATATGTTATCTTATTAATTTCCCGTATTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGAT[CT]CCATTAATGTGAGAGATTTCCCTGATATGTTATCTTATTAATTTCCCGTATTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATTAATTTCTTG[AG]GGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTAATTTCCCGTATTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAA[CT]CAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTAATTTCCCGTATTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGC[CT]GGCTAACCCAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATTTCCCGTATTT CCTCAATGCAGA

7598c	56	A G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAA/GJAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTAATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47	C G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACA/C/GJCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTAATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30	A G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTJ/GJTGATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTAATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116	A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAAATGAATGGGTAGTCTCTATCTTCAAGGTCCCCAAATA/JCCTTGAGGTTCCCT
7998b	94	A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAAATGAATGGGTAGTCTCT/JCCTTCAAGGTCCCCAAATAACCTTGAGGTTCCCT
7998a	75	A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTJATGATGGGTAGTCTCTCTCAAGGTCCCCAAATAACCTTGAGGTTCCCT
8071	119	A G ---	---	AAATACAGAAATTTTATTAAGAACTGTTTAAAGTAGAAAAAACCTGTCAAGAAAGACCCAGGTGG AAAATGGGTTCCCAATAAATGGAAATTTTAGGGCAACAAAGCTTAAAGGCC/JGJCAAAAGAGA AATAGCACCACTGTCATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTTGTTAATCACTGAATC TGGGTTTCTCTGTAATCCACACAGAGCATGCACACACACATTTTATCAT
8467b	93	C T ---	---	AAGGCTTCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA/C/TGGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAAGGAAAAATTAAGTCTG
8467a	70	A G ---	---	AAGGCTTCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG/JGJCGCAAAATCCACTTTGCTGTAACTGTCATCCGAACCTCCCTTCAGAGAGCAAGCAAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAAGGAAAAATTAAGTCTG
8498	84	C T ---	---	AGGGTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG/C/TJAAATACITTCATTAAATCGAAAAAGAAAAATTCCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCITTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCCTTCTCTCAATACAGAACCCAGGAATGTAATTTCTCACTCACTCAG

WI-18562	29	GA	---				CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	AC	---			---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAAAGTATAATTGTAACACACAGTCTCGCACAGTTC AC
WI-18683	22	CT	---			---	TAAGTGTTCAGGACTGGACTC[CT]GGTCCCTTTATTAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCAAAGCCTGCCCTGCAGT
WI-18520	75	GA	---			---	GACTTTGGTGATTTAATTGCTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTAC[A/G]CCGGAGTGGTAAATACTACCTACTGCCAACAAACACGGGCATCCACTCTGCTCTCA TGCTCTCTCCGTGAGAC
WI-18563	94	AG	---			---	AAATAAAGTTTTATTGGCACACAGCCCAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	TA	---			---	GTCCTATTCAATTTAGCTAGACCCATTTCATTCTGTTAATGGCTACATTTGTTTTCATTGTGAGAC T[A/GTCCCAATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCAG
WI-18723f	94	GA	---			---	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAAA[G/A]TATAAGCTTATTTGGTGAATCTTCATCCT
WI-18723g	71	TC	---			---	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96	AG	---			---	TTTATTACAATATTTAGGTGGCACATAAATAACAAAGTCTGA[G/A]ACAGGAGGTAAACATTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18619	44	GA	---			---	TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGGCAGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGAGCCTCCAGGTGGAAGGGTATTTTAAATAAAAAATAA TGGAGCTACAACCAACCCCTG
WI-18535	107	GA	---			---	GTAAATAAAGTTTTATTGGCACAGCCAGCTCGTTTCATTATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGGTCCCGTG
D17525	107	CT	---			---	AGAGTGGTCAGAACACACAGGCCGCAATCCAGGCTCTATCACTACTAGTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACCTCAGTTCTTCATAGATGGAAC[A/C]TGCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAGATTAACTAATAGATGATGATGACACTTAAACAGAGTGATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAAGGTGCTGATGTCTACCGGCAGACGAAG

DWU-133c	313	A G	---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTGTTACCATCCT TTAATAGATCTACACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C	---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTGTTACCATCCT TTAATAGATCTACACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T	---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTGTTACCATCCT TTAATAGATCTACACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC ITCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T	---	---	ATGAGATCCTTTAAATCCTTCATGAACGTTTGTGGTGGCCACCTCTACGICAAACATGAAGTG TGTTCCCTTCAGTGATCTGGGAAGATTCTACCCCTTGACCAACAGTTCCTTCAGCTTCCATTCGCC CCTCATTTATCCCTCAACCCAGCCACAGGTGTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAGACCATAAAGGGAAAGGATTCTGTGGAATATAAAGAT
DWU-387	169	G T	---	---	GTGTATAAATGCAACTGTTGATTCTCTCAACATGGCTCACAATTTCTCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTAAACTGCACCTGCCAACAAGTTCACCTCATATATAAGCATTTATTTTA CTCTTTGAGGTGAATATAATTTATATTACAAATGCTTAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCAACCAAGTATCAAGTAATAACACAAATGAAGTGTCAATTATCAA
DWU-447b	172	---	---	---	ATTTTAGTGCTTTGGGTTAAATAATCAATTGCAAAAGTATTCTGAACGTCAAGCTGCCCGAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT CCATTATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAAATGCTTTCTGTTAG GCCCTTCTTCTTACATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A G	---	---	ATTTTAGTGCTTTGGGTTAAATAATCAATTGCAAAAGTATTCTGAACGTCAAGCTGCCCGAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT CAACCATATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAAATGCTTTCTGTTAG TTAGGCCCTTCTTCTTACATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C G	---	---	GTAAATTCAGTTTTCAGTTCCCTCTTTTGTGCTGCTTCTCAATTAAGCGTTTAAAGGTGAGTC/GAT AAATCAACTGTCATCAGGTGAGGTGCTGCTCCATACCCAGCGTTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	TCATACTAGGGCAGTATCTCTCTAGCTAGTGCCCATACAGAAAATTCCTATCACCATACAAAAATTA A/TJGCAGTATTTATGTTTTAAAGCACAGGTGTACCGAAAAGTGTGAAAAGTCTGAATTTATGGGT CTATGCAATGCAITTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	AAATCCAGGCATTCGAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACCTTATTA AGAGCTCCACAGTGAAGATGGAGAGGTGAACCTGCTTTGAATATCCAGATGTTTGGTC[AG] TGCGTATGGCAGTGAGCAGGTATGTTTGGCTTTGCTTGCACTGAAATTTAAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATTCAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	AACTGCATATAGATAATTTATCCAGGATGTGGCTCATTTTCAGCTTGTCTTCTACTGTTTGT ATATACAGTTTTGTAAACCATATGATTGA[C/A]AAGAAGAAAGTCTATGCTTAGCCAGTCAGTACA CCCAATTTTAAAAATAACATATCTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTATCTCTAAATTTCTAGTCTGATTGGC
DWU-59	94 C T ---	---	CATTCTTTGTGAAGGTAAATGGACTCACAAAGGGGAAGAACATGCTGAGAAATGGAAGTCTACCGG CCCTTCTTTGTGAACGTACATTTGGC[C/J]GAGCCGTGTTCAAGTCCCAGGTGGCAGACTCGTTTTG GTAGTTGTTTTAACTTCCAAGGTGTTTTACTTCTGATAGCCGGTGATTTTCCCTCTAGCAGACATG CCACACCGGTGAAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C ---	---	CTTGATCATGGGTGGAATTTTGTATCTGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	CACACTGGCATCTAGGCCCTCGCCCTGCATTGCAGAAAGGAGAGCCAGGTCCCTCTGGAGAA[C/J]G CTGGTTCCCCAGCCCCACACCGGCTTTGCACACACACAGGCTGTTGAGGCAGGAGGTGGGTAAAGCGT AGCTGTAGACCCCAAGCAACCAACAGCCCTGGGACCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[G/J]GAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAACAGAGATTTCTCAAGGGCAAAGTGGCTTCT A
WI-18036b	97 T A ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAAACTTCTAGAAAATACAAAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAACTTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT[C/J]AACTTCTAGAAAATACAAAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAACTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	TGTAAGGTGACTTCTATAAGCTTCCCTAAACTGTCAAACCTTTCATTTACTGAGATTTTTCAGGCCAAT GTGTC[TT]GTTGGTCTGAGATTTGATTATCAGCTGGGTAAAGTTAACTGTTCCCTGTTTCA

WI-18063	105	GA	---	---	AGGCTTAAACTGATAACAATTTGCCCTTAAATCACAATACAAAAAAGCTCTGCACCTTTCATTCCTTCCTTC
WI-18078	86	AT	---	---	CCATGTTTTCTGATTTGATGTAACCTTAAATTTGT[G]ATCCTTTAAACAATATACTGTAGCTGCA
WI-18091	90	TC	---	---	AGTTGAAAGATCAGAGAGGTTATGGTTGGTAGCTGAACCTCAGATTCAGATTCMAACCTGGTCCAGTG
WI-18119	38	TC	---	---	TTGTTTTTTCAGCATCAG[A/T]GTCCACTAGCCAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18142	66	TG	---	---	CCAAAGCTCAGTCAGTATTAATCACTGCTAAATTCATCCCTTTGTTAATTCATCAGACACTGTGGT
WI-18178	68	TC	---	---	TTTCATCTCTAGAAGTTGACTTTGCGGGCTTTTTATACCTCCATATCTCAACTGTGAAGC
WI-18244	35	GT	---	---	GCATCTCTAACAGTTTTGGTAGTGTTACAGAGGAT/GCTTGTAAATGGATTGGAGTACTTAC
WI-18245	115	GA	---	---	CACATTTTCATCTGCTCTGAATAGTTCACCTAACCAACTACTGACACAGTTTTAATTTTGGTCTT
WI-18261	26	GA	---	---	TTCAAGATAATTACAATTGGAAGGGGACCATAATTCACATTTTAAATCGAAAATAATCTATATAQ
WI-18268	88	CT	---	---	T/GCCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA
WI-18299a	107	CA	---	---	GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCCAGATTCAGTCCATGCGCTGGAGTTAGTCTGGGG
WI-18299b	101	AG	---	---	GT/GTGGGGGATGACACACACAGACACATAGATCTGGCATCTGATAGCAGGGCATAACAG
WI-18299c	77	GA	---	---	TCAATCTGAAAACCTGCTGAAGCCAGCATGCGGTTG/GTGGGAGGTGATTATGCGTGGGGAAGATG
WI-18299d	67	TG	---	---	GGCACTCACCCGACAGCAGCATCTAGCACCCACAGTGACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18299e	101	AG	---	---	ACAGATGTCAGTTGTTGAAATTTGGCCCATTAAGATATGGGGCTTTTCTTGTAAAAAGTCATTCAAA
WI-18299f	107	CA	---	---	AGGCTTGGCAAGAGTTTGCTATACAAAGGAGGACAGAGAAACATGA[G/A]CTGGGGAGTAGGCTCT
WI-18299g	101	AG	---	---	GACAGAAGGTGGGCTGTC
WI-18299h	107	CA	---	---	GATTGAAGGGATTGCTTTATTATTAA[G/A]TGAAAGCGTGATAGAGGAACCTGTTTAAGATAAACAA
WI-18299i	101	AG	---	---	CTTATAAATACCTCCCAATTGTAGAAAGTGAAGATTG
WI-18299j	107	CA	---	---	TAGAGGGAAAGGAGGTGGGCTGCTGGGCGCTCAAGACATGAGAAACGGGTGGTGGCTCCAAAGC
WI-18299k	101	AG	---	---	TTCTTACTTCCCCATAGATCTCTGACATGTGCTGCAAGGCCTCCAACTGGAAC
WI-18299l	107	CA	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAAATTTT
WI-18299m	101	AG	---	---	ATCTATTTGGGTCTGAGAAATCCACAATTTTGA[G/A]GTAATCTTTTGCCAAATTTATGACATACTCG
WI-18299n	107	CA	---	---	CAG
WI-18299o	101	AG	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAAATTTT
WI-18299p	101	AG	---	---	ATCTATTT[G/A]GTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATACTCG
WI-18299q	101	AG	---	---	CAG
WI-18299r	107	CA	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAAATTTT
WI-18299s	101	AG	---	---	ATCTATTT[G/A]GTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATACTCG
WI-18299t	107	CA	---	---	CAG
WI-18299u	101	AG	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAAATTTT
WI-18299v	101	AG	---	---	T/GJATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATACTCG
WI-18299w	107	CA	---	---	CAG

WI-18299b	52 GA ---	---	TCACAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCAITTAACITTG[G/A]TTTGCCAAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18299a	48 CT ---	---	TCACAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCAITTAACITTG[G/A]TTTGCCAAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18307	76 GA ---	---	TCAACTGTACCAAGTTTAGCAGCAAGAGGATACTCTCTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCGGT[G/G]ATGCTATGTAAAGCATCCACGATGGTTTATTTGACTCTGCAATCTGCTGGTCAC
WI-18324	72 CT ---	---	TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAACTCCGGGGGGTGGGTACTGATT TATC[G/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48 TC ---	---	ATGAAAGTCACCTCAATCATAGGGTCAAGAGAAAGAAATGTTTTCAGAT[G/C]TAAATCTATGAATA GGTGTGATCTGCTTGCATTTAAGAAACAACACAAAGTCA
WI-18395	77 GC ---	---	TCCTGACATGATCTGAAATAAAGTGATTGGTTGAATTTCTCGGAAATTTGAAGAATAAAATG ATTATTCAG[G/C]TGTGCAATGGTTTATACATATCTCTCTCTCTTATGCAAGCTATG
WI-18398	62 GT ---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAAGAAAAAAGAAAAAAGGTT[G/T] GATAACATTGCCAGTAAACATAATTCAAACAAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18396	21 CA ---	---	CTCGTTGGTATCTCTCATCC[G/A]TTCTCTTTCGCTCTTCTAAATTTAAGAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACTTTAATCACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18409a	20 CA ---	---	AAGATGGGAAAGAGGAAATC[G/A]TTTCTTACTAGAGATTTTTCCTTTTAACTCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAAGCTCTGGGGCCCAAGGCCCAAGTGCTA
WI-18442	62 CT ---	---	AAAAAGGAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAAAAATAGTTTCTGG[G/C] TTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGGGAAACACAGAGAAAAAAGG TTTATAGTGGGAGAGAGGA
WI-18452	38 GA ---	---	TTGATGTTAATCTGTCATTCTGGAGATCGGCTAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTTCCAAACCA
WI-18489	102 AC ---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGCAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGC AGTAGTAAAGAT8AAAGACTGCAAGGATTCAACAA[G/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
EST5b	93 A ---	---	CTGGTGGGAGGAAACAAATTTGGGTATATTCATACATGGAACCTTTCAGAAATAAGAAAGGAA CAAACCACTGAATCACAACAACATGGACAAATCTCAAAATCATTTATGCTGATGGAAAGAAACCATTC TAAGAATACACAGTACAT

EST5	93 A	---	---	---	CTGTGGGAGGAAACAAATTTGGTATATTACAAATGGAACCTCTTCAGAAATAAGAGGAA CAAACTGAAATCACACAACATGGACAAATCTCAAATCATTTATGCTGATGGAAAGAAACCATTTCA TAAGAATACACAGTACAT
EST6	48 C	---	---	---	TTAGCTACTTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACCTTTCTAAAGCTCT GAACAAAGCTTTTCTTCTTTGCAACAAGACAAAGCAAGCCACATTTTGATTAGACAGAT
EST8	158 A	---	---	---	GGACAGGACCTCTATTCOCGCCCTGGTGCAGCAGCGGCTGATGGACTGAGGCCAGGGGATCTGGGOC CTCTCTCAGGGCGTCTCCAGGACCCAGAGCTGTTCTGCTTTCCTAGAGCTGTGGCGGCA GATAGCTGTTCTGAGTTGCAAGCAGCATGGAGATTGGACACTGTGTGCTTTTGGTGGGT
WI- 18740c	104 G	T	---	---	TCCTCATTGTTGGGATGATGAGAAAGATGTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATC[G]GAGTAGTGGATAATTCATTTTGATGGCTCTATTTT TGGCCA
WI- 18740b	96 C	G	---	---	TCCTCATTGTTGGGATGATGAGAAAGATGTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATC[G]GAGTAGTGGATAATTCATTTTGATGGCTCTATTTT TGGCCA
WI- 18985a	105 C	T	---	---	CCAAAGTCTCCTGTGCTCATAAAGAGTTTGGGATGGGAGAGATCCAGACATCTTGGGGCA GCCAGGCCCTTGCCTTCATTTTACAGAGGTAGACAAC[G]TTGATTCCAAACAAACCCCTTCCOC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAOCCATTGTGTGTTTCCCTCTT TGAAGCAATGACAAGCACTTTACTTTACCGGTGGTTTGTGTTTCTTAT
WI-18746	114 G	A	---	---	GCCAGAGCTGAAGCTCTTTTCTCTCTCGGCTGGAAGAACATCAAGATACCTTTCGGTGGATCA AGCTGTGTAAGCTGACCGTTTATATTACTTTTGAAATATCTT[G]ATCCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112	212 G	A	---	---	CCGTGTTCCACACACACAATGGCAAGCATAGTCGCCTGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGTCTATCTCATGACAACACAAAGAAACCGAGACAAA TCTTTTGGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G]ATCTCTTCAAACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A	C	---	---	TGGTGGCTGGCTAGTAGTTTCTACAGAACATAATTTGCCTCTATAGAAGCTATTCTTAGATCATGT CTCAATGGAACACATCTTCTTCTTAGCCCTTACTTGAATCTGCCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCCCTGAAATTTTCACTGTGAATGCTTTGATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCAATAATTTT[C]A/C]ATGATTAGCCGTGTAAC
WI-19057i	175 G	A	---	---	CCCATTTATTATAGGOCAGTGATGTCTCAAAGAGTAGAGGCGTCTACTGGTCTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGACGTCCAGGCCAGCGACGCCACTG TCTTCATGCAAGGAACACAGTGCAGATCCCAAGCTC[G]ATCTCTTTCATCTTGGTTTGGCCACA

WI-20103	168 C T ...	---	---	TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCAATGATACAGGATAAACTGGGATGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGGTCTCCCACTTCTTCAATCTGCTCAAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGTAGAGCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ...	---	---	GCCTTACCCATTTGCACATATACATATGCACCCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA/GA/JTTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCACATACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ...	---	---	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAAGCGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTTTTA/GJACACTGTTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ...	---	---	GTCCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATAGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGA/GA/JAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156 A C ...	---	---	GTCCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATAGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA/GCJAGTTGGA AAAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47 A G ...	---	---	CAGTAAAGAGTGATTCAGTTGCAGTAATACACTGACAGGTAATA/GJTATAACATTAGAAAA GCAAAATCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTCACACTGGAAAATGAAGGCAGTTTCCAAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ...	---	---	GCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCAATCAGGCAATA ATTGTTCTTGGAACTGACCCGACTGTCCATGCTCTGTGGGACTTACACATTCAGTTTGACAGI T/CJTGAAAACCAACTGGAGCTGCTTTCCAAAGATGTTCTGTGCTTCAAAATAGGAATTCATG TTATTTCTTCTTGGCTTAAGCTCTTATATCTTCAATGACCTAAGCTGA
WI-18845a	49 G A ...	---	---	GAGTGCCATACCTTCTCCAGGCTCTGCCCCAAGAGCAGGAGGTGCTG/GA/JAAAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACTCCCATCCCGTAAGACCTCTTCCCTTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ...	---	---	AGCAGTGGCCTTATTCATCCAAAACACGCTCTTGACCAGGCTGCTCCCTTGTGGCAGCAAGGGC ACAGCTAATTCCTACTACAGTGTCTTTAAGTGAAAATGGTCGAGAAAAGAGGCACCG/GA/JGGAAGCCG TCCTGGGCTGGCAGTCCGTGGGACGGGATGTTCTGGCTGTTTGAGATTTCTCAAAGGAGCGAGCAT GTGTTGGACACACAGACTATTTTAGATTCTTTTGCCCTTTTGCAACC

WI-20146	31 T C ---				TGAGCTCTCTGTAATTCATTGAGCAGTTAGCTTC/CATTTTGAGATAAAGTCAAAATGCCAAACACTAGCTCTGTATTAAATCCCATCATCTACTGGTAAAGCCTCATTTTGAATGTGTAATTCATATACAGGC
WI-18922	74 G A ---				TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACTGGAC TTAAGC/GA/JTCTGGCTCTAATTCACAGTGTCTTTTCTCCTCACTGTATCCAGGTTCCCTCCACAGAGGAGCCACCAAGTCTC
WI-18763b	53 A G ---				TTTCTGTGTGGGGTCAACCGTACAAATGGTGTGGGAATGACGATGATGGA/JG/JATTATTAGAATGTACCATAATTTTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCATGTGTTTTGCCAA
WI-18763a	38 A G ---				TTTCTGTGTGGGGTCAACCGTACAAATGGTGTGGGA/JG/JTGACGATGATGGAATATTAGAATGTACCATAATTTTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCATGTGTTTTGCCAA
WI-18771b	75 G A ---				CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAGAAAGATGTTGGGAACAGAA/G/JAAATAAAGTGAAGTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---				CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAG/JG/JAGATGTTGGGAACAGAGAAATAAAGTGAAGTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---				GGGAAAAATTTGAGACGCAATACCAATAGGATTTGGTCTTGGTGTGTTGATGAAATTTCTGAGGCCT/C/JTGATTTAAATCTTTTCAATTTGATGTTGATTTCCCTTTTAGGTATATTGCGCTAAGTGAACCTTGTCA
WI-18742b	51 C T ---				ACAAAGTCCTGTAGCCCCCTCACCTTTCCCTGTTTTCACATTTTGCCAAATGAC/JATCGGGTTTGGTTTCTGTGATATTAAACGGTTGTGTTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGAGTTTACC
WI-18882	94 C T ---				GTGTGTCCAAAAATGGGGTCTGCTCTGCTACCTTTGACCCCTTCCCTTCTGCTCTCTCTCTCTCATCATCAATCCCAACAACATCCTCTGCCA/C/JACACAAACAACGTAAGTTTCATTTGGGCAAAAAATTGA GC
WI-19970b	167 G A ---				TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCCGGCCCCGGCAGTGCAGTCACGCGGGGAGGAGGCTGCCGTTCCCGAGTTCCCTCACTGCGGGGACAGCAAGGCCCTTCTCACTGGTTGGTCAAG/JATGACCTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAACCAAGAAATCTTTTAAACGACTGACCTTCCCTTAAAAACAGA
WI-19970a	126 T C ---				TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCCGGCCCCGGCAGTGCAGTCACGCGGGGAGGAGGCTGCCGTTCCCGAGTTCCCTCACTGCGGGGACCAAGAAAGGCCCTTCTCACTGGTTGGTCAAGGTAAGTACCTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAACCAAGAAATCTTTTAAACGACTGACCTTCCCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGGAGATGTTGTGAGGGTTATTTTTTTTAAATAGTTCATAAAGAAATTT GACATAGTATCTTCTTCTCAAGACGTGGGGGAAATATCTCATTAIC
WI-19067c	153 G C ---	---	TATTGCTGCTTGTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGGAGATGTTGTGAGGGTTATTTTTTTTAAATAGTTCATAAAGAA ATACATAGTATCTTCTTCTCAAGACGTGGGGGAAATATCTCATTAIC
WI-19067b	151 T C ---	---	TATTGCTGCTTGTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGGAGATGTTGTGAGGGTTATTTTTTTTAAATAGTTCATAAAGAA ATACATAGTATCTTCTTCTCAAGACGTGGGGGAAATATCTCATTAIC
WI-19067a	57 C G ---	---	TATTGCTGCTTGTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTGC TGCACATTCCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTT CTCTGGGCTCTAGGCTCGGAGATGTTGTGAGGGTTATTTTTTTTAAATAGTTCATAAAGAA ATACATAGTATCTTCTTCTCAAGACGTGGGGGAAATATCTCATTAIC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCTTGTAGTTATTTTAGGACAGCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCCTCCAACGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATGTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATGGTTAGAACCTCCTATTATTAATCTGGG
WI-18944	147 A G ---	---	CAAGGCAAAAAATATCAGGAGCTTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC(AVG)TGTTTAAATTAATTAACAATATAAAGTCTACAGTTAATTATGTGCATA TTAAAAACAATGGCCTGGTTCATTTCTTCTTCTTAAATAAATTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATGGATGTTTGCATAATACATAAA GTTCTGTGTAATACAACTAAATTAATGCCCCTCTTCACAGTCAAAGGAACTGGGTGGTTGGT TTTTGTGCTTTTTAGATTATTTGCCATGTGGGATGAGTTTTTAAATGCCACAGACATAATTTA AAATAAATAAATTTGGGAAAAGGTGTAA(G/A)ACAGTAGCCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGTAGCCTCACGAAACTGGAATAAGCCTTCGAAAAGAAATGCTTGAAGCTTGTA TCTGATATCAGACTGGATTGTAGAACTTTGCTGATTTTGACCTTGTATTCAGTTAACTGTTCCC CTTGGTATTTGTTAATACCTGTACATACTTTGAGTTCAA(C/T)CTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGACGTGCTGTGGGAAGACAAAGTCTGTGGCTTG

WI-19042	193 A C ---	---	TTTGTGAGTTGCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACCTTGTGCTCAAGGACATGGTGAGAGTCCAACAG ACACAAATTTATCTGCGACAGAACTTCAGCATTGTAAATATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGTATTAACTATCTCTTTGGACTTCTGAAGAGACCCTCAAT
WI-18984	208 A C ---	---	ATTGGCCCTGTACAGTTTGCATTATTTATAAATTCATTAAAAACACTACAGGTGTGAATGGTTAAAA TGAGGCCCTCCAGTTCAATTTTCAGTTATTTCTGAGTGTGACAGAGCTATTTCGCACGTATTAAAT GTAACCTTATTAAATGAAATCAGAGCAGTAGACAGATGTTGGTCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAATGCTAAATGCTAAATTAATCACTGGCATGTTGACT
WI-18851	90 T A ---	---	GCTTCAATTGGCGATTGATTGAGTGCCCAACAATGTAACAGGGTTGGTAGTTGTTACTCATTTTGAAT ATACCTTTTCTTATTGTATTCTT[A/G]ATAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	ACTCCTCTGCTGTGCCAT[C/G]ACTGTCTTTGAACCAGGAAAGTCACAGAGTTTAAAGAGAA GCAAAATAACATCCTGAATCGGGAAACAAAGGGTTTATCTAATAAGTGCTCTCTCCATCAGCTTG CTAOCCTAACACACATTCCTCTGATTTCGCTGAGGACGTGGCATCTACTACGTACGTGGCATAAC ACATCGTGTAGCCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---	---	TGGAATTCCTTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAGGGTCAGTA TGG[C/C]TTAGGGAAACATTCCATCCTTGAGTCAAAAAATCTCAATTCCTCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	CACGGTTCTCTGCATGTTACCAGAGGCTTCTGGTCTAGCCAGCCCTGTATGACCCGGCAATA TCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---	---	CACGGTTCTCTGCATGTTACCAGAGGCTTCTGGTCTAGCCACG[C/A]CCTGTATGACCCGCAAA ATATCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---	---	TTAGGAGGTGGGGTGAACCTGCTCTTGGCAGGGATTTGTGACACTGCATTGCTGGGCTGTTCCTT/ CJCGGCTCTTCTGGACCTTGACCCGTGGATACAGGCCATGTGCCATGTTTGGGTCTCTGGAGGG TGGTGAATAAAGGC

WI-18972a	112 A G ---			AGGCTGTGGCTTATGTACCCACAGAGGGGCTCTGAGAAAGTCTGGCTGGGATGGCCCTGCC CCCTCCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCA/GAGTCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTTCTGAACACCTGAGGCTTCTGTGGCCACCAAGGCACTACGGCTTCTCTCC AGATGTGCTTTGCCCTGAGCACAGACAGTCAGCATGGAATGCTCTTTGGCCA
WI-19016b	184 C A ---			GTITGCAACCAACATGTGCTCTTTTCAGTCATTCAGTGTCTTTAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAAITTTTGTATGTATTAACGAAGTTCAAGATTAGAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC/TTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTGGGCTGGATGTTCTGTGTGGGGTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---			GTITGCAACCAACATGTGCTCTTTTCAGTCATTCAGTGTCTTTAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAAITTTTGTATGTATTAACGAAGTTCAAGATTAGAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC/TTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTGGGCTGGATGTTCTGTGTGGGGTTGTCTGTGCACTGTAG
WI-20096	21 T C ---			GGTTTGGGGCATTATTTTGT/CTGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCC ACCCTCATCTAGAAACAATCTCTCTGCCAGACTTG
WI-19591b	156 C A ---			TGGGGCAATTTTAAACCAACGAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGCC CTTAGGGTGGGAGCTCTCCGCA/CTACCACTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTAICTAGGGATTGCACCTCTTACACGG
WI-19591a	45 T A ---			TGGGGCAATTTTAAACCAACGAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGC CATGATATAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTCCCTACCACTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTAICTAGGGATTGCACCTCTTACACGG
WI-20310	125 G A ---			TCCTCAGCTCTGTCTCTGTCTGTGGGTTCTGTGTTCAGGCCCTCCAGGCATGGTTCTTCAT TTAGGTAGGAACAAGGCAAAAGAACATACAGCCAGCTCTCTAGAGGCTCCA/GATCAGAA CTGGACCTTTAACTACAAAGGAATCTTGATGAATTTTGTAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAGTGCACTCAGGCAATCTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---			CTCTCCCTAAGGAGCTTGGCTTGCAGCCCATTCAGCAGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAGCCCTTAGTATTGTGACATCTGCCCTTTATCCTGCTCTCT CCCCAGTGTCTACACTTGGGCAAGCAGAGTGGTGGCAGCCAGCCTTGAGAGCTCTGTAGACC GGAAGGAAGGGGGCTATTG/GAGGTGATGGCTCTGCTGCTCTGCTT
WI-19359a	39 T C ---			GACGTGGACAAAGGAGTTTAAATGAATACITTTTGTGT/CTCATGTTCAAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACCTAGGTTAATAATA GGCTATTGTCCACCCACTCTTCGGGCTTGTGCAATATTCTGGGCTCAAGTGGGAGGCCACGTG GGAACAAGGCTCAGAAAAACAAGGACATGCAGCCTCCCTGAGCCAGTTCTCT

WI-19766b	93 A G ---				TGGCCTCAATGACTGGTACATTGGAGAAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTC[G/G]GACAAACAGAAAGGCACACCAAGCCTGAAACCCCTC
WI-19766a	31 G A ---				CGGACACAGCAGAGTTACACGCTAGGGATGTCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCTCCTCACCCCTCCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---				TGGCCTCAATGACTGGTACATTGGAGAAGCT[G/G]TGAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCAGACAACAGAGAAGGACACCAAGCCTGAAACCCCTC
WI-20512c	59 T G ---				CGGACAACAGCAGAGTTACACGCTAGGGATGTCCTGGAGGTTTCTGACCATGAGAGGCCCCCTCACCTCCTTACCCCTCCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19599	230 C G ---				CTTCTCTGTTGGCTTTCGATTGTGCGATTGGAAAACCACTTGGAGAAGGGACTTTCCTGGCAAACCTTAAAGACTGGTTAAATTACAGGGCTTAGGAAGTCAGTGGAGCCCTTACTGA[G/G]AAAGCTAGAAAGGAAGTGAATTCCTTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCACGCCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19909a	29 T C ---				CTTCTCTGTTGGCTTTCGATTGTGCGATTGGAAAACCACTTGGAGAAGGGACTTTCCTGGCAAACCTTAAAGACTGGTTAAATTACAGGGCTTAGGAAGTCAGTGGAGCCCTTACTGA[G/G]AAAGCTAGAAAGGAAGTGAATTCCTTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCACGCCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20341	221 G C ---				GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGACCCCTTTTCCATAACCCCTTCTACATTGGAAAGAGCAGCACACCTTGATACAGAAATGGCTCCGTGAAGTCTTTTAAACGGACAAAGGTAATCACAGCTAACAAACGTCATGTTGGCTCACACGTAACCAACACCTCTTTTTCAGAACAGAGAGCGTTAAAGTAAGGGCA[G/G]TCCAAAGATAACACTGCTA
	82 T C ---				TGTTGAAATAAAAAATTTCCATGGTCTTAAATTGAACCTGTATGTTACTTTCTTTTAGAATATCCTTTTTCATTAAATAAT[G/G]TCTAAACCACTCTATGTGTCAACCTTCTGTTTAACTAAGATATGGGT
	82 T C ---				TTTTGGAAGGCCACAAAGTCACCAAGCTCCATGAAGTGGGCGAATTTGGTCTTGTGTTGGAAAGCTCTCAGGGTGTTCCTCCAGAAA
	29 T C ---				CCAGAAATAAGCCCTGAATATCTCTTTCT[G/G]TTAAAAATAAATTTTCTCTTTGCTCTTCCAAATAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATATAACACTACCTAGGCGGGTTTTTCTTTATACCTTGTTCTGTACTGTGGAATCAACTAA
	29 T C ---				TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTCTTAGGGGCTAGAGACATTAGGAAGGCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCATTGTTTAGCAGGAGGCAGGAAGATCTGGGCTCTGGCAGCAAAAGCGTGTGGTAATTTGGGTGACGTCATGCATCCCCATGCATTGGTTT[G/G]ATGCTCCAGTGAGCTGTGGCAAGTCT

WI-20113	60 TC	---	TTCTGGTACATGGTAAGTCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGT/CJGGA AACAGTAAAGCAAAATTACACACAATTAAGGAGGAATATTTTCAGACATAGGATATTTAAACAT CACTCAAATACTGGAGCATGATTCAGCAATAAATCTATCCATAAACACAGGTAGATAATGTGACCA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 GC	---	TGATGGCAAAGTACAAAGGCTCTGAAGAACACAGAGTAACAAGAGCAGCGCAGTCAGCGTGTGGC CACTCCACAGCAGCAGAACACTTGACTTCATTAAAGGCAAG/CJCTTTACTCTGTTACTTTTCCTC CCACATAGTTTAAACCAATAGAAAGGCAATCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAAAACAGATGCA
WI-20721	72 TC	---	CCTGCAATCACAAAAGTGAACCTAGTTGATATTTTGAATCATACTTGAATTAACCAOCTTCAGAAA TTCAT/CJAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 AG	---	CTGGATTTTAATATTTCTGGCCTAATAACCAATGTAAATCAATAAAATTTGGTCAATATCTCCACCTC ATTCTGCTAACATGTTTTCGAAGATCCCTAAGTAAGTATTGACGACTGAGACTAGTCGGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT/GJAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 CT	---	GCCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACAGTGGGCCATGCACCTCTG GGGTGCGATGAAGAGACTGTTGGTCTATGGCGGTGA/CJTGCTCTCCAGGCTCATATGGATGTCT CGAGGTGCACAGGGAACCTGCTGCTGTGTAGAGCTCTCTC
WI-19348b	98 GA	---	GCCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACAGTGGGCCATGCACCTCTG GGGTGCGATGAAGAGACTGTTGGTCTATGGC/GJA/GTACAGCTCTCTCCAGGCTCATATGGATGTCT CGAGGTGCACAGGGAACCTGCTGCTGTGTAGAGCTCTCTC
WI-19635	98 AT	---	ATTAGTTCGTGTGGGCCACATCAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACACAATG TTAAAGGTACAGTAAATAACAGTATTATJATCTTATTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGCTGACTGCATGCAGATATGTGTCTGAAAGAACTTTGCCCT T
WI-19641a	46 AG	---	TCCAAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG/JATTTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTGATTTTGTATTTACAGAAGATGTGAGGCTATCTCATTC AGTTATTAAATGAATGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTAAATTTTAAAA AATCTCAGAATGAGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52 CA	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTATCCCCCTC/JAGGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTGTATGGACACAAGTTTTCATGCTATTA
WI-19673b	180 CT	---	TCTGCCATGATCAGATTGATGAAGAACATGATGGTCACTAGTAGGTAACTTTCTGTGTCATTGSCCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTGTCATCACCACCTGTAATCTAATAGT GAAAGGCCAAATGATGTCTCAGTATCAGTGTGAAACATTTTCTGCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCACAAAAAACACAGCCC

WI-19673a	35	GA	---			TCTGCCATGATCACAATTGTGATGAAGAACAATGATG[A]TCACTAGTAGGTAACCTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCAATCACCAGCTGTAATCTAAT AGTGAAGGCAATGATGTCAGTACATGATGTAACCAATTTTCCCTTGGACCACTGAAAGAA TCTTGAGGACCTGAAGGCTCAAGGTCACACGCTCAAAAAACACAGCCC
WI-19724	35	AG	---			TTATTGGGAACAAGGATTGTAATTTGGTA[A]GCTGAGTCACGGTGGCCCTGAGTAGTGTCTC CTAGAAAGCAACACGAGATTTGGTTTCTCTT
WI-19307	196	TC	---			TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCCACAAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTGGATTGCTTCATGAGAAATGGTGGCTGGGATGGAGTGACATTCCTTGGCTGT GGTGAATGCAAGAAGGAACACAGGCAATGATTCATAGAGGCCCTTAAAGAGACCCCG[T]CTGG AAATGGCCATGGTCTAATTTGGTGTGAATAAACTAACCTCTTTGGCTG
WI-19269	85	AT	---			CTTCCCTCATCCCTCTCCACCACACCATCCCGGAACAAGTCTCCAGGATTCCTGCCACTGGC CATTTGGAGTGTCC[A]TJTTGGTAGCAATGTGGAACCAACACAGGCCCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTTGAGGGCTTTGGCCACTTGTCTCATAGGGAGCTCG ATCTCCTCATCATCTGGACAGGTGAAGCGAATTTCTCCGGGCTAGGCA
WI-19846	122	CT	---			CAATGGACTGAATGAGTGGTGGTGGGGTGGGACACACACACCTTCAATACAGTCAAGGTGG CTTCCAGTTTATAGAAACAGAAATCTGATCTCAGCCTGAGACGCACAGAGAGGT[C]TJCTTCCCTG ACCCAGCGCACTCAGAGCCAGGCTGTTTCAAACTGCAATTAACCTGCGCCAGAGATTCAAC CGTAGGCATCTTTAATAAATACTCACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	GA	---			CACAGATGGTGTAAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATTAATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTATAGGCCAAGGTTTGGATCTGTCTGGACCT CAATGTG[A]CTCTCGAGAGCAGCCAGCTTAGCAGCAGATACCTTACAGCTTGTATCTACTCAA GTGATGGCCCAACAGAGCTTCTGAACCTCTCCTGGGGAGGTAGCTGACAAG
WI-19076	40	GA	---			TTGGTTGGATACTTGTCTGGAACAAAAAAGCAGTTTAA[T]G[A]GTATCAAAATACCTTTTAAAAA GTATCTAGCACAAAGATTTTCTGTAACTAGATTATGTGTAACTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCTTATCCAAATCTATCTGCGCTCCTGAAAACTGCAGA AAGGCATTTGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTATTCTT
WI-20218	26	TC	---			CCACACACTCTGGTTTATAAGCTA[T]CJAGGACAGAGCAGAGATGGAACCTGAAACACAGGGTAG AAATTAACATAAATTGGAGGGGAACAGTGGGATGCAGAAAGATGACACAGCCACATGTGCCCCA GTCAAATACCTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTCTATCTACTGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	TG	---			CAACCTTTTGGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAAITCCTCTTTTAAATATCTCCAGGCTTGAATGGGAGGGGCTGGGCTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT[G]CCAGAGAAAGCGGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTGCGCTTCACTCTGTCGACTCTCTCATGCTGGGACTGTCTTTCGGGG

WI-20361a	192	GA	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAIGG CITTATGCAAGATGACAGAAATATGTGAATCTGATTGTCGCCAGAGTTACACTCTGCACCTCCAAAGCTA CAACAGTGCCACAGCTGAGAGGTTCCCTATACCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTC AAATGGGAAATTCCTAACTACAGAGACAAATGGTCTCTACAGTAGGCCCG
				GAGCCAAACCCAAACAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAAT[G/T]CATAAACATCATCTTTTACACATGGAGAGCGAGGTAGGCCATAATTTGTTCA AATTCATCTTTCTCAAATTTTAAATTTTAAATCCCAAAGGTGCTATTTGAATTCCTCAAAAATA AACTGCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20572	75	AG	---	CATGACAAAGACAAAGATCAAGGAGTAACATAAAATTAAGTTGAATAAATAGTATACAGCAATC TTCACCTTTTAAAGAAATGTGAGATCCTTTTGGTTTTTATTTCTTAAAGTACAAATGCTAAAC[G/A]GAGCCGAGCTCTCCGCAATTCAGG
				TGACCTCATCTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTCAGTCTGTG CTGTACTTCAG[G/T]TAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAA AGCTGTAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCTTCAACCAGACTAT CCAGAGCCATTCCATGGGGTATTTGGTCTGCATCTGTGAGACACTGAGCT
WI-20593	79	AG	---	TTCTTGCCAAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTGTCTCTCA[TC]ATGTATCT TGTCCTGCTGCTTTTGGTTAGCAAGGTGATGAATACTTTTAAAGTTTTGTTGTTCTTTCTCGT GGTACAGTGAATACTGATCTATCTCTGGCTAGGGTCAATTTACAAATTTGCCATGGAACTGAGC AAAGGCCACGTTGGGATAAAATCACTACCATCGACGCCACCACTATT
				TGACAAGGGAGAGAGGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGGTTGGTCACCTGTAGCTGAATTAATCTCTCATATTCGGATGCTCAATTACAGT ACCATTCAGGCAAACTTTTCTTAAACGCCCTTCACT[G/A]GTTTCTTTTA
WI-19066f	239	AG	---	TGACAAGGGAGAGAGGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGGTTGGTCACCTGTAGCTGAATTAATCTCTCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTA
				TGACAAGGGAGAGAGGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGGTTGGTCACCTGTAGCTGAATTAATCTCTCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTA
WI-19066g	184	CT	---	
WI-19066f	148	TT	---	AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTA

WI-19066e	147 GC ---	---	---	TGACAAGGGAGAGAAGGGAATCTACTCATTCGAAGGAAATCCTCAGCTTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTCAGCTGATCGTCTTAGCCAGTCCAATCTCAGGAGAACTGG CATATGTTCTGC[G/C]TTGGTACCCTGAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066c	100 GA ---	---	---	TGACAAGGGAGAGAAGGGAATCTACTCATTCGAAGGAAATCCTCAGCTTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTCAGCTGATC[G/A]TCTTAGCCAGTCCAATCTCAGGAGAAC TGGCATATGTTCTTGGTTGGTACCCTGAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066b	87 CT ---	---	---	TGACAAGGGAGAGAAGGGAATCTACTCATTCGAAGGAAATCCTCAGCTTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGA[G/C]TCTCAGCTGATCGTCTTAGCCAGTCCAATCTCAGGAGAAC TGGCATATGTTCTTGGTTGGTACCCTGAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19086a	72 CT ---	---	---	TGACAAGGGAGAGAAGGGAATCTACTCATTCGAAGGAAATCCTCAGCTTAAAGCTTCAGTGAGCCAC AAGCA[G/C]TTAAACCCATGAACCTCAGCTGATCGTCTTAGCCAGTCCAATCTCAGGAGAAC TGGCATATGTTCTTGGTTGGTACCCTGAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-20660	105 GC ---	---	---	TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGATATTG[G/C]TTAATAAGGGAAGCATTAAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTATTCCATTCTGTTCTGACAAAGATAGAACAA AAGCTATCCACCCGCCCCCAAAATACTGTTTAAACAACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGTCTCTGCGAGCCTCCCTCAGTCTCC TCCACCCGCTCTTCTTCCAGCCTGCCTGCATGCATGTCACCCCTTGGT[C/T]TTCGCTCCATCGOC TTGAAAGCTCTGAA
WI-18768	120 CT ---	---	---	TTCCCAAGGGTCTGTATTGCAGCTAAGCTCAATGTATGTTAATCTTCTAGTTGCTTGTCTTG GTCCTTCTCCAATGATGCTTACTACAGAAAGCAATCAGACACAATTAGAGAGCCTTTTCCATAAA GTGTAATTTTAATGGCTGCAAAACCGCAACCTGTAAGTCCCTTTTAAATGGCATGACAAGGTGTGC AGTGCCCATCCAGCATGTGTGCTCTCTATCTTGCATCTAAGTCTGCTCC
WI-19087	37 A G ---	---	---	GAAGCCAGAGATTAGCCCGGATTCGGCATCTGTCAACAGGACAGAAATGTCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACTTTGGAGATCAGAAAATTCATATTAAGCAAAGTGATACAAACA CAGTGATTGGGAATGCCT
WI-18790	49 AT ---	---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTC[G/A]GTGGCCAAAGCCAGACACTACCCACCTT CCCCAGTGGCCCGTGGATCCTGGTCTAGGCTGGACACAGGATTCAAGAACACCCAGGCTGCACA GAAAGAGCAGATGGACCTGAGTGTGGTACAGCCCTTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA
WI-18987	35 GA ---	---	---	

WI-18919	26 C T ---	---	TGGATGAAACCACAGGGATTCCGGAC/TJGCCAGACCCCAATTTTATACCTTCTGCTCTAGACCTC[G/A] TTGTTTTGTTGTTGTTGTTTTTATATTTTATACCTTTGGCCATACCACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ---	---	CTTCTGTCAGAGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G C ---	---	CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCA/GCAGAGATATCTCTGCTCTAGACCTGG CTGGAGTTCAAGCTTGAATTATATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T G ---	---	CTTCTGGTCAAGGCTTTGGACAT/GTCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTGG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G A ---	---	TCAGAAGCAGACATGGCATCTGTTCCCTTCTGCTTGTGTTGTTGTACCTTTCACGAGACCTGAATT TTAGAAATGCCAGTGTGTCAGAGTGAGTGAGTGAATTTCTCTCTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTATATAACATATCAACCA[G/A]TAGCATTAAACCATTTTATTTCTGTCCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	48 T A ---	---	CCAAGTTGCATCCATGTTTGTATTTCTGATGAGACTAGAGTGACAG/T[A]GTTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGACATCTCTATGAGATGGGATATGCAGATGGCCTATGGAAATGCAGCTGC ATAATTACACATTATCAAGTCTCTTACAAATTTATTTCCGAGCATGTACAGCTAAGTAGACCCA ATGGGAGAGAAAATGCCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C ---	---	CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAGCCCTAGACAGGTAAGAACGACACACATTGGATG GCAGCATGGGTTCTTCCCATTTATGGGCATGAAATATGTTTGAATAAGGAACAAGCATTATT CCTTGGCAACAGCTCACTAAGAGGCTTTTGTGCTGAGTCAAGCAACACATTGCCCTGCTGCCC CTTGGAG[G/C]TGCAATTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214 T C ---	---	TTGAAATCCAGTCTCTGGCCCCCAGGAGGTCTGTACCATAGATGTCTTCTCTACTGGGTC GTTCTGGCTTTTGTAGAAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATGATGTTCTTT TGTTCAGAGCAATGTTCTTGTATTCTGAAACTGGAACCTGAACAGTTTGGCTTTCTCTCTAGTCACC AAGCATACTT/CJCTCGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ---	---	GTCTCCACAGAGTCTTGCACCCCCAGCCCTGTCTGCTGTAAAGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTCCAGGGGGTGGCTTAGTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CACGGTAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCATCTCTCTCAATACAGCC/T[C/G] CCCTTGCACTCCCTATTTCAAAATAAAATTAGTGTCTTGGCTGTCTGT
WI-19135	20 G A ---	---	CAGTTACCTGCTTGGCTC[G/A]AAAGTGTATCAATTTGTAAATTTAGTATTAACCTCTGTAAAGT GTCTGTAGGTAGCTTTTATATATATAGGACAGACCAAAATCAACCTATCAAAAGCTTCAAAAGT TTGGAAAGGGTGGATTAGTACAGCACATTTGGCTTACAGTAAAGTGAATTTTATTAAGT GCTTTTGGCCATATAAATGCTGATATTTACTGTGAACCTAGCCAGCTTCAC

WI-19236	54	G A ---	---	TACACAGAGGGTGGCACTTGGACTCTGAGGGTTGGGTGTGGAAGGGGAAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTACGCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACOCCTTTTCATAGGGGAAGAGTGCACACTCTGGCTATCTCAGGGGAATGGGAAAAG AATCTTCAAGGGCAAGAAGACTCGTGGGAGGATGCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTCCAGTCTCCAGAAAGCAAGACTGCCCTTCATTCAGCCTTGTGACCTCCAGCCTTCTTAAGG CTCAGCCCAACGGGACTCTGGTGGCTGCCAGCTTGTAGCTATCTATATTAATTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGAGGCTGTAGCCAGGAAACCCCTCTTCTCCCTGGT CTGGCTCTGCTGGAGCG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACTAG[C/A]ATTTACCGGTGTGGGCAC ATGGGTGTGCCACCTGGACGTGTGACGATGTGGCGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA C/TGGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACTAGCATTTTCACGGGTGTGGGCAC ATGGGTGTGCCACCTGGACGTGTGACGATGTGGCGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGT[G/C]GGCTCATGGCAGAGCATT CAGTGCACGGTTTAGG
WI-19235	173	A G ---	---	TCAGGAGGTGGAGTTCGTGCTCAGCTCCTCTGTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTCCTTCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTGTTCACAATGGTGGAA[G/G]GCTTCATGTAAATATGATCAGGACCCACC TCCAGTCTCTGAAAGTGTGACAGTGTCCAGCCGTTCTGCAGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTCACCCAGTTTAGTTTGGGATGATTTGATTTCTGTGTGTGATCCCATTTCTAA CTTGGAAATTGTAGCCCTCTATGTTTCTGTAGGTGAGTGTGTGGGTTTTTCCCCACCAGGAAGT GGCAGCATCCCTCCTCTCCCTAAAGGACTCTGCGGAAC[C/T]TTTACACACCTCTTCTCAGGGAC GGGCGAGGTGTGTGTGTGTTACACTGACGTGTCCAGAGCAGCACTT
WI-19117	134	A G ---	---	AAATAATGCAACGCGAGGAGGAGAAAAGAAATGCACCTAAGACAAGAACTCTCTCATAGAACATTG ATCTGTTTACAGGAAACAAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A[G/G]TAGCTATTTTTTCCCTAAGACATTTTTCATTCATGAATATTTCAAGTTTTTCATACTGTACA CATTTCTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263	CT ---			CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTACACTCTGTCTCTCTCTATCTCTCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCACAGCAAGGGGTGCAGCCAGGGTTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCATCTCTTTTCAGAGCAC TTATCCACTTGCTCTCCTCTACCTCAGCACCTGGGGTGGAAAGGG
WI-19134a	162	T C ---			CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTACACTCTGTCTCTCTATCTCTCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCACAGCAAGGGGTGCAGCCAGGGTTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCATCTCTTTTCAGAG CACTTCATCCACTTGCTCTCCTCTACCTCAGCACCTGGGGTGGAA
WI-19224	112	CT ---			GGTTTACCAGTCTTCCAGGGAACCTCCGATGAAGTGTCCACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCTTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTCATAATCCAGCAGGCCAGAAAGACTTCC AGGAAACTCATTCAAGGAGGTGAAATGATGATGACTCTCCAAAGATGAAAA
WI-19201	179	T C ---			GCAGCTCCTAAGGACCCTGGCCATTAGCTCTTGCTTTTGATGGCATCTCTTCCACCTGTCTCTC CTTTGCTCCTGTGTGTTAGTGGCAGGTATGACAACCTCATCCAGTGGAAACAGACCTCAGCTGCC CTTCCGCCCCCAGCTTTGCCCTGCAGGTGCACCGAAAGGACTCTGGGGGATAAAATTCAAAAA GTGTGATGTGCTGCTCAGAGGTGAGACTCCATGCTGCTTGGCCTCAA
WI-19034	45	T C ---			GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGAAATGACTCTTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGTCTGTTTGAAGTGAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTCAGCATTTAAGTCTGTCTGCAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25	CG ---			TGTTCTGAGTCACGCTGAGGAGAGCTGCTTCACTCAGGAGTTTCATGCTGAGATGATCATGAGTTCA TGCAGCTATATTTCCCTTTGGAAACAGAAATGAAGCAGAGGAAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTGAAAGTCTAGAACTCCTGTAACTTTTGAACCTCAAGGGAGAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A G ---			AAAGGAGGGGAGAAATCTTTTACATAAATGCCCTTGATCATCTCCAGTCCCTCAGTGGGGAA[A G/AAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	G A ---			AAAGGAGGGGAGAAATCTTTTACATAAATGCCCTTGATCATCTCCAGTCCCTCAGTGGGG[G/A/A AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T C ---			GGCAGCAGCTTTTAAATTTGAACACTTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTT[C/JAAGATCCCAATTGCAAAGGCCACTGCTGGCTCA CTTCTCACA
WI-18501	121	CT ---			CAGAGGAAAGTTTATTAGTACCCACAGAGGAACAGAGAAACAGACACAAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTGGCAGGACAGAGGGGGCG[C/TGGACAGCA GCGCATGCCACAAACATTCA

WI-18017	87	C A	---			ACAAAGAAATGGAATAGTTTGGAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAATATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G	---			TTATTGGTTCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTAGAAACNTCGATTCTGAATATCCC[A/G]TGGCGGCATATGCAAGGAAGATGA
WI-18254	64	T C	---			TATACGGATCATGTAATTTGTGTGACCACACTACCACAGTCAATTTGTAGAGCAGTTAAATCAGT[C]GCCAAATCCCTCTTCTCTTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117	C A	---			CAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAAGACGGCTTCTGGCNCCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGTCTAAGTGAGCCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTGGGIGGTTCTTCAG
WI-18295	40	C T	---			ACCACACATTTGTGAGAGCCTATTGTGGAGAACAAACAG[C/TT]TGGGAAGTAAAGGTTGATTACT TCCTCTCCAAAGGATGATGTTTAAATGAATCCCTTNCCTTAGCTTCATTCATAATGCCAAA
WI-18459b	64	T C	---			GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT[7 C]GAGTAATTACAAACATAATTTTANATGACAGTGAATTAATAACGTCTGGGTAAAGCCAGAG GGGAGGAGGGCGTCTTCA
WI-22585	56	A G	---			TTATTTTAAATTTGCATCTGAGATAATAAAATTTATCTGACAAGTGAACAAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGAGGTATCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A G	---			GGGCTGTGGAGTAACAGAACTTGATGGAAATTTGGC[A/G]TCTGTGTAGATGATCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---			GCCTTGTCTTTTGTCTCAGAGGCTCAGATGGATACGCAAGTCTCTTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG[A/G]GGATCCAGCAGTGAGATCAGGCAAGTTCTGTGTGCACAGACAG GGAACAGGC
WI-19888a	98	C T	---			GGCAGGATTCACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTGA[C/TT]GGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTTATGTATTTTCCACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C T	---			TGAGACCATCTCTCAACAAAGAAATCAGTCAGTTGAGCACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C/TT]GTGCACACAGTACAGTGCACAAATCCAGAGGGGCAACACACATTGTAAAT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---			TCAGAAATGCTTTCCACTGCCCCCAACCAAGAAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCCTGGAGGTGACATGACAGGATTAGTCTCTCTGT[TT/C]CTTGGT GCAAGTTGAACCAAGTATGTACCAATTGCATCAGAGCATCTGTTCCCTGTGAGATCCCCACTAG

WI-20561b	94 T C ---			CGTTGCTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGGCATTATTG TACTTCAGATGAAAAATCCTTACATGT/C/GGAATCAATGCTCTTTTAAATTTTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---			CGTTGCTATTTAAGATGGCTGTTTAAAGTATAAAGCAGTTTGAGCAACACTGATTGGCATTAA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGCTCTTTTAAATTTTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---			GCCTTCATTTCTGTCAACCCACCTGTCCACCAGTTATGTTGGCCTTCAATATATATGGCGTTAGAACAT A/T/AATAATCTATATCATATATTTATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116c	59 T A ---			GCCTTCATTTCTGTCAACCCACCTGTCCACCAGTTATGTTGGCCTTCAATATATATGGCGTTA/TAGAA CATATATAATCTATATCATATATTTATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116a	22 C G ---			GCCTTCATTTCTGTCAACCCAC/C/GCTGTCCACCAGTTATGTTGGCCTTCAATATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133 G A ---			AAAGATTGTCAGTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGCACATATTACAACACAG NTCCCAAAATGGTGAACCTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTAATAAACGC/ G/A/TGTGAACATAATGTTTAAAGATTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAAGATAATAAT ACAGTAACACTACTTTTTATTCTTTGCTCTTTTATCCCTTTTCAGGTTTCGATT
WI-21444	39 A G ---			CTGGGCAGCAAGTAACCATTTTAAAGAACTACTCTCAAC/A/GIAGTCTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACTTATTGGAACATAATCTTTGTATTTTATTCGAGGAAGAAGAATCT ATAAGATTGACTTACTACTTATGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI-21034b	148 T C ---			AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGTAGAGATTTTGTAGAGAGTGGTATTAGAAGGATACAG CATAAATTTAATTTGTAACATGCTTATCTAGCTAACCTAACTCTGTTTCTGTAGAACTACTGGTCATGG GAGATTGGATAGAT/C/GCCTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI-22091c	205 G A ---			GGCGTGATTGTGATGCAATGTCCCAACCAAGTCAAGCTATCATTAATGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTACCTCCCCCTTAAGTGACTCATATTTTC ATTACTTGTGCTGTAGCTTTTAAAGGTTTAAAGATGTAGCATTAAGTGATTACTTACTTGAGGGCA ACA/G/AJAATTACGGCTTAAACACACACTAAATCATGAGGCTCAGGGATTG

WI- 21805a	45	A T ---	---	CAACTGCTCTGAGGCTTCTACTAGCTGATTATATATCTATATTAT/AAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTCTCAAGGGTGGATATGTTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGGCTTTTGTAGCTTAAGTCTGTTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTGAAGGCTGTTTTGTTAATTGCTG
WI- 21778b	155	T C ---	---	AAAAATCCATAAATATTGAACCCCAAGTTACAGAGAAAGTTGCTAACTTTTTTATTGAATTATTGAC TCTGCCCGGTGCTGTTGCTGGCTTTCAACTCCAGTCTGTCAATGCCCTGTGTAGTGGGTGCCAG GTCTGGGCTTCTGAGGTCCT/CJGGTAGAAGGAGGGCAGGTGGT
WI-20907	241	A C ---	---	TGAGTCAGTGGTCAGATGGGGCAGTTGGCTCAGCTGCAGTCCCTGACTCCGGAACACACTGTGCCTCT CAAATGATCTAGAGCTCATCTTGGGGGTACATGAGGGGCAGTTGTTCTAGTACCCCATTTAGCCG ATGGCTCTTCAAGCCAATTCACACTGGGAAACACACCCCTCACAAGATGCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGTAGAACTAAAAACATTTTAA/CJAATTATCTA
WI- 21449b	222	C T ---	---	AACAGCAGCAGTCACITCCAAAATGCAAAAAAATTACAATTTTATAGAATAAAATTTATAATGTTTA TAATGGGGTCAGAAGANTTGAAGGTACAACAGAAATCAATCAGCAGCACTGGAGGCGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGCTCCACACCC AAATCATACCCCTCAGCTTCCCA/CJTJTGACAGAGCCAGTGTCTCTGGGTTAG
WI- 21558a	157	G A ---	---	GCTTACAAGGAAGCCTGTGGACAGCGAGNTGGGTGGAAACGACTCCAGCTGGAAACCTGCCCCTC CCATCCCCCTTAGCGCTCTTGGCTTCCGGCTGATTTCTTGACAGCAGTCTTGCCAGGGCAAGG AGCTGTGGTGGGGGGCAGTATG/AJAGCCAGGGACTCCCTCCACAGATGAGGCTAGGGCTGCAA AAGGCCCCCGTGAAGAGAGATGTGGTCAAGGCTTATGGGTCTCTCCACC
WI- 22187b	178	G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAAACCAAAACAAAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAAATTCATGAAAAATTTCC CCTAAACCATAACAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 22187a	110	C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA/CJA/AAAAACAAAAACAAAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGGAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 21609b	146	G A ---	---	TCATGAATATGAGCCTCCATAATCTCTCCCTTGTAAACAAACGTGCAGTCCGTTACAAGCTGTAAA AACAAAGCCCAACCCAAAGACATCAAGAGGCAAGAGCAGTGGCAGTGAAGAGGGAGCCTGTAAAG GATGTTTCAAAG/GAJAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAAGTGCAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAAACAA/C/TGTGCAGTCGGTTCACAAGCTGT AAAAAAGCCCAACCCAGACATCAAGAGGCAAGAGCAGTGGCAGTGAAGAGGAGCCTGT AAGGATGTTCAAGGAGGTCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTGGAG
WI- 22512a	104 T G ---	---	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCTAAATCCCTTGTGGCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTGTGATCTGT/GACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGGCAGGAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG/CJ/TATGTGACAG TTTC/GJTGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG/CJ/TATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATACTTATGTGTACTTCTTG[A/G]TTTCA TCATACAAGACAAGCACAAAAAGCACCACCCATGCCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGTTAATAACTTATGTGTACTTCTTGATTTC TCATACAAGACAAGCACAAAAAGCACCACCCATGCCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTAA AAGAACTACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAGGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACCTAAAGGGCCGTGAAGGCGATGATTGGTTTTGGCACACAGAGTGGATAACCAIT/AJACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTTGAAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGCCCTTCCCTCTCTCTGACAC CAGCAAGGGGGAGGCACCATCACCGGCCCTGCCCATCATGATCCCAATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGGCTTGCT[C/T]GTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

WI-21661	117 G C ---	---	---	GCTTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTCCAACTTTAGAAATGATAAATAAGAAATGACATTTTAAATAAAATAG/CJTJTAGTCACAGTC ACACAAAACACTACCTTCTAAGGAAAACGTGCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAG GA
WI-21980a	25 T C ---	---	---	TCAGTTTAAACACACATTCAACAAGGAT/CJAGATTAAATTAATGTACAGGTGAGCATAAAAGGGAGATTAA TAAACCAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTACTCAGGATAAGTTTATTATTAATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G ---	---	---	TGCTTGATTAATGTGGTGTACATTATCCTATTTACAGATGGAACAGAAAATACCAGCTTTTTT AAA/GJTAGCAATATCTATTATATAATAATATTGAATAACACCATAATAATATCACTAAGGA AGTAATCTAATGTGTTGATTTTCAGAGGGAGAAAACATTACCTCIAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGSAAAGGGACAGGGATTTC
WI-22457a	112 G A ---	---	---	TTGCTATAATTTCCITTAATAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA CAACACAGTAAACATACCTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAAATTAACATAAG GAACAGAGTCCCTGCATTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCC AAAAACCACTGAACCTACCCAGCTGAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97 C T ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAGGTGTAATAGCCGTATGACGACCTTCGCGTCATACCTAT AATGGTTAATAACAGCATTCTCTACCC/C/JTAGTGATGCTCTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 A C ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAGGTGTAATJACGCTGATGACGACCTTCGCGTCATACCT TATAATGGTTAATAACAGCATTCTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 G T ---	---	---	TTACCTTCCAAACAGGCCACTTTGGAGAAAG[G/J]AAGAGAAATGCTATTAAATCAATAAGCCAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACCATCATCTCTGCCACAGAACC TTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTTGGGACCTGAAGCTTCAGCATCCCTT CTTAGGG
WI-21703d	197 A/G ---	---	---	CAACAGGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCGAGGGGCTC TGCATCCCTTTCTCAGCAGAGCACCATCTTCACCTCTCCTGGGAAAGCAGCATTGGAGCCTACACCA CTTGTCCTTTCTCACCAGGGTAAGAAATGCAGGTTATTGCAGAGGGGAGTGAGTCTGGGAA[G/JG] TGGGACAGACAGACTAGGGGCAAGGACTTAAGGGAACCTGTGGGGGAAGAG

WI- 22703c	134	A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC TGCATCCCTTTCTCTCAGCACAGCACCATTCTCACCTCTCTGGAAAGCAGCATTTGGAGCCTACACQ AGCTTGTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAG TGGGCAGAGCACAGCTAGGGCAAGGACTTAAGGAACTTGTGGGGGAAGAG
WI- 22663c	139	G A ---	---	CCCTTGTAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTGAGCCGGCGCTCGCTAACTTATT CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTTGCACGTGGTGCACCTACAG GC[G/A]GAAGAGCTTCCTCATTTGCTGAGGGCTTTTCTGAATCCGTTTGAATGTGGGT
WI- 22663b	55	C T ---	---	CCCTTGTAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTGAGCCGGCGCTCGCTAACTTATT TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTTGCACGTGGTGCACCTAC AGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCTGAATCCGTTTGAATGTGGGT
WI- 22663a	38	C T ---	---	CCCTTGTAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTGAGCCGGCGCTCGCTAACTTATT TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTTGCACGTGGTGCACCTAC AGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCTGAATCCGTTTGAATGTGGGT
WI- 22631a	52	T C ---	---	TCTTTATCTCTGCTGCTGCTGAGTATTCTGGGAATCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACCTAACAAATTAGTTTCTGTAATATT/GJTTCTAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAAACCATTTAATATCAAAAGTATACAGCATTTAAGTCAGCTTTTCGAAGAACTTTTATT AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTCAGTCTGATTCAGCACCATT CAAGTTTAGGCAAGGATTTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI- 20258	157	G T ---	---	AATCCACACTTTCACGAGGGGACCAAGCTGCCATGTCTCCAGGCTCACAGCAGCGGGGCTAC TCTGCTGTTGTTGGTGCAAGGTGGAGATGGTGACGGCGCATTTGGAACCCGTAAAGGCATGACAACG GGAGCCCGCGGGGTGTTTCAAGTTCGCGTTGACGAGGTGCTGGCTGGCAGCGGGCTCTACAGA AGGAGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAGTACC
WI- 22714	212	C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTCCTCTCTCTGCTAACTCTGACAGGAGTGTGTGGGAAACGAAGT CTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCTCTGTAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA[C/A]TTAGTAGGGGGCCAAACATCTTAACAAGCTAGTTGCT
WI- 22734a	44	G A ---	---	TGGGGCTACTTTAGATGGGATGGGCTCAGGGTCTGGGAAGGCTT[G/A]TCTTAGAAGACATTACCCA AATGATGAGAGGCGAGCCAGTCGTCGAAGCCATAGTTGGATGGCGAGACTTTCCGGCAGAGGAAAT AGCAAGTGCAAGGGGCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGGTGAAGGGCGCCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117	A G ---			TGATATGATGCTGAGATTGGCTTCCAAATATGCCTAGGAAGGAAGAGTGTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAAGTGTAAAGCTTGCTAAGGGT[A/G]TTATTCTATTTT TGGGATATGTTGGGAATT
WI-22750	48	G A ---			TGTAACTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[A/G]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACTAAGGAGAGTCAGCATTTGACCATTTCTGACTGTGCT
WI-2275a	60	A G ---			TGCTGTTCTTTAGTTGATGACGTTTATCAATGTGCTACTGTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAATAAATCCCTAAGGCGCAGCAATAATTTCTGCTTTGAATCCTTCATTACAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGGGATGATGAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143	C T ---			CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGCAAGAAAGTACCCAAAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCATGACAAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAG[A/C]TTAGCAAACTGATTAAAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---			TCTCTGCTGCTTGAGCCCTCATCCGACCCCTCCAAAGCCCTATGCCACACACCCGTGCCACATT CCCCATCTCCCTGCTGCTCCCATCTCAAGTCCAAATTCGAGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CT[G/A]TTGGCGTGGTATGTGGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31	C T ---			TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCATTTGCTCCAAAGGTTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122	A T ---			CCATATCCAGTCTTCTTGAAGCTTCTATTGACTTTATGGGTTCAAGTTATTATATCCTTTATCACTAT GACTTTCAATTTGATTTTATTTGTTTCTTCCATTCTCTGTCAAACCTTT[C/A]TTTGTGTTATAA ACTGTTTCTAAACTTCACCTTAATCTCTATCTGTATTTCCTGAGTTCCCTGAACCTCTTTTAGAGG
WI-21186	95	G A ---			AGCGAGCATCAGAAATCAGCTAGAGGTTGACTAAAGAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTCGAAGACCTTCTTAAGTGTGCAG ATGCTGTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTCTTTTAA GGAGAGACAGGAATTCAGAGAACTGCTAATTTAAGCATATGATTGAAT
WI-21187a	94	A G ---			CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAATCAAAATACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GNTCTCAGTAATGCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTGCAATCAGCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAGCAACCTGT

WI-21190	39 TC ---			TTTCCACATACCAATGCACCTGTTTGATAAACTATT/CJGTGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATATTATAACAAATAATTATTAAATCTGTACTATTACTGC TTTAGTTACTAGTGTATTGAGAAAGGAGAAGTCAGCATAGTTATTTCATGTATAATAAGCTT AACACA
WI-19937d	186 GA ---			ACCATGTGCATTTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTAGACAAGCAAAAGCACCTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 CT ---			ACCATGTGCATTTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTAGACAAGCAAAAGCACCTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCCTCAGCAAGTC[C/T]GTCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 CT ---			TCACCTTTGATCATAATCCCTGTAAAGCTAAAGTTATTCA/CJTAAACAGGAACCTCTGTTTTC TTATTCAAATGTACAAAGCTGACGGTTACTGTACATATTGCTAGCAGGAGACAACTGGAAATACT AAACAAATACTGGAAATTCACATTACAGACAGACGAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCTATTGTGGGTTGCT
WI-2122a	42 CT ---			CAGTTTGGTACAGGAAGGGCCCATGAATGTGGCGGGAACATTCCACAGGAG[AG]CAAGGAGAAG CTGTTCTCTGG
WI-21254	53 AG ---			AAGGAACTGCATGGGTACAAT[G/T]TCCAATTCATACTTAACAAGGTGGGGAACGGGTCACTCT TGGCCTGCTCCAGAACAAGGGCGAGTCTATGCACTCTG
WI-21054	23 GT ---			GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCCTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGTTGCAITTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCAGTGAAGTCAITTCCTATCTT/CJAITTAGCCAGGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTATGGGTGACTATCCTTGCCTAAT
WI-21059b	181 TC ---			GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCCTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTGCAITTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCAGTGAAGTCAITTCCTATCTTATTGTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTATGGGTGACTATCCTTGCCTAAT
WI-21059a	63 CT ---			GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCCTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTGCAITTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCAGTGAAGTCAITTCCTATCTTATTGTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTATGGGTGACTATCCTTGCCTAAT

WI-20442	37 T C ---			---	TCCACGTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAAGTGGCACAAATTTAAGAAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43 T C ---			---	GTGACAAGAGGTGAAGCAAGGGACAAGGGGCAGCGAGGGCAGTCT/CJCTGGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---			---	ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCAATTAC ATCAACGTTAAATTTTGCCGACAGTCTTTCATTGCTGATCACATTTTGATAATGACAGATCCCAACAT GAAACTCTGGAAGCAAAATGAATATTACCTTGCTCTTTCATGCAAAATTTAGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCCAGATCTAAGGAATTTGTAGAGGGATCTTCT
WI-21149a	167 G A ---			---	AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTTGGCAAGATAGTTGACTAAATACCACCT AAATAGTGGCTTTTTTTTTTAAACAATGACCTTAATTTATCTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCAACTGGAAGCTTTTACAC/GATGCITTCAGAATGCGGCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188 A G ---			---	GGTGCAACTTGGAAAATAATGGTTTAAAAACAGGATAAGCATTAAAGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTTCTCTTTATCCCGCAAGTGAGTTTCATGCTCGGTGAAACCA GACAGTGTGAATCTGTTCCAGCCCCAAATCTGCAGCATTAGGGATGAGTCTC/A/GJGAGTGATTTCT GAACTGAGCACGCACTCATGCTGCATGGGGAACCTCTGGGAGAAAGAGCCT
WI-21382d	125 C G ---			---	CCATTGCAGTCCAGAGATGAGAAACTGGACCAGAGGCAATCATGAACAGACGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAAGTGGGGGGGTTTGGATCCAGTGGGATNTGGCTCC/CJGJAGGTT GCAACCCCAAGGAGTCTCTGGAAGCAGCACCACTGCTGATGGGGAGCAGAAAGACTGCCATCCTC AGTCAGGGTCCGAGTCAAGGTCCGAGGAGACTGCTGCTCCATAGTCTCGCAC
WI-21437a	201 G A ---			---	TCCTGAGTTGGAGTCTAGCATAGTCCCTCCCTCAAAGAGGGACAAGGGTCAAGGGGCAGAGC AAAAATCCAGTCTGTTCAACCCAGGAGACTGCCCTTTGGGATGGAAAGTTTCTGGAGCTCCCTCCATT CTATTCCTGTGGGCAGGAACATGCCAGGGCTGCTGGTAAATGGCAGGGGTCACTTTACCAGGGCG /ACAGGCATAGTGTGGCCCTGCTGCCCTGGGGCCACCCTGGGAACAGT
WI-21202b	156 A C ---			---	CAAAATAGAAATTTCTTGTGAGTGGATTGACTTAATTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAAAATGGTCAACATATATTTTAAAGTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCA/A/CJGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---			---	CAAAATAGAAATTTCTTGTGAGTGGATTGACTTAATTTATTTCTGTATAAGCTAAATATGTTGTA TCTGTTTTATGAACATGATTTTATAAAAAATGGTCAACATATATTTTAAAGTTAACTGATTTATTGA GGGAGGAGGAGAGAGTTGACAAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA/GJTCCAAAGTCATCTAATATAAACCATATTTACATAATTTGTAGG GACAGTATACTAATCTACATAATAAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCAGTATCAACTTGAGTACCTC/GJTTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATAAACCATATTTACATAATTTGTAGG GACAGTATACTAATCTACATAATAAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75 C T ---	---	---	GGATTTGAGTCCCAACTTGATCTCAAAATTCACCTTCTTGCAATGAACAGCTCATTCCTCTAAAGTT TCAGTTTC/JTTTACCAGTAAGGAAAGGTTGGACCAGACATGTTGGCCGTAATTCCTTGGTAA CTGCCCTCTGCAATTTGCTCTGAGGTTGTGTCCCTAGGACTAGGTAGGATCTCTCTTCTTCTGCC TTACCTAGGCATAGTGCCTGTATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20329a	68 G A ---	---	---	CGATGCTGCTAAGATAGGAGGTTAATTCCTTACATGGTGAGTGGGTCACAGAGACAAGACATCAAT C/GAJCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGCTGCTTTAAAACAGTAACCAATCAAAAAGAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATCCACAGAGCCCTTGAAGGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	---	TTCTGGCATTCAATGTACATGTAAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAAATCACAATTTGATCTAAGTTTCACTTTAAGAAACATTATAAAGGTAATT AAACTCTAGGTGTACTTAT/JCJATGGAACACTAGTTTATTCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTTAAGGAATATAAACATTGAGA
WI-21504	147 C T ---	---	---	TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCATTAGAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAAATACAGTGGGGGACGGCCGTTCCGCTCCAGCTGGGTTTCCCC AGATGCAACAAT/JTJGGGGTTCTGGCTTCTCCACTGGTGGGGATCGCGCCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	---	CTGCACCAGGGAGACAGCTGCTGGCAGGGACTAATAAACCCCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAACCGGGCAGGGAGGGGCGAGAGAACTG/AJCACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	---	TAGCCCTTCTGCCAACATCTGCCAATNTGAGGCTGGGTGGAGCTGGCCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGTCCAAACCCAGGCTTCTCACTTGTCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAAGTGCCTTTTGGAGAAGGCA/JGJAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCGCTTCTCCACCCTATTTCCCTCCCTGAAG

WI-21475b	117 A T ---				TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGGCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTQ/ATJCTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGACGTGGCTCTTTGGAGAAGGCAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCTTCCCGTTCTCCACCCCTATTCTCTCCCTGAAAG
WI-20893d	207 A G ---				TGTTTGTTCCAGCCACATCTTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTCTACTGAGGAATACAATCATTTGACGTAAAGTTATCACCAGCACTCC AGGTCAGGCCAAACCTTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC/AG/ACATAACATTTGGTAGAGTAACAAACAAACCCACAGCCTAAATG
WI-20893c	179 T C ---				TGTTTGTTCCAGCCACATCTTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTCTACTGAGGAATACAATCATTTGACGTAAAGTTATCACCAGCACTCC AGGTCAGGCCAAACCTTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTTGGTAGAGTAACAAACAAACCCACAGCCTAAATG
WI-18941c	71 C G ---				GAGCTCAAGGGAAGACCTTACCAGATAGGGACTAACTGGAGGGTGGAAAGCAACAAAGGTGAAA GGTATC/GJGGTCTGTGAGACAAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGACATTTCTTATCCAGTGCATGTCCTTAAAT AAACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAACAAAGCG
WI-21552b	166 C A ---				TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCTTCACTCAAGCATTTATCCATAGTTACAAAGAA TCCAAGTATACTCTTGATTTTAAATGTA/C/AJAATTAATTTATTTGAATTTAGTTACCCCC ATTGTCTATCAAAATTCATCTTATTCATCTTTGTAACCTATTTATTGTA
WI-21552a	66 G A ---				TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCTTCACTCAAGCATTTATCCATAGTTACAAAG AATCCAAGTATACTCTTGATTTTAAATGTAACATTTAAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATTCATCTTATTCATCTTTGTAACCTATTTATTGTA
WI-21512	54 C G ---				TCCTCGTACTTCATGCTCCCTCCCTGCCAGAACCTTACAAAATATTTCTGT/C/GJTAGAGAGGA AAGAGCTGGTCTGCTCTGGAGGCAACGTCCAGGTCCGGGAAGGCACTCGTGGTGTGTGATCTGTC TCAGTGTGGAGGTCTCCACTCGCCCAACAGGCAAGCTCGGGCCAGAGATGAGAAATGCTGTAA TCCAGTACAGGGGCTGCGTGTGGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---				CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACCTCTTAAGGCAGGACAAAGCAACTTTCATT ATTCTTAGTTAGACCAGAACTTTAAATTTTATTTCTCTTTAACTGTCAAAATACACCAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCGAGTAA/G/AJAGTAG TATCTCTACATACCACAGTATACAATGATGCCTTCTCTGAGGTTTAGGAAC

WI- 21514b	133	C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCCCAATCTTCAAGGAAGGAGGACACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAATAAATGAGG ANTTTAAAGGCTCAGATGGGTAAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100	A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCCCA[AG]TCTTCAAGGAAGGAGGACACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAATAAATGAGG ANTTTAAAGGCTCAGATGGGTAAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27	C G ---	---	ATGAACATGTTGCAGTGGCGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATCTACCTGTATGAGGGTACTT
WI- 19576a	113	A G ---	---	TTTCATCGGTTCTTAATACAGTACAAATCCTTTTGTGAAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATT[C/AG]TCTAGTTCAGTGATTAGT CACAGAANTTAACATCTGCCAGATGTACACAAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141	A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAAGGCGAGTGGGCACTTGGAAAGTGAACACATGGAATA AGCAGCCTATCTCTTACCAACCCAGAAAGTTCTTGGGGCATGTGATGGTAGGCCAGACCCCTTTCCAA GGGAAT[AG/C]TACTACATAAGCCTACACTGTACTGTGAGAGTCAATGGTGGAAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTTCAGANTTCTAAGGCCAGCAT
WI- 21574a	235	C T ---	---	AAACCCAGAAATTTAGGTACTTTGTATTATGAGGAACCTACTATAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGGGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACCTTACTGCCTACTTCC[C/T]GTCTGTCAAGGTGGGA
WI- 21644c	151	T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTCTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTCACCATANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGAT[AT]TCAATCAAGATCCATGGAAATGATGCAGITTAACATGTGTCTCAGC TTGCCTACTGACCACCTTCCCTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55	G A ---	---	TGTCCTTTAACCTCAAAAGTCCAAATAAACATAATAGACATTTTGANTATAGCTAT[C/GA]TTTTAACA AACCTCATTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTAATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAAACCATACGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151	C T ---	---	GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGCAAGTATCAGATGACTATTTCAAGCTTATAGA GAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTACATACATTAAGATAAGGATGGACT CTTTCAGTGAGTATTAT[C/TA]AGGACACAAATCGACGGATGTAATCTATTTGANITATACCATAGGCC TATCTATATTTGGCCCAAGGGAAGGTAAGGATGGGTACTGTGGAACCGGA

WI-21981	61 T A ---				TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTTGAAGAAAAAAATTA/GTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGGGATAAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCGTGTCTTGGGAATTACAGGAACATAAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---				TCCAACTAGCCTCTCAGTATTAGATGAGGATAGAACAGATACGGTGTACACGCGCTCTCCACTGCT TACTGTGTACCAAGAAGGCAGAAAGCAGCTCACCCAAAGCCTAACCTGGCC[C/T]TGTCITTTTTCAG GCTTCTCAGGATGCCACAGCACATACTGGGGAAGTGGGATGCAGGAGAGCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---				TGAAAGTAGCCCTTCTGGACAGAAAGAAATATTTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTCGTCATAGACAGGGTGAGCTCATGGTGGAACTCTCTCTT GTCTGTAGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCCAGTGGATCTCCCC ACAACTTC/TCTCCAGGGGCAGGATTTCACCCAGGGCCCCAGGGTGCOCG
WI-19105a	33 T C ---				TGAAAGTAGCCCTTCTGGACAGAAAGAAATATTT/GTGGTCCATGTGGTTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTCGTCATAGACAGGGTGAGCTCATGGTGGAACTCTCTC CTTGCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCCAGTGGATCTC CCACAACTTCTCCAGGGGCAGGATTTCACCCAGGGCCCCAGGGTGCOCG
WI-21760c	81 C A ---				CAACCTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGCTCTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCAC/CACCTCTGCTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---				CAACCTAGTCACTCTACTGATGCAAAATGATTTGGAG/GTGGTCTCTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCTCTGCTCAGTTTCAGGGCA
WI-21569b	198 T C ---				TCTGCCATATTGTTCCAGCACCACTATTACTGTTATTACTCTTTGAGGAAACACAGGNATTAAG AAATCTGTTTGAATTTCCATGATGCCTAACCTCTATGGTTAAAAATCTTTTCTTACCAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAAGAAATTTATCTCTAC/T/G AGAGACAATTCATAGTTCATAATCTTTCAGGGTTGCTTACTTTGGGGGGC
WI-20934a	72 T G ---				CCAACTGCAACATAGTCTTCAATCTTAAAAAGTACATAGTAAGGTATGAAAAACATTTGTATTCA GAGAA/T/GTCTAAGACAAAATGGTCAAAATATTCAATGGCCTGGCACTAGTGGTAATTCACAGCAGAC AAACAGCATGAGAAAAAGCGGGGAGACAGTAATAAATACGTGCCCATTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCTTAAGATGGCAGATTAGAAAGACCTTNTTCCCCCAGGAGA
WI-21561	55 T G ---				TTTCCATTTTATTACCGCGGCCATCAGAACATAGCATCTATACCTTCGAACCT/GJCCTCTTAAC CTCTCCAGGCAAGAAAGGAAAAAGTGAATCATATTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAAAGATTTTGGATGCATTGTCCCCA

WI- 22082b	67	C T	---			CAGGAC TTGGTTGCTG TCCCAACTGCACATAAATGTCCCTTTTGGTTTGAGTTATGGTTGTGTC /TGTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTGCTTTATCCGGATGACGG AGGGTACACGGGGCTGGCTCAGTTCGGCCGAGGAGGTATTCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAACTCTTTGCTGCAACCTCT
WI- 20993	139	A G	---			AACACAACTCCATGCTTTCAAGATTCCCACACCCAGATACTAAGACATAATTAATAATTTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCCCTGG GCTTCTAGTTAAAGTGTAGTATACATTAAAGACAGTATTCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCTATTTCAAGGCTCTCCTAGCTCATCCACACATCACC
WI- 21723b	125	A G	---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCA[A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI- 21723a	82	G A	---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI- 22132	99	T G	---			CAACAGATGCTTGAGCCAAAAAGCAAAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCCTTAATCTGACTTGCCCTTTACTATCCTTT[G]CCCCATTTCTCTAATCTCTTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCTCTAGTTTAAATGTCTGCCCCAAACA ATACTAACCCATTGAAGGATAAATACTATGGAACCTTTTAAATGGACAGTGGG
WI- 21006a	106	A G	---			TGACAGATCACACCACATTTTGTGTAACCTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACACAGAGAGAGGCAAGTACAAAAATGTAACC CCACCAAGTGCATGTGAATGAAAGTGCAAAAGGGCTTCATTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCCT
WI- 21761b	138	C G	---			CTGAGGCCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCCTGGCTTGGAAATAACTGAAAAGATTTCAT TTTCCTTTGTGTACAAAGGATCAAAATATTTTCACATCTCTCTTCTGCCAGTTAAACGTGCCGTGG CT[G]CAATACACACCAAAAGCCAAAGCGTAACCTTGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI- 21079c	166	G A	---			AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG[G]A/ATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTATAGGATGGCAAT

WI- 21079a	50 G A	AATGAAATGCGACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG/AJCGCAAAATCAAGT TGTTTAAATACCAGTGTGCAGCTTTGATTCCTCCATGAATTAAGCTGTGTGCTCACTTGTTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGAATTTACAACCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI- 22129a	45 T G	TCTGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAAGT/GJTTATATAACAGTCATTGCT TGGTAGAATCCAGTGTCAATAGTGTAGCTTAACAGTTAACTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAAATAATTTGGTTGCAAAATCCAGNAAAGGGCA TTAACCAACATGGGACTGATCTCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 A G	TGGAGTTAAGTGGGCTCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC/AJGGGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGAGCCTCACCCAGAGAGCCTCACTGCATTGAOCCACACCCACCACTCAAC CAGCACACAGGCACAGCGGGGACACGCACACACGNTGCACCTCACCACG
WI- 18916b	42 C T	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC/CJTGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACCTGGACACAGCCTCAAC AATGCCACCTTCATA
WI- 18916a	35 G C	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAG/CJCTCAGCCGGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACCTGGACACAGCCTCAAC AATGCCACCTTCATA
WI- 19828c	200 A G	TTCCCCTTCCCCAAGAAGTGGGCAAGAAAGCTTTGTTAACCTCTTTTACAGATGAAGAAAAACAA GATCAGAGGTTGCTAAGTGTGTAGCCTAGTCCAGGNCCTTGCCCAATTCCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCCTCTGACCCCTCACCAACCCCAAAAT[AG]CTTTTAACTCTGGAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI- 21863b	47 C T	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTG/CJTAGCTGCATGCCACCCCTC ATATCCACCCCATCCAGCCTCTGCCCCCAGACACCCCAAGGCTGCTGCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGTATCCAAACACAGCATCT
WI-19860	51 C G	TTGACCTAAAGCCTAGCATAAATTTAGCTAAGTAGAATGTTTCCAAAAGATG/CJGJCTGCATCAGTAT CTCCATCCCACATAATTTCTGTTGATTTTGCCATTCACCCATAAATGGTGGGATCTACCTCCCT CCTTGCAATTTGAGCTGGNCTCTGATCCTGCTGCTAAGGATCTGAAGCC
WI- 19889b	80 C T	ACCCAGCTCCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACCTGAGGGCAAG AGGAGTGAGGGG/CJTACAGCAATTTATTTCCCTCTTTCACCTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCTTGGCCACAGTCGTAACCTATTGC

WI-19891c	172 C G ---	---	TGTTGGCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATTCGTTGGTGCCCCCTCCCCCCCCG ACTCCTCTGTCCTGGAAACGTGGCTTTGNCCTCCAGACACAGTGTAGATGCAAGCTCTCTCTCAGCGG AGCTCCGATCCCTCAATTTGCCATCTGCTGACTC/GJ/GCTCTCCCGGGCGTGGGGCGTGTCTGT CAGCGAGCGGGCGGAGGAAGGAAGGAGATCCAGGGTCTGCTG
WI-20155a	81 C T ---	---	GCACCTGTAGGGGTAGCTTCCATGTTCTCCAAAGCAACGGCTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGGC/TJGCAAAACTGCTTTGAGGAAATNTCCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTTCAACATACTATGAGAAATACAGCTAATGAAGTGTGGCAGAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAAGTCTCTCTGTCCAGTCCAGAGAGACTTCTC
WI-20270b	91 T G ---	---	AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCGTCAGTGTACAAT ACATTCATGTCAGGATAAGGAGCAT/GJACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTGTITTOCCCGAGAGGGCTGGGAGGCGGGTGGTGGGA
WI-20270a	53 G A ---	---	AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGACGC(GA)TCAGTGTAC AATACATTGATGTCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTGTITTOCCCGAGAGGGCTGGGAGGCGGGTGGTGGGA
WI-20622	130 T C ---	---	CCACTTCAATATTTTACAAATGCTCAGCGAGCAATATGAAAAGCTTCAACACTTTCCTTTGTGA ACTTGTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/GJ TACTAATTTTATGATGTTACTCATATTTTATTCATATACITTTAATGACATCATTGCCCAATACATA CATATTTCTNTAACTTTATTTTACAATAAGCCAAACATCTGTCATGCAG
WI-20768b	190 C T ---	---	TCCCACTCAAACTCCACCCCAACCTTCTCTGGAAGCGAGGGCTAACAGGACCTCTGCGCTGCTGC TCAGGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATACCACTCTA CAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCACACATACTGCTGGGA(GJ)TCAGGGGACTC GTAATTCGCTTGGTCCAACCTCTCTATGGGGTTAGCTGCCCTCATTC
WI-20768a	71 C T ---	---	TCCCACTCAAACTCCACCCCAACCTTCTCTGGAAGCGAGGGCTAACAGGACCTCTGCGCTGCTGC TCA(GJ)GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATACCACT CTACAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCACACATACTGCTGGGACCAAGGACTC GTAATTCGCTTGGTCCAACCTCTCTATGGGGTTAGCTGCCCTCATTC
WI-21909	153 A T ---	---	TGTTTGCTTTGGCCAGGTACTCTACTGCTTTACATAAAATTTATCTCATCTGTGCACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACTTAAATTAAGGATATTGTTGGTCACTCTTTAAAGAAA TGCTTTAACATACCAAG(AJ)JAGTGGAATCAATAGATAAAATATTTAAGTCTTACAAAAGCGTAC GACACTAAAGTAATATAGGATACCACCTAAATTTATATTTCTATGTATGGAAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTTCTTCTGGAACATATTGGAACACTTGTTTTCATAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCATTATGAATCTGAATTTCTA/GJTAAAT ACTCTGGTGCAATTCATTTCATCTGCAAAAGCACTGGCACAACCACTCTTGGCGGTGCAGCTCTCGG AGAACATCTAATAATTGAGTCTAGTCTGTCGGGAACCTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAGGATGAATTTCCACATTTATTTTNCATTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AACTGAGGCGAGGAATGGCATGGCGTGGGTACCGCTGGACCTGGACGTTGTGCTTCCAAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGGAGGCATCATAGAAAAAACCCTCAGCCAGAAAGTTAGGACATTGTGATTTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCGAGGCTCTGGTGTC/GJTTCATTGCAAAATAAAACCCA GACCGGTCACTCTTCAGTCCCTCCAGCTCTATTATTTATGATTTGCTCTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GACGTCTCTGAGGGCTCTGCCAGGTGGATTAGGTCAAGAGAGGTTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGTGAGAACCTTGCTTTT [C/T]TCCAATCTCTCTTCTTAGCCAGAACTTTGCGAGAGGCCCTTTNATTTCTTCCCTCTATTCC CCTCTTTCCCAATGTGCTAAGGTCCCAATTCAGAGCCCTCCACG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTACAGCCATAGTGAGGTTCCCCCATGTCTCAGTACCAGA[G/G]GTTTGAGTAC GGTCGTTAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCTGGTGGCAGATCTATACCCTCTGGCTCTGAAAG GCTTGCAACCAAAATGGGAGCTGGGGCTAAGGCATATTAAACAAGGCTCCAAAGGACCCCTT TCACTGGGTCTAGCATCCAGCTCTCTCAGCAAGGAGGATGTGGT[C/T]CCTTGTTTCTG AACAGGCCCGAGGGCAGCCAGGCATGCCATCACTGCGACACTCAACCCCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAAATTTTGTGTTAATTCTATACAGAAATGGTCTTTCTTGAATATTTT GTAGGGATGGATGAATTGAAGTGAATTAAGTCAAGATAAGGGGGCAACTCTTTAAT[G/G]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCTCACCCAGCTACACTTTACCTTGATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGGTCGCCCTTCCAGGCAGGCCAGTGCT [C/T]CTGGATGGCATCAGCACAGGCTCCCTGCCCCGGCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---	---	---	ATTTCCCTTTCTGTGTTTCGTATTTCCCTTTTGTGAGTAATNAGCAATACACTGAT[C/T]GGAA ATCTGCATGATTAATAACATTAAAGTTTCAAAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCCGAATGCAAAATTAGGTATCCCTCAAAATGCACATTCTCCTCTAGTT T

WI- 21763b	154 A G ---	---	CATACCCTTTAGTGCCACATTGATCTTAGTTAACAGTCTTGTTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGACCCAGATACTTCCAAGTGGAGCCAGCCCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATT[GA]GACAGACATTGCCTGTGCTTCTACCCAGCAGCTGCTAGTGCACIT GA
WI- 21763a	135 T C ---	---	CATACCCTTTAGTGCCACATTGATCTTAGTTAACAGTCTTGTTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGACCCAGATACTTCCAAGTGGAGCCAGCCCTCAGACTGTTCTCAGTCACT T[CG]CTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCAGCAGCTGCTAGTGCACIT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCCAGTGGGGTGCACTTCTTCTTATCTTAAAGCCACTTGGGTA[AC] TCCATTTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAAGTCCCTGGAGGGAGGAGGCTTCTTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGGGCATATGATTTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTT[CG]GAAAAAATACACAATGGGAAGTACACA
WI- 21965a	112 A G ---	---	CAGGTTCCACAGAGGCTTTTATTTCAGCCACTCAGGACCCCTGGCTTCTGCTCCAAAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCACAGCC[AG]CCCCACAGGGTCTCTGTT TCCCAAGTCTGATGGATTTCAGGCAAGACCTTCACACATTCACCCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI- 21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAAOCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGTTTCTAGTCAGAAAGTCTCATGGACTTCTTCTAAG[CG]GTGTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATAGGAGGAGGAGCAGCTGCTGGAG AG
WI- 22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAAGGAGCCTGAGAAGAAATTTTCAACTATTGACTATACAGAG TCTTCAATTTCCAAAACAGTTAATAGTAACTTGGTGGCACATACACATGCAATTTGAATACTCTGTAT TATTGAGTAACTAAAT[TC]JAGGNTCCCTGCATCTCTTCAACA
WI- 22250b	132 C T ---	---	ACTTGCTTTCAGGAGGCACTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTGAGGAATGTGCATTCACCTACTGTAGTGGTTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATGC GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI- 22250a	89 G A ---	---	ACTTGCTTTCAGGAGGCACTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTGAGGAATGTGCATTCAC[GA]TGTGGTTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATGC GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR- 04932-2b	192 G C ---	---	GCAGCCATCTCTCTCCAACACCTCCAGGCCACCTGGGGCCAGAGCACTCTATGCCAGCAGCAC CTAGTGGCCCCAGTACGGACCCGCCCTGGCCCCAGGTTCTGGGCTCTCAGGACGTCOCAGCAAGTGGA GCCAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCCAACCTG[GC]GAGTGTCTC TTTGACGGGGCCCGCTGCTCAGCTGCTCCTGGGAGGTGAGGAGGAGGT

UTR- 04932-2a	149 C T	GCAGCATCTCTCTCAACACCTCCAGGCCACCCCTGGGGCCAGAGCAACCTCATGCCAGCAGCAC CTAGCTGGCCGAGTAGGACCCGCTGGCCCGCAGTTCTGGCTCTCAGGACGTCCAGCAAGTGA GCCAGAGGTTTG/C/TTGGGACTCCAGGCCAGGGGATAGGCCAGCCAGCCAGAACCTGGAGTCTTC TTTGACGGGGCGCGCTGCTCAGCTGCTCTCTGGAGGTGAGGAAGAGGT
siFIBBb	412 G C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siFIBBa	341 T C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siILV2	61 T C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1001 7c	70 T C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1001 7a	33 G A	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1002 3	63 A T	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1009 6	36 G C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1011 8	107 C A	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1012 0	89 T C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1017 8	42 C T	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT

stSG1019 3	136 GA ---	---	GGAAACAATACTACCTAAGGACAAAATACTATTATTAATAAAAAAGTCTTCTAGTGATATATTGTGTAACACATTTCTGGAGCTGGTAGGAATAACCATTTTATTCTGTAGTGCCATCTATACAAAACCTTTTAC
stSG1020 2c	143 GT ---	---	T[G/A]TTTGAAAACCTGAGATTTAAGTTGCAAACT AAGCTAACTTAGTGATGGTGGCCACTCAAAGTCTTTCCGAGGGAAGCTAGTCTGGCTTGGGAGAGTCAGCCCTTGGTCACTCATACGGGGCTCCAAGCTAAGGGCTCAAGGCAAGGAGTCCCACTGCTTCTCGCTGTCA[G/T]CAAGACCACAAAGGCAGATGCCACTGCTGCTCTTCCCTTGTCTACTTCT
stSG1020 9b	75 AG ---	---	TCCTTTTCTCTTTTCACTCTCAGTCACCATGATTCAAAATAAACTAAATTTCTCCTTAAGATCCCACCTTATTTTTA[G/G]CTCCAAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	TCCTTTTCTCTTTTCACTCTCAGTCACCATGATTTC/TAATAAACTAAATTCCTCTAAGATCCCACTTTATTTTTTAAGTCCAAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	TACTAGACATGCAAAATGAGAAGATTACATTC/GTGAATATTTAAAGAAGTTATATTTGTTTGACATAATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATCTGA
stSG1025 2	108 AC ---	---	ATAGGTTTCAGGAACAAAATCATTAAATGGAATAATGAGAAGAAATCTTTATTTTGGACCAATTTTAGGCACCTAAGAGTTTCTTTCTCTCTTCCCTTCCCTTGATCA[G/C]AGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTCTG
EST10915 0	123 AC ---	---	CTGTATTAAATTAAGAAGGCATTAATGAGGGACGGAAAAATCTACCTGTACACAAAAATTTCTGTACTTTAACAGCATCTCAAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAG[G/C]ATTTTAA
EST11023 1	166 TA ---	---	GAACTGAGTTATTGGAC TTTTTTGTTAAACCAACCCCTGAAAGTTTCCACATGTGAAATATAGATACAACAGTGAACAAAAATATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAAGTAAACAGAGGGCAATTAGTCAATTAATAAAATAAGTACATGTTAT/GTGTAAATAAAATTAATTTACAAAGGCTTTTCCACTCGTGGATTGATTCCTTTTGGAGGGGAGTAACTCTGG
EST14096 8	71 GC ---	---	GGGATGTATATTACAGATAACACAACTCACAATAATATACCATCAGACATTGAAAACTAAGGCCATCTGTGA[G/C]TTTATTTTAAAGTTGGTGTTTGCACATAATGATCTTAAAAAAAATGAATTACCAAAACCAAGATTCTCTCTAAATGAAAAATTTAATGCAGGTACAGGATACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125 CA ---	---	TGCAATTTGTGAAGGACAGGAGGGGCCAACCCCTGGGACCTCATCTCTGTAGATGTGAGGTGCGCAGGGATGCTTAAGTCTTCTCTGTGCAGAGACCCGAGGTGCAGAGATGATCTTCTCA[G/C]CCCTTCTCAGGGGCTGGAG
EST22555 7	60 GA ---	---	TCAAGCATGTGTAAGGCACCTGCCCCCGCCAGACCCCTTCTAATCTTGCACACTGGAAGGT[G/A]AAACCTGGGAGAGAGAAGACACTCCCTCCCTAGCTTCTACCTGGGCAACCCCTCCAAAGATGAGCATTCATCTTGGAGACCAAAATAAAAAAGGACAAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---				GTAAACCTTGCAAGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/CTTGACATGGGCCAAAGACTTCCAGACAAAGCACCGGAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---				CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAACCTTAACCCCTCAGGCTGCTCTACTCA/ A GTTGGTTGCTAGCCTCACTGCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56 A G ---				GAGGGGGAACCTCAAGAGGATTCCACAGTGAAGCAGATCATGGGGCAAAAGTC/AG/CTATGG GGCCAGACTGAGGTGGACACACAAAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCGGC ACAGCACGGAGTAGCCAT
STS- R37410c	201 A T ---				TGTGACCATACCAACCTATGCAATAAAGAAAGAAAAAATCCTCACCTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGTATG T/AT/TTTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---				TGTGACCATACCAACCTATGCAATAAAGAAAGAAAAAATCCTCACCTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATG/TTGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGT ATGTATTTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---				TGTGACCATACCAACCTATGCAATAAAGAAAGAAAAAATCCTCA/CT/TTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAGTTCATAGCATTTT GGAATTTATGGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGT ATGTATTTGTGAGTGGTCTCTAGTGGCCAAT
STS- R42778	74 C T ---				TATCGTGGGAAGTCCAACTCATACCTATGCTGCTTTTCTACTGCTAATATGGATGCTCTTGCCA GGCTC/CT/TTAAATTTGCTGTAACTGGAAGAAACCTTCTACTCTCCACAAACCTGAA CAATCTGAAGAGATGCATAGCGGATGGTGGCTTTCAGCAGCTGCGGAGGTGGAGTGGAGGCG ACTGCTAATCAGTATGGGTTTCCCTCCGGGATGGTGAATAATGTCGGACCTAGATA/CTGACCGA AGGTAGCACGACACTGTGAGTGCACATAA
UTR- 04350	125 C G ---				GAAATAACCTAAACTGCAAGCAAACTACCTGTTAATAAGAAATGTTCTTCTGT/CTGACAGTTG AAGTGGGTGAGATGGCATAGCAATGAACAGTGGGAGCCATGAGGCTCAGATGCGGGGCAAA CTCCTCTGTGAAATGTAT
siSG1026 6	55 T C ---				GTATAATTCAGCATAAGCCAAAGCCTTTTAAATAACCAATACTATCATTTTATGAATCTTTTACA AGAT/GAAGCACAGTAGTACAATAATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
siSG1028 2	70 T G ---				CACITTAGATATGAGGAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAACCAACATAG TTTTCATACCACGTTGAAACCATGTGTTGATATGCAATAACAGCAAAATAATTTTTCAC/CA/TTG TCAATGCCAATGCATTGAAGGCCAGAAAAATGAGAAAAAGGATAACAAACCTTTTGATAAAAAAGGTA AGAATTTCTGTGTG
siSG1031 0	128 C A ---				

siSG1033 1b	116 T C ---	---	TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCAATTCGG GCTCCAACCTGTCTAGGAAGGCTAGACCTCAAAACACCAACCTCCATTCGTCATTCCTCTTTGG CTACTATGCTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGACCTCTC
siSG1033 1a	107 A T ---	---	TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCAATTCGG GCTCCAACCTGTCTAGGAAGGCTAGACCTCAAAACACCAATTCACCTCCATTCCTCTTTGG CTACTATGCTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGACCTCTC
siSG1243 b	225 G A ---	---	ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAATCCTCTCTTG AAATTATGTTCAAGCCAGCATGGTAGCTTATGCCTGCAATCCAGCACTTCGGGAGGCCAAAGAGA AGGATGCTTTGAGCCAGGAGTTGACACCCAGCTGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTTC[G/A]AAAGTATTTTCAGACCAAAAGGAGGT
siSG1345 b	60 G A ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTGCTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
siSG1345 a	54 T G ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTGCTT[G/C]TTACGGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
siSG1385 b	117 T G ---	---	TTAATGTATCCAGGGAGGGGCCAGGGATGGAGGGGAGGGTTGAGGAGCGAGGCGAGTTATTT TGGTGGGATTCAACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT[G/T]CAATCATTAAGAA GACAAAGGGTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAACATGGCC CCAGCAGCTTCAGTCCCTTTCTCGTCG
siSG139	69 T C ---	---	TCGTCTCCTTTCCAGTCTTCTGCCAGAAGCATCCCATGATGTTGTACCGCACAGCACTTTGTGCT T[G/C]GCTTTAGCACTTGCACCTGGCTGGCTGGCTGCCACTGATTGTGTAATGTTGCTGCTGCC
siSG1427	103 T C ---	---	GATCTGTTCCAGACAAGGCTGATTTCAGAGACTCCACGTGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCCTCCACTTCCAGTTGGCTTCTGTCCTCATTCAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTCAAGTCTCTCAGCTTGGAAATCCAGCAGCAAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
siSG1471	50 A G ---	---	CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGGTCC[G/C]TCCCTTGCATGA AATGTGGGAGAGGGAATAAAGTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
siSG1483	44 T C ---	---	CANAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGT[G/C]TTTAAATCAAAGTTGAGA ATGACGAATTCAGAATTTCTTCATACATAAATGCTTCTTCCTAGTTCTGCAGATGGGTA
siSG1896	67 T C G ---	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCACTCTTGAGGACAAAGGCCAAACCAAGTGTGCA [C/G]AATGTGGAGGATGTCTGTTCAGCTGTAGTACTAATGCAGGAAACCCCAATGCAGAAAGAGGAA AATGCCTGA

siSG1847 b	95 GA ---	---	TTGCAGACAACAATGGAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGTTAAATAAAACAAGTGAGAGACG/GATTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATTAACCTTGATCACTGTGCT TCAACACAACCTG
siSG1847 a	49 CA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC/C/A/CTAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATTAACCTTGATCACTGTGC TTCNAACACAACCTG
siSG1897 a	83 AG ---	---	CTTAATGCCCTTCTCTCTCTGACAGGAGACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTT/G/GCCCAACCACTTCTCTCCCGGTCTCCCAAGATGACT
siSG2022 a	86 TC ---	---	TGCTTGAGGTTTCAAACTCGAGATATCTATGGCAAGTTTATAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATATACAT/C/ATTCCTAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTGT TGTTATTTTTCTCCCTACAAATATTTCTGACTCTGTAGGACAGTGGCCTCAGTTGGGGGTTGAC T
siSG2076	104 CG ---	---	AAACGTTGTCCCAAAATTTGTTCAGTTTCAAGATATAAAATGAAGCTTCTGAAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTTGACATT/C/GJACATCACAGTGGGGCATTTT
siSG2108 c	71 AG ---	---	TTGAGCAAAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAATGATTTGAGGGCTCCACAGAGA GAGC/GJTAAGGGGAAGACTTTTATAGGACAACCTAGAGTAAGTAAGCAAGCAGACGTTTGAATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
siSG2108 a	49 TC ---	---	TTGAGCAAAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAATGATTT/C/GAGGGGCTCCACAG AGAGAGCATAAAGGGGAAGACTTTTATAGGACAACCTAGAGTAAGTAAGCAAGCAGACGTTTGAATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
siSG2141 b	173 AG ---	---	TTATTCAGGGGACAAAGCTGCACAAAGGAATGTTCTCTTATTTTAAACAAATGACTGCGGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAAATGGCAGCACCACTGGCATGGCGATGGTGCAGGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG/GJAGTTCCTTATTATATTATTTAAGGC AGTTTTCAGAGCACTGGCAATCTTGTGTCTGTG
siSG2141 a	113 CT ---	---	TTATTCAGGGGACAAAGCTGCACAAAGGAATGTTCTCTTATTTTAAACAAATGACTGCGGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAAATGGCAGCACCACTGGC/TATGGCGATGGTGCAGGTG GGTGCAGTTCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTTCCTTATTATTTAAGGC AGTTTTCAGAGCACTGGCAATCTTGTGTCTGTG

stSG2148	50 A G ---	---	TGGGAACAACCGGCTATAGTCTAGTGCATATTTTAGACCGTGATTTCTGAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTCCACAGAGAGCTC ATCAC
stSG2175	68 C T ---	---	CTCAATGAGACTCCATCAGCCAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTGTGCT [C/T]GCCGCTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCCGACCTTTTCCAT ACCTGGGCAGAGGGAAGGAGTGAAGGACCA
stSG2189	41 C T ---	---	CAAGTGTGAAAGCTGGGATTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACTCATCGTAACTTTGAGCACCTAGTGTCTGAGTACTTCGTATAGGTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGTTCTGTATGAT[C/T]TTATATTATGTAT AATGTCTTACCTGATGATACCCCAACATATTACTAGCCTTAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	CATTTCCTGCTCCTGCTCCAGTACTACCCCGTCCAGCAACTGCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
stSG2257	65 A C ---	---	TCAGTGATTGAGGAGCTGGCTAAGTCATGCTAACTCTGTGAGGCAGGCTATCAGAAGGCGAG[A/ C]CTGTCAAGAACTCTGCCAAGCACTGGCTGCTCCTCAGGAGAATTTCTCCT
stSG2306	67 A G ---	---	GTCAATCAGCGTAGAGGTCACCTGGTATAAACAACAGTAGCTATATGATAATTTGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTTCCAAACTGATACACCATGAGGTGAACACTTTTCACTGTTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCGCAAAAAACA AAAAAT/GTTGCAGTGGAGGGGCTGTGGAGGGTGAATG
stSG2339	63 T C ---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAATTTGCTTGACTGCAGAGTAACCTGCTGTCAC[T/C] GTTCTCAGAGTCAACATTACGGTGACTGTCTATTCTGGCTGTGCTTCTCTATTCATCA
stSG2465	76 C T ---	---	CAAGACTAAGAAGCCGACCCGAGTGGTCCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTCAAAGTGGGGTATGCA
stSG2549	140 T C ---	---	TTGCAGGCTTGATTCCACAATAACAAGTCATGTATAGAGAATGTAAATGATACTTGAAACCCAA GATATATAAATAATTGAAGTCATTTATGCCTTTTGATGACTGGGTTAAATATGCAAAGCAGCTAAAG GAATA[T/C]TACACCACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	AATTGCCAAATGGAATTCAGAGGATTTTAGACCACCTTTGCCCTGTTCATTCCTCCAGTTTGGT CCCAATATAGGCCCTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCAT/G]GAACAATC CCGGCCCAAGATTAAITAT
b			

siSG2577						AATTGCCAAATGGAAATTCACAGAGGATTTTAGACCAACTTTGCCCTGTTGCATTCACAGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[G/T]ATGAACAATC CCGGCCAGATTATAT
a	121	CT	---		---	
siSG2700						ATCTCTGACTGCTTTAGTGGGAAAGGAATCAATTATTTATGAAGTCTCCGGCCCC[G/A]AGTCAC TCAGGTTTGGGGAATAAACCCTGGTCCAGAGCAGAGGAGGCTACTTGAGCCGACACCA
siSG2724	58	GA	---		---	
b	101	TG	---		---	AAACAAGCTTTGTCATTTCCACTACATTTTGTGTCTTTTATTAATATTTGCAAAATGCTATAAT TTAATACTTATATTCCAATTGCTTGCAATAATCA[T/G]TTTTTAACTCTGGGGTGTGAAAGAAC GTGGCCGATCTTTACTTTCCAGAAAGGGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G/
siSG2776						AJATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAAACCACAAA ATATCCACTAATCCCGAATATAGTAAACCCTGTCTTGTCGGAATG
a	65	GA	---		---	
siSG2791						AAGGAAAGGTGGAGGGAAGGAAGGAATTACAATGGTTAGAAAGAGCAACTAAAGATTATTTTC TATTACTTCTGAACGGTAAACTTAGCAATTTTAAATAATTT[G/T]GGGCCACTTAAATCTATTA
b	109	GT	---		---	AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG AAGAAAGGTGGAGGGAAGGAAGGAATTACAATGGTTAGAAAGAGCAACTAAAGATTATTTTC TATTACTTCTGAACGGTAAACTTAGCAATTTTAAATAATTT[G/T]GGGCCACTTAAATCTATTA
siSG2791						AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG CCGCAATTTTCAACACACATTTCTATGAAACTAAGGTGGATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACAAC[G/T]GAACAAAAATAAGAAAGAAACCCATGAATGCCAGGTTTA
a	100	AG	---		---	ATTTTTTTTC
siSG2826	85	CT	---		---	ATGGTGCATTGTAAAGGCAATTAATACTTTTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCCCAT
siSG2850	88	GA	---		---	ATACTCACGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCTGCAATTTCTGTGGTGTGAGC AAA[T/C]GCCCCTTTATTTTAAATGATCCAGACATCTGGGCAGCATAGCT
siSG3031	71	TC	---		---	GTCCCAACTCTCTCTCTTAGAGAAAAAAGTGTGATTACCTCACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC[G/A]TGAAAGAGCATCAAGCCAAAAAGGCAAAACTGGCTGAGGC
siSG3058	81	GA	---		---	CAGCATCTCCAGAACATTCCTAGAACTGAACCATTTCTGTCATTTGAAAAAAACAAGCCAAAGTTC CAATCCAAAATAATAAATGAACGTGCT[G/G]GATAAACATTTCTTTATGGTTCCAGCCCCCTACTTT AGTT
siSG3092	94	TG	---		---	AAGAAGTACTTTGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTTGTCAGTGGAGTC[AG/GTGGGGTGTGAAGTGTCTGAAGTAG
siSG3230	95	AG	---		---	ACATCTATACCCAGTAAGATGCAAGAAAGGAATATCTGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTGGTGTCTTACCACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGTT[G/C]GTACTTGGCTTAAGTACTCATGCTTTAT
siSG3245	160	GC	---		---	

siSG3265	42 T C ---	---	AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAAT/GC/GCATTGTGGAATAGTTTCTCAG TTTTATTATGGAAGATGATGATTTTACAGCCACATTCAGTGTATGTTCTTAATAACAAATCGAC AGGACTGTCTGTTTCACTACAAATGGAGGACAGCTTTTTCAGGCAATGGGATTTCTTGATAATGCTAA ATCTGCTTGTGAGCTGAAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAA
siSG3269 b	141 C T ---	---	TGTAATTACTGTGTCATCCTATCCATTCCTTCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TJTTAGATCCCCAAGTCCCTGACACATTTTCTTAAGAACT
siSG3269 a	24 A G ---	---	TGTAATTACTGTGTCATCCTATCCATTCCTTCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAGCATGACTGTAGATCCCCAAGTCCCTGACACATTTTCTTAAGAACT
siSG3284	130 C T ---	---	TTAACTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATTAATGACTAAATTACAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA/C/TJ TCCCTAACTTTTGTAAATGCTGTAAATGGGACATTTGTTGTTTGTATACCC
siSG3292	99 A T ---	---	GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA/A/TJ/TACAAATCAAAATAGCATTTTCTTAACCTCAA TAAATGTCATATCTTTAGTCTCACT/C/AJCCAGTGTATCCATTTTCCCAGCCGTAGAGCTTTCTG TTTCTGTAGATTTGCCTGTCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTGCACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTGTTCATTCCTTTTAA GATCCCCAGTATTATTTCTAANTGAATGACTTTGTTGTGGAAATATAAATCTGAGGACCACTCAGAG GG/C/TJATAAGGGAACCCCTCTTTGCTTATAGTTTATAGGACTTTCT
siSG3369	69 C T ---	---	CAAGACTGTAAAGAACGTAGGCCCTTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAGGAATGACATTTCCAACTGTCACTTTGTAGC/G/TJCTGGGT CAAAGTCTAAGAGGACAAATAATAGAGACT
siSG3398	125 G T ---	---	TCTTACTCTGTTAACTAGTCTGGAGTAAAGGATGCAATCACG/A/GJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCACCTCAGCCAACTGAGTAGCTGGCTGCAGGACAAAGTCACCATGCTTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43 A G ---	---	GTAAGACAAAGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCGCCGACCTTTTAACTGAAT GTTGAAATCATTTCTGCTCTTTGCTGGGTAACACTGAT/AJCAAGTTGCTTAACCTTTGTGAAACAC TTTCTTATCTGTAAACAAATGGACAAACAGAACTTTTCTTCCCTCTC
siSG3424	173 T A ---	---	GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGCCCCCT/AJGAAATAGCTTACTCTGTTTTCCTATC
siSG3436	88 T A ---	---	

siSG3463	103	C T ---	---	GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTATTTG AAATAAACAAATAATGCATACACAGCTCAATGGGTACAC[CT]TGGAAACAAACCTTGCCTTGACTATATTA CTGA
siSG3491 b	71	G A ---	---	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTGTGGCAATAATTTCTACGAAACAGGACGATTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTCTATTAAACTCAITTAATACTATTTCTGTGATG ACAGAAATAAGTTAAC
siSG3523	33	C T ---	---	TAGCCATCTTACTCTAGTCTCTTTTGGGTTTAC[CT]GCATATATGTGTACAAACACACACACACC CCTAATTCCTCAATGCTCTGGCAATAGTTTATCTCTTACTGGTCTC
siSG3536	213	A G ---	---	AGTACAAACACAGATTAAAGAGCTCAGCAGTATTGACACGCTGGAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCAAAATACAGAATGGCTTC TGTGATCTGGCCTTGGTGAACCGCATCTCACTGTCACTTCTATTGTTTATTTGTTAAATGAGCTTG TGCACCATTAG[A/G]TCTGCTGGGTCTTCTCAGTCTTGCATGAAGTATG
siSG3583	112	G A ---	---	GAAAAGCTTAACATACGATCCATGTGCAAAACCCAAACAGGATCTACGAACTTGGCATGATCCA CATCGTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
siSG3586 a	60	G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTTAAATTTAAAAATCAGGTGTGGTGG[G/C]ACG CCTGTAGTCCCTACTTGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
siSG3589	101	T C ---	---	ATATAGTGTGGTAGCATTATAAATCCTTTAAAGCAATCTGGCCATATCAAAAGGCAAAAAAAGT GTATATACCACCTGGCACAAAAACCCCAATGA[T/C]CTATTTCCAAGAATGTATCCAGATGMAA GTATCCAACAACAAAAAGCTATATACAC
siSG3590 a	70	A T ---	---	GAGAGATGAGCTATTATTCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA AA[A/T]TTTCTCTGATGTCCTTGACCTGTAGGAAACACATTCAGTTTCTACACT
siSG3619	78	A C ---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTTA[CA]ACAACACTCCAGAGAAAACTGGGCTCTATATTTAAAG
siSG3644	40	T C ---	---	ACATATGTAAGTCCCATTTAGTAGCCATATTTAGGATGAGAT[G/C]GGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCAITATGAATAATAAGTTATCTGGGAAACCGCCATTGTCCCAACATTTACTAA GTGCTCTACTA
siSG3646 c	70	G A ---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAATATATGATGAACAATAATATGCTTACT GGT[G/A]ATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAAATATATGATGATAACAATAA(G)TATGCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAAATATATGATGATAACAATAATATGCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCTGGTGTCTCCCTCTGAAGCGGATGACCATCCAAACCTCGGACTCACCT GAAATATCCTACGAGGC(A)CTCGCCCTCGGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCTGGTGTCTC(A)CTGAAAGCCGATGACCATCCAAACCTCGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCGGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3698 b	145 G A ---	---	TCCTGCCCTTTGTTACCCCTAGAGAGATGGACCCAAATCCCCAGGGT(G)CTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG(G)AAGAATACCCACCCCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCCTGCCCTTTGTTACCCCTAGAGAGATGGACCCAAATCCCCAGGGT(G)CTCTGACTTCCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTATTGGGAGAAATACCCACCCCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAAGCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGOCATCCTGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGTGAAG(C)TACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTCT
stSG3725	104 G A ---	---	GCCAAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAATATATTATTACCAGCCAACAGCAACAGCCCC(G)A)AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTGTAGAAAGATGATTTTG AGGGCTTCAGTATTAAAGGGGAAAGCAGGCTGGAGGGAAAGAGAGAGGATATGGTCC(G)A)TT GCTGACTCCATGTGTTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAGAATCCACATCATTGTTGGTAGCAGAGGATCTTAT(A)AAAGTCCCTAAGA CACTGAGGGCATAAACCAACAAATAAAATAAAGGAGTGATAGGCTAAGCAGTATCTTCCCCT
stSG3880 b	115 G C ---	---	GACAAGGGGGAAGAGATGCCAGAGACAGGGCTGGGGAGCTGGGGTCCCTGAGTGCAGGGCGC CACCACAGTCTGTGGGTCAAGGCCCTCTCTGGGAGCAGGTCTA(G)GGCAGGAGGATGCAG GGTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT

siSG3880 a	36	G C ---	---	GACAAGAGGGAAGAGATGCGCCAGAGACACAGGGCTGCGCGCAGCTGGGGTCCCTGAGTGCAGGCGCCACACACGCTCTGTGGTCAAGGCCCTCTCTGGGAGCAGGTCTAGGCACGAGGATGCAGGGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTCTCGCCCT
siSG3895	44	A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTGTA/GJTTTTCCTTCCATTAACTAAACATGCCCTCATAGATATATTCAATTAGTGTATCACCATTGGGAACAAGATGCTGATTCGTCAACTGAAAT
siSG3902	104	T C ---	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCGGACTCTGGTGGGAACCTGGCTTCCTGATAACAATCATCTATTTACCTAAATGTGAACCTCTTTCTTTCTG/CJTCAGCTCAATAGCTTAACATCTAAATTCATGTTGCTCCCTTTGCTGGACAAT
siSG3935	50	G A ---	---	GGGTGCTGACGGACAGGCACACCCAGCAGTTCAACAAGCAATTTGTCCG/AJCTAGTGTGCAGGCTCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACTTCTCGACGT
siSG40	25	A G ---	---	GAGGAAGAGGTTGAAGAAGTGCCTGA/GJAAATATATTTAAGATTTCTTGGGGAGAAATCTCGTGCCTAAACCTGGTGATGGATCCCTTACTATTTAGAAATAAGGAACAATAAACCCCTTGTGTATGTATCA
siSG4009	32	A G ---	---	GTGTGGGCTGCTGATGAATGGCGGCTG/CJGTACTCTTTACGGCTTACACTTTTATGCTCCTATGAATCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCCACACTGCTTACA
siSG4033	123	T C ---	---	AGAAAGCTTGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATTGAAACTACAGTGCAGTAACCAAGAACCTTAATGTTTCAAGCATAAAGGTACTTTT/CJGTGTGAACAGGTGGCAACAC
siSG4038 a	29	G A ---	---	GCTGAGACGCTGTACAGCCACGCCCTGTG/AJCGCAGGCCCACTCTGTGCAATAAACATGTTCTGCCCATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGAGAGACCTGAGGGTTCCATCACT
siSG406	53	T C ---	---	ACTGTGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAAT/CJGGTTTAGTTTGTCTGAAGACTGGCCTTATTAATGGACAGCTTCTCTAACAGAGATTATTAACITTTATCAGGTGTTAACATCTGTTTCAGGAACATGGCA
siSG4095 b	55	G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTGAGATACTATTGTCTGCTAGATGATTAG/GJATAAAAAAGTTTGCTCTGTAATACITTTAAAGTTGCTTATCTCATCTGTAAACCTATGTGCTTTGAGAAATCAAGCCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4095 a	27	A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTG/CJGATACTATTGTCTGCTAGATGATTAGGATAAAAAAGTTTGCTCTGTAATACITTTAAAGTTGCTTATCTCATCTGTAAACCTATGTGCTTTGAGAAATCAAGCCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4120	65	G A ---	---	TGCATGTTCCACATCTTTCATACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAAC/GJATCTTTTCCCTCAGAGAGCCCAAGTTAAACAGGTTCCAGCACCACTTAATCCACCGAGCT

siSG4128	54	A G ---				CTTGGCAGATAAGGGACTCGTTGCAGATATGACTTTCCTTTGTGTACATTCTT[AG]TATATTTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTCACCTCCTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAATGTTCCAGAGG
siSG4209					---	CACGAAACAGATGCAGCTACACAGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAAGC AGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGGAACCTTGACAGGCGGCACTCCCTG[GA]GC AGGGGACCAACGAGGCGACAGGTCTTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
siSG4209	128	GA ---			---	CACGAAACAGATGCAGCTACACAGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[AG /A]CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGGAACCTTGACAGGCGGCACTCCCTCGGC AGGGGACCAACGAGGCGACAGGTCTTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
siSG4254	65	GA ---			---	CATTACCCAGAACGCCATGGAGGACCAAGC[GA]CCACGGCCGGGACTCCCGGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCCGGGGCTGCTCTCCCCCAGGGCGACGCTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCCGGTCATG
siSG4301	81	T G ---			---	TGCAACAGCTCTGAGAGGAATCCTTGGCAGATCAAAAGAGGGTAGTGGCTCCACACATTCCAT TTAAGCAATAAATTT[GA]GCTTCTGAGTAGTTGTTCCAGTTTACCCAAACATTTTG
siSG4331	71	T G ---			---	CTCACAAGGGCCACACAGAAAAAGATACAAATACATTCATCCAGCTAATATTTAGTTTTATGACAC AGAGT/GTTTTCAACAAGTTTAAGTGTCACTGACCTGAAGAGCATGTTAAAAAGTTTAAGTTATCACTT GGAGAGCAGATTTCTGGCCTCGCCCTTGATTTCTGTTTGGGGGTGTC
siSG4340	76	GA ---			---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAGTGAAGTAATGATACAGAAAGTCAAAACC ACATGTTCTC[GA]TAAAGTGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
siSG4361	109	A C ---			---	TTCCCAACCATTTAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTTCTTGAAATTTCCATAAGGGATAAAGTGCATCTTTTGC[AG]CCTTCACAAC TAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
siSG4361	24	T C ---			---	TTCCCAACCATTTAGTGACAGAGCT[GC]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTTCTTGAAATTTCCATAAGGGATAAAGTGCATCTTTGCACCTTCACAAC TAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
siSG4376	73	A G ---			---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTGTCTTCCAAAGGGAG AACAG[AG]CTGGAACTGCGGCTCTGCAAGAGGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
siSG4381	50	T C ---			---	GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTT[GC]TCAGTCTTGTAGT ATCCACAGTAGTGTCTGTCCATGTACAAAGTGTCTGCCAGAACACCCATTAAATTCATGCC
siSG4410	79	A/G ---			---	ACCAATGGTTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAAACACCGC[AG]TGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGACGAGGGGTGGCTTGT CAGCTGGGT

[illegible]

[illegible]

stSG8362	88 G C ---	---	---	TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTCTCTGTTAAGAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGA AT
stSG8010	62 G T ---	---	---	CACATCTGTGTTCTGGAGCAAGGGAACACACAGAGGCCAGGAGTTTGGGTGTGCACCTGG[G/T] GTC TTCAACTGGGTGGAACCAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAGAAGATAGA TGCTT
stSG8022	53 G A ---	---	---	AGCTCCTGACTCCCTGTTCAAGTGACGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAAACTGGAAACTCTACAAATCAATCGCTTATTCTTTATTTTCAGAGGGCAGGTTT TATCAGCACACGCTGATCTCC
stSG8032	67 G C ---	---	---	TGATTGTTAGGATAAGTGGGCATTGTGTTACAAATTACTCCAAAGAAATTCAGAAAATTGTGTGTT G/C]TGGAGGCAGGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46 C A ---	---	---	AGCTGGCTCTTCTCTGTCGTGTCGGAGGCTTCACGTCCTCG[C/A]CCGTGGTCCCTGGGTGGCC TGCAAGACCAGGGGTGGGAAACAATGOCAGGGAGAAATTCCTGTACATCAACACGGGAACA
stSG8064 a	23 G C ---	---	---	AGCTGGCTCTTCTCTGTCGTGTCGGAGGCTTCACGTCCTCGCCCGTGGTCCCTGGGTGGCC TGCAAGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAACACGGGAACA
stSG8072	59 A G ---	---	---	CACCATCATACATCGAGTAGGCTAGGAGCAGGAGGGGTGGGTCTGCTGTCTTAGGG[G/T]GGC AGAGGCAGAAAGGAAGTCCGAGTATTAGTGCCGCATGCAGTCAAGCCTGTGCTGTTCAAAA
stSG8100	40 A G ---	---	---	ATACACCCACACACCCCACTCAACCTTGATCAAAITCCA[G/A]AAGTGTAACATAAGATATAAGAA ATCATGACTAGTTAAAGATAGCAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCTTGGAAATGGG
stSG8102	138 T C ---	---	---	AAGGCTCCTTTGAAAGCATGGTTTATTGTTCCATTTAACTGTTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTTGCATATATTTGAGATGTACAGTGTGATGATACATGTATGTATACAATGTGAAA TGAT[C]TGTCAATAATCAATAATCAATGTTGTTAGGAAATGTGATGGT
stSG8105	110 A G ---	---	---	CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCTGTGCTTGTAAATACACAGATGACTAGGCC CACCTGGGAGTTCCTGTTGGAGTCTAGGCTGAGAAATATTC[G]TTCTAACAAAGTTCCAGGTGA CCCTGAGGCTCTGGACTGGGGAACATGCTTTGAG
stSG8130 b	96 T C ---	---	---	GTGTGATACATTTGGGAATGGAGGAAATAAATGACTGGATGGTGGCTGCTTTTAAGTTTCAAAT GACATTCAGACAAAGCGGTGCCTGAGCC[T/C]GTGCTGTCTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36 C G ---	---	---	GTGTGATACATTTGGGAATGGAGGAAATAAATGA[C/G]GTGGATGGTCGCTTTTAAAGTTTCA AATTGACATTCAGACAAGCGGTGCCGTGAGCCGTGCTCTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124 T A ---	---	---	TTGTGGACTTCAAATCTTCTCCATTTTAAATGACATTATGCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAAATTTGTGAACACAAATCTAAGAAATGAATGAGATGTTT[A/C]TGAAA TCTGATTCAAACACATTATCTTAAACTGACTCTCTGTCAATCCTCTGTCTCTGTGAAGG

[illegible]

ESTD- AT3a	--	--	--	--	AGACCTCAGTTTCTCTCTGTAAAGGGAAGTTTGTTCTTGGATCTCCATGGGCCACGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAAGTGGAGGAATTTGAAAGGGCATTG GAATTCAGAGCAAAAGACAGATATTAAAGCTGGGGAATGTGG
ESTD- B3AR	--	--	--	--	GGCTGCCAGGGGTTCTGTTGGAGGGCCCTAGCCGGGGCCCTGCTGGCGCTGGCGGTCTGGCCACC GTGGAGGCAACCTGCTGTCTGTCATCGTGGCCATGCCCGGACTCCGAGACTCCAGACCATGACCAACGTT GTTCTGACTTCTGCTGGCCGAGCCGACCTGGTGATGGACTCTGTTGGTCCCGCGCGGCCACCTTT GGCC
ESTD- BA511	--	--	--	--	GGCAACATAGTGAAACCCCATCTCTACAAAATAACAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCAAGATGGTGCCACTGCA
ESTD- BCL2	--	--	--	--	AGCTGGATTAACTCTCTCTTCTCTGGGGCCGCTGGGTGGGAGCTGGGGCGAGAGTGCCTTT GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGACGCTGGGAGAACAGGGTACGACAAACCCGGAG ATAGTATGAAGTACATCCATTATAAGCTGTGCGAGGGGCTACGAGTGGGATCGGGGAGATGTGG GGCGCGCCCCCGGGGGCGCCCGCCGACCCGGCATCTTCTCTCCCA
ESTD-BCR	--	--	--	--	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCGGAGACTCATCTGCGCAAGA GACCAAGAGGTGAGTCTCTGTTGCCGGGAAAGGAGGAGGTGACAAAGTCACTCTGCTTCAA ATCAACCATCCGTTGGACACTGTGTGGCTGCCATCTGCTGGCACA
ESTD- BRCA1a	--	--	--	--	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGTTTTCGCAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	--	--	ACTAATGTAGAAAAATCTGCTAGAGGAAACCTTTGAGGAACATTCATGTCACTGAAAGAGAA ATGGGAAATGAGAACATTCGCAAGTACAGTGAGCACAATAGCCGTAATAACATTAGAGAAAATGTT TTTAAAGAAAGCCAGCTCAAGCAATATTAAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	--	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTACCCCATACACATTTGGCTCAGGTTACCGAAGAGGGGCCAAGA AATTAGTCTCTCAGAAAGAACCTTATCTAGTGAGGATGAAGGCTTCCC
ESTD-C1R	--	--	--	--	ACACAGGTGCTGGCACTGGGCTGGGGATCCTCTCCCTAAATTTGCTCCGGGAAGACATTCATCAA CCCAGTCAGTTTGGGGACAGCCATGCACCTGAGCCTCTGGTAGCCTTCAACCATGCATTCATCTAA GCTCTGCAAAAT

ESTD-C7	--	--	--	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAACTCCTGCTGGA
ESTD-CB22	--	--	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAAATCAATATGGAATGAGGAGACATCACCTGGAATGTTAG
	--	--	---	---	---	GCAGTGCCTAACTGGGGATGGACAGACAAATGGCAGTGGCAACCCATAGGGCGGATACAAAAGAC
ESTD-CB23	--	--	---	---	---	AGGCAAGGAAGGGTAGAACCATCAAGAGGAATAGGCTGTGAACCCCAAGCAAGGAGGACCTAG
	--	--	---	---	---	TAACATAATTGTGCTTCATTATGGTCCTTCCGGCCTTCTCTCACACAC
ESTD-CB24	--	--	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC
	--	--	---	---	---	TTCAATTATGGTCCTTCCCGCCTTCTCTCACACATACAGAGGCCCTACCAGGACCAGACAGCT
ESTD-CB25	--	--	---	---	---	CTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGAACCTGAAAAACGTGTCCCAACCCGA
	--	--	---	---	---	GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAA
ESTD-CB26	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAA
	--	--	---	---	---	AAACGTGTTCCCAACCCGAGGTGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAG
ESTD-CB27	--	--	---	---	---	GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCGACACAGTGGAGCTGGTGGGTGAATGG
	--	--	---	---	---	GAAAGAGGTGCACAGTGGGTGAGCAGACAGACCCGAGCCCTCAAGGAG
ESTD-CB28	--	--	---	---	---	GTTTCTTTCAGACTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTTCGCCGTC
	--	--	---	---	---	TCGTCTCTCGAACCCAGGCATGGAAATCCACGGACACAGGGCGTGAGGAGCCAGAGCCACCTG
ESTD-CB29	--	--	---	---	---	TGCACAGGTACCTACATGCTCTGTTCTTGTCAAACAGAGTCTTACAGCAAGGGTCTGTCTGGCACC
	--	--	---	---	---	ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB30	--	--	---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT
	--	--	---	---	---	TGTGTGTTGGGCTGGTTGCATTTGAGGAGTGTCTGAGGAGTCTGCTCATCATCACTATCTTCTGA
ESTD-CB31	--	--	---	---	---	TTTAGGAAAGCAGCATTCCTTGAGCATCTGAAGTGACAGCCCTTCTCTCTCCACCCAAATGCTGCT
	--	--	---	---	---	TTCTCCTGTTTCATCTGATGGAAGTCTCAACACCAATTTCCATACC
ESTD-COL2A1c	--	--	---	---	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA
	--	--	---	---	---	GTGGTGACATACGTTGCTATTTATGCTCTCTCTCTGTCATCTTCAGGGTGTTCAAGGTGGAAGGT
ESTD-COL2A1d	--	--	---	---	---	GAACAGGTCCTGCTGCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACAACTGCTGCTTTTG
	--	--	---	---	---	GTACGCTATTGAGCTGTAATCAACCATACCGTACCT
ESTD-COL2A1e	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC
	--	--	---	---	---	AATAGACTGAGTTGCTGGACCTGGAACACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC
ESTD-COL2A1f	--	--	---	---	---	AAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAAAACACTATCATGGAACAGC
	--	--	---	---	---	ATT
ESTD-CPT2	--	--	---	---	---	GCCGCAATGCCCCGGGAGTTTCTCCAATGTGGAGAGGGCCTTAGAAGACATGTTTGTATGCCTTAGAA
	--	--	---	---	---	GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCACTTCTCATCATGAAAC
ESTD-CPT3	--	--	---	---	---	TGGAGGCGCGGCATAGTCTCATGCCTGTAAATCCAGCATTTTGAGAGGCTGAGGCGGGGTGATCAG
	--	--	---	---	---	TTGAGGTGAGGAGTTTGAACCAACCTGGCCAACAT

ESTD- CTLA-4	--	--	--	---	---	---	ATGGCTGGCCTTGGATTTACAGCGGCACAAAGGCTCAGCTGAACCTGGCTACCAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTCTCTTCCCTGCTCTGCAAGCAATGCAGTGGCCAGCCCTGCTGTGGT ACTGGCCAGCAGCGAGGCATGCCAGCTTGTGTGTGATGATCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	---	CAGCCAGCGTGGTGGTGGTACCATCCCGCAGAGAACAGGTACGCCACCATATGCACAGGT TCTCATATTGAAGCTGCTCAGGGTTCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	---	AAAAAACATTTTAACACCTTTTCAATCATATACACCAATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAAATTACTTGCATCTAAATGTCATAAATGATTAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAATATTACATATCTGGATTAAATATGCCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	---	CATCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCGCCCTACCCTTTGTAGTCCATGGGAAGGCTCTCTGCGGGCGGTG GGGTTGTGTGGCTATGTGGTGGTCTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATTTGGGTATT GCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	---	TTTGAGACCACCTGGCCAAACATGGGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGAGTGAGCCAAAGATCACACCCTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	---	AACTGATTAGAACCTGAAATACATAATTTTATCTGAAAAAGTCAGATTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAAATCCAAATAAGTACACTGTAATAAAGAAATTAACAGAATATCATTTGT TTATTCAAACTATTATCACITATTTTATTGGTAAGCCATACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	---	AGGTTCCACATTATTGCTGATGTTTGGTGTATTCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTGTTTATTAAATCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCTC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAATATGGTCAGGTACAGCTGATATCCC AGAAGTGAACATACTGCTCTAGAACCCAGAGTCATACTGGATGTTCTGTTCGGTCTTCACGAIGG CAGGTATGAATATAATACTGTCTCTTTATTGGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATGTATTT CTTAAACAATAAATCTGAAAGTCCAAAATTTACTCCTTGATCCATGGACTGCAGAAATAAATGTATTT TAGCTGTCAGAAAACAATACTATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGTAATTTTGGAGAGGAATCTTGTTTTCATGAGTAG
ESTD- D4S95	--	--	--	---	---	---	CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACTTCTTCTCTTCTAGAGTCTACCGG

ESTD- D7S399	--	--	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DM	--	--	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGCTGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGAGGAGGTGGGAGGGAGACA GAATGCTGATTATCTGGTGGAACACAGAACTTCTGGCCTGTGGGTAGGGCAGCTGCTTCCAAAGCC TCCTGATTTGAGGAAGGGAGCAGAGAGGAGAACAGAGT
ESTD- DRD1	--	--	--	---	---	---	TCCCAGCCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAACGGTCAGCACCCACCTGAACCTCGCAGATGAATCCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAGAACTAAGGTAC
ESTD- DRD2	--	--	--	---	---	---	TCTGCCCTTGGTGCAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCCACCACTGACTCTCCCGGACCCCG TCCACACCGGTCTCCACAGCACTCCCGACAGCCCGCCCAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	---	---	---	AAGCAGTGCCAGGATGAGCGGAGTAGGAGAGGCGATAGTAGGCATGTGGCGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCAAGGTGTAGTTAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGAGGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ER8B2	--	--	--	---	---	---	TCTTTCAGGATCCGCATCTCGCCCTGGTTGGGCATCGCTCCGCTAGGTGTGAGCGGCTCCACAGCTGG GGTAGGGGGTGGTGGTCACTGCGGGGGCGGTGCAGACCCACCGGGCTGGGAGGACTTCACCC CGCTCACTCCGTTCTCGACGAGTCTCCGCTCGTACT
ESTD- ETS2	--	--	--	---	---	---	ACTCAGTGCTTTTAAGTGAAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCGGCGCTGGCA GTCCGTGGAGCGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCATGTCTGTGACACACAC AGACTATTTTATGATTTCTTTTGCCTTTTGCAACAGGAACAGCAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	--	--	--	---	---	---	GATAAGTACACTGAGGCCCGAGGAGTTATTGCCTAGTAGCCCAACTGTGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCC AGCCAGTCCCGGGGTGGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	---	---	---	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTAAAGTATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTTCAATGGATACAGAAATTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTTGTGTGAGTGACGGGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACGAAAGT ATGTAATACTTCACAAAATACTAATAACCGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	---	---	CAAAGTAAGCACCCTAAATGTTAGCTATTACTATCATTAATTATTATTTATTTTATTTTGG AGATGGAGTCTGGCTCTGCAACCCAGGCTGGAGTGCAGTGGCAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTGATGCCATTCTCTGCCCTCAGCTCCGAGTAGCTGGGAATACAGGCCGCCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGCGGAGTTACCGT
ESTD-IL1B	--	--	--	---	---	CCACTACAGATGGATAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAAATGCATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCATACTATTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCTCACCCCTCCTTAGCCGTGGGAGCAGGAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCCCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAGACTAAAGAGGGGCCAGATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCACATTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATATTCAAAATTTGAACCGTAGCAAACTGCATTGGTATTTAGA AAAAATAAAAAATTTCCAATATGTAGTGTGTATACCTGCCTCGCCATGCAGCATCATAGCCTGT GGGAACCAAGGAGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGGCTGTCCCTGCTGCCTGCA AGGTTTTGCTTAATCTCAATCAATGCTCTTCACTTTTAGCAGCTGTGGGTTTTGTGTTGTTTC TCTGTTTTGCTTAGTATCTGACTACTTTTTAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACACATTTTATAAAATTTTTCACCTG
ESTD-MOC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCCCAGCTCTGTCCCTAGCCGAACCTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTTCCAGGGTTTGGTCTAAGTGTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCACTGTTCCCTGTTTAGCATGG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAATAATACCAGATCCACAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	---	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTCTAAAAAAGAAAAAAGAAAA AAATTTAAAGGGGTACTTATATCCACACTGCACACTGCCTAGCCAAACGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATCTGAG AAACCTCTTTTAAACCTCACCTTTTGGGGTTTTTGGAGAAGGTTATCA
ESTD- NPPA	--	--	---	---	---	TGTCCCTAGGCCAGCCCTGCTTGTCTCCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD- NRAMP	--	--	---	---	---	GGAGGAGGAGGTGGGAGGGGGTCTGTCTCTCCAGGTCACACAGACAGAGAAAGCGGCTCAGTG TATCCCAACCCCAATGTGGCGCTGGAGATGAAGAGGAGTTGATCGAGGT
ESTD- NRAS	--	--	---	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTATGTAGGTGATATTGGATACITTTTGTGTGATTATATATAGCAATTTGAGGG ACAAACAGATAGCAGAAATGGGCTTGAATAGTAGTCTTATTTAACCTTGGCAATAGCATTGC ATCCCTGTGTTTTTAATAAAAT
ESTD-OTC	--	--	---	---	---	GTGACCTTCTCACTTTAAAAAATTTACGGAGAGAAATTAATATATGCTATGCTATCAGCAGA TCTGAATTTTAGGATAAAACAGAAAGGAGGTATGTAACA
ESTD-PAI1	--	--	---	---	---	GCCACCAACCCCAACCCAGCACACCTCCAACTCAGCCAGCAAGGTTGTGACACAAGAGAGCCC TCAGGGGCACAGAGAGTCTGGACACGTGGGAGTCAGCCGTGTATCATCGAGGCGGCCGGCAC ATGGAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGCCCCAAGTCTAGACAGACAAAACCTAG ACAATCACGTGGGTGGCT
ESTD-PAR	--	--	---	---	---	CTCTTCAGGAACCAACAGTCTTACCAAAACACGACTTATGCTGTCGAGAGGTACAACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCACTAGCTCTGTGAGTGTCTTCTCACTTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCAGTTAGGCTTCTGTATACCCATGCC
ESTD- PBDA	--	--	---	---	---	CCTTCTATGCCAGATGGAATTCAGTCCCTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCGTGGCTGGGAAGGGCAGGACTAATCCAATCTACCCGAGCTTGCTCGCATACAGCG GACAGTGTGGTGGCAACATTGAAGCCCTCGTACC
ESTD-PS-1	--	--	---	---	---	GGGAGTAAACTTGGATTGGGAGATTTTCTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACACCATAGCCTATTCTGTAGCCATATTAATTTGGTTGTGCCCTACATT ATTACTCTTGCCATTTTCAAGAAAGCATTTGCCAGCTCTCCATCTCCATCACCTTTGGGCTTGT CTACTTGGCACAGATTATCTTGA
ESTD- POMP1	--	--	---	---	---	ATGAACATGGTCTTTAATTTATGATATGTTTGTATTAGTATCTTAAAGGGCTTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGTGACAGGGTGTCTTCAAGGCTCATACAGA TTCTGAAAATCATGTGTCCTAGAACATTTTGAAGAGGTAAGTCTTATGAAATTAATCTT
ESTD- Pai/RDS	--	--	---	---	---	ACCTACAGACGTGCTGATGTGTGTCCAAACCCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGAAGAGCGTGGCGAGACCTGTGAAGGCT

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ESTD-FDS	--	--	--	---	---	---	CCCGAGGAATCTGAGCGAGAGCGAGGGCTGGCTGCTGGAGAAAGCGTGCGCGGAGACCTGGAAAGG CCTTTCTGGAGAGTGTGAAGAGCTGGCAAGGGCAAGGTGGAAACAGGTGGAAACCGAGGGCGCAGACGCAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT CCAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	---	CTTCGTACGGGAGGTCAAGTCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCAATTTCCC CTGCTGACAGTATGACACGCGCACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCCG TCCTCTGAGGCTGGAGCCACTGAGAAATCAGCTGGAGGAGCCACCTGGCTGGGGCCAGCCACT CCGAGTCGGGATGTCACTACCGGGCAGTACCTAGCGCTACCGGAGG
ESTD- SPTB	--	--	--	---	---	---	TGAACACCCCTGTGGTCGGAGCCAGGTGTGTCTCTCTGGAGCCTGAGGAGTGTGTGTGTGTG CAGTCCCCGGCCACCTGCTGTGTGAGCCTGGACATACACCTTCACTCCTTTGGCCCCGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCTGTGTGTGACACCCCTGTGTGAACCCCCAACCCCTGCCTCC CCCCAACGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	---	TTCACTTTGTGGATTGTTCTTTTGTGTGTCAGCACCTTTTCAACATGATGTATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGTGGGATATTTGAAGAGATCTTTCAGTCCATGTCTCTAGAGAG TTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTAAAGTCTTTAATCCATTTTG ATTGATTCTGTGA
ESTD-TAT	--	--	--	---	---	---	AAATGGTCAGGACCCTGATCCACAAGAAAGTGGTACCATTTTCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCACTTCAATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACACCTTTCTCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THFB	--	--	--	---	---	---	TGCGGCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTTGATTTCCAAAGAGAAAGATGCCAAG CACACGAAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCACTTCATCCA CACTGGATTGCCCAACAAGTCTGAGTGCCAGCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACACCAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCCTACACACAAATCAGTCAGTG GCCCCAAGACCCCCCTCAGATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGCCCCAACTTCCAAATCCCCCGCCGCGATGG
ESTD-TYR	--	--	--	---	---	---	TAGTGAAGTTTTCATCTCCTGTCAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTTCAGATCCCCCAAGCA GTGCATCCATTGACACATATAATATGCATCCAGACAAAGAGGTCAATAATATTGATGTCGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

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ESTD- TYP1	--	--	--	---	---	AGTAGTGGAAGCTAACGAGCCCTCTCCTCACTGATCAGTATCAATGCTGATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCAATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGTATTCTTTTTCACCTTTATTACCTCTTTCT AATACAGCATATGTTAGAATTAAAGTTCTAGGCATACCT
ESTD- VB12	--	--	--	---	---	TTCCAAAGGCCCTCAATACAAAGTCTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACAAAGTCAAGAGTCAAGAGGAAACACCATG ACTCTGAGATGTCACCACTGAGAACCCCGTTATATGACTGGTATCGACAAGACCCCGGGCATG GGCTGAGGCTGATCATTACTCATAT
ESTD-VWF	--	--	--	---	---	AGTAGGAAAGCAAGAGTTGATTAGTGMGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CGACGTGTCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCATGAGAAACGCCCTT CATGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAACTTAAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCAAAGTTGAATGTCAGTTCGCTGTGGTTAGATGCAGGATTTATATGATCGGTTAACC TCT
EST71770 6	--	--	--	---	---	AGCACACCTCTCAGTCAAGCCTCAGCACAGATGCTTCTTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGACAGAGAGTATTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAAGATACAGCTGTTGGTGAAGG AGTGCCCAAGTCCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST52418 6	--	--	--	---	---	CAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAAGTCACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCGGGAGTTGGCGAGTAGCGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG
EST13586 3	--	--	--	---	---	CCCACTCTATTTGCCAGCCCCCAGGGACAGAGCTGATCCTTGAACCTTAAAGTCCACATTGCCAGGA CCAGTGAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCCCCG GTCACTC
EST51976 7	--	--	--	---	---	AGGAGAACTGGGCCCCCATGCGGGGGGACGTGGAAAGGCCACTTGAGCTTCTGAGAGAGGACCTGA GGGACAAGGTCAACTCTTCTTACGACCTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAAGGAACAGCAGGAGGAGCAGCAGGAGGAGGATGCTGGGOC CCTTGGAGAGCTGAGCTGCCCCCTGGTGC

EST11458 6	--	--	--	---	---	CCACITTTGGTAGTCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGITTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCAATTTTCCACAGTGGT CCCATTAACAAACATTCTATGAGCCAGGAGAGAGATTACGTAITTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTATCTGCCCTCTCACAGGACTGIGGCC
EST39852 8	--	--	--	---	---	CGGTCTTCCAGGTATTGTTGCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATCCATAAG GCATTTCTGAGGTGAGTACACCTTCCCACTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGTGGTGAACCTGTCTCTTGGCATTGCCGGCCCTCTCTGGGGCCCGTGG TCCTCCTGTGCTGTGGTGTGCTGTGAGTCAACGGTCTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGAAACGATGGTCCCAAGTCCGCGATGGTCAACCCGGACACAAGGGAGAGCGGGTTAOCCTGG CAATAT
EST38027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCCACTTGCCTTCATGCGCTGTGGGCCAACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTCATACATGGATGAGGAGACTGGAACCTGAAAAAGG CTGTCACTCTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGATGATGGTGTCTTAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTCCAAATAGAGCCTTACCAAAAGTGAT TACATAAAGAAAGTCAAGTGTGTTTACTCCTCATGACCAATATCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAGAACTGTCTCTGTCAACCATGGAGGATACTATAACTGTGAAGATAA ATTCAGCCACAGAGCTGCCAGATC
EST76807 EST44438 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAAGACCCCTGTGAGCCGATTGTCTATCTCCAGCGCCCTGTCTC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGGGACCTCAAGCTCGACTTCAAGGACGTCTT GCTCCGACCTAAGCGAGACGCCCTCAAGAGCCGAGCGGAGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAAATCTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAATGATTAAGTAAGGGAACCTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGACCTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTGGGTTTAGCGTGGTCTGATGTTGCTACTA TAGTCCAAAGTGAA

EST10398 2	..	--	---	---	---	TGCTGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTATGAAGGGGCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCAAACGCGAGAAG CATGTTTTCTTGGGCAAGAAGGTATCTACCAATAGTGCTATTAGGCCATTGG
EST36751 7	..	--	---	---	---	CCAAGTCGTTCAATTTAGCTTTGAGGTTTTAACTCGATTACTTTTTCTATTCAAAATCTCTGTAAAA TTGAAATAGAACTAGTTTTCTGATCTATGTTTCAAGTTAAACAG
EST40582	..	--	---	---	---	CACGTGGAAGGAGCTATTTTTGGAGGCTTTAAGAGTAAAGAATCTGTCCCAAACTTTGTGGCTGAC TTTATGGCTAAGAAGTTTTTCACTGGATGCATTAAATACAAAATATTTTACCTTTTGAAAAATAAATG AAGGATTTGACCTGCTTGCTCTGGAAGAGATATCCGTACCGTCTGACGTTTTTGAACAATACAGAT GCCTCCCTGTAGCAGTTTTACGCTCTCTTACCTA
EST18288 3	..	--	---	---	---	GGCTCTATACCCCTGTGGTCTCTCCACGCTCTCTGGACTTACAGAACTGGAATGTTGCTGCTGAGAA GATTACAGGTTTCATCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCTGACGGAGCCAGTGTGG ACAGCACCTTGGCTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	..	--	---	---	---	TTCCGGCAGCCCCCATCTTGGACCTTGGTCCCTCAGGGGCCAACCCGGGCACTCAACGCTCT CGCTCTCGGTAACATCCGGCGGGCGGCTCTTGAGCACATAGCTGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTGCAGGGGCCAGCCCTGCAGAGAGAGGGGTCTCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCCACTG
EST58707 7	..	--	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCTTAGAATACACGAGACCGA ATGTATCAAAATGGACATTCAGCAGGAACTTCAACGATACCTGCTCTGTGTAGGCCAGGTTTATAGCA CACTTGTACCTACATTTCTGATTGGTGGACTCTTGTGCTTAAGAACCTT
EST74167 6	..	--	---	---	---	AGACATGAAGGAGTTGAAGCCTACAAATCGGAATGGAGGAACTGGAGGAACAACCTGACCCCGTGGCGGAGG AGACGCGGGACGGCTGTCAAAGAGCTGCAAGGCGGCAGAGCCCGGCTGGCGGGGACATGGAGGA CGTGGCGGCGCGCTGGTGCAGTACCGGGCGAGGTGCAAGGCCATGCTGGCCACAGACACCGAGGAGC TGCGGGTGGCGCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	..	--	---	---	---	CGCTGGTGCAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGGG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTCCGGATGCGGATGACCTGACGAGAGCGGC TGGCAGTGTACCAAGCGCGGGGCGCGAGGGCGCGAGCGGCGCTCAGCGGCATCCGCGAGCGCGCTG GGGCGCTGGTGGAAAGGGCGCGTGGCGGCGCCACTGTGGGCTC
EST36770 4	..	--	---	---	---	TGTAGCCAAAGTCACCTGCATCATCATTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGATTTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCATTATGAGTCCCAAAAT TCAAGCTCCCGATAGGGCTGGCCTGACCAAAATATACTGGGTTTCTGTTCTCTTCTTCTGATCAT TCTTCAAGTTATACTCTTATTTGGAAGGCCCTAAAGAAGGCTTATG

EST26021 1	--	--	--	---	---	---	TAATGTAGCTCATCCACCAAGAAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACAATTCCTCTGCAGCACTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAAATGCATTATGGAGTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTCTTCCITTTGCAACAAGACAAAGCAAGCC
EST51212 0	--	--	--	---	---	---	ATCCTGAGCTCGCCAATAAGCTTCTGGTTCTACTTCTCTTCTCCACAAGCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCTGGAGCCTTGTGCTCCACTCAATACAAAAGGCCCTCTCTCT ACATCT
EST20118 2	--	--	--	---	---	---	GTCCGAATCCTCCTCTGAAAGTGGCCGGTTTAATCTGCTCATGACGCTGCGGCTGGTGCAGCT GAGGTGAGGGGCTTGAAGCTGGAGTGGGTTTAGGAGCGGGTCTCTGCTGCATCCTAAGCTCT GAGAGCAACCTCCTTGAAGCTGGAGTGGGTTTAGGAGCGGGTCTCTGCTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	---	ACAATCCAGGTCACACATTCACAGAAGAGGGGGTGGTCACTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTACAGGTGTTAATATAGTAAAG GAAGCTTGAGCTCATGACAATTTGAAGCTGACAAATACACAAGAGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAACATGAAGTTGTTTTGAAGTGGTGTACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
EST34088 2	--	--	--	---	---	---	GTGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCACACAAGAGACCGGCTCAAGG ATCCCAAGGGCCCAACTCCCGAACCACTCAGGGTCTCTGTGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCCCTTGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAAGAGACCCAGAAAT CACAGGTGGGCACGTGGCTCTACGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAACT
EST74082 0	--	--	--	---	---	---	TCCAGGTGGCTGGAAOCCAGGCCCAAGCTCTGCAGCAGGAGGAGAGCTGGGCTGGTGAAGCATG TGGGGTGAGCCCAAGGGGCCCCAAGGCAGGCACTGGCTTCAGCTGCTCAGCCCTGCTGTGAC CCAGTCACTGCTCTTCTGCCATGGCCCTGTGGATGGGCTCTGCTGCCCTGCTGGGCTGCTGGCCCTC TGGGACCTGACCCAGCCGACGCTTTGTGAACCAACAGCTGTGGC
EST45311 0	--	--	--	---	---	---	GCCCTCCTCTCTCCAAATCTGTCCTATAGTTTCTCTATTAGTGAACATACATGCACTCTTTTAGT GGATAGATGCACACAACACACAGCCATTATGGGGAAGGATCCAGGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTCAGTAGTA CATACACATCTGTGTCATTGTTGAAT

EST65258 8	--	--	---	---	---	TGCCCCATCACGGCGCGGAGACATGGCTTGCCACAGCTCTGAGGATGTCACCAATTAACAGAAAT OCAGTTATTTCCACCTCAAAATGACGCCATGGCCGGCGGTCTTCTGGGGCTCGTGGGGGG ACAGCTCCACTCTGACTGGCAGCTCTTGATGGAGACTTGAGGAGGGAGGCTTGAGGTTGGTGAG GT/AGGTGGCTGTTCTCTGTCAGTCAGGACATCAGTCTGATAAA
EST38216 3	--	--	---	---	---	ATGAGGATGAAGGTGGACAGGAGGAGGAGGCCAACCTGTATCCCGGGCTGCAGATGTCGCTG GACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 2	--	--	---	---	---	ATACTAGTACAAGTGGTAAATTTTGATACATTACACTAAATATTAGCATTTGTTTAGCATTTACCTAA TTTTTTCTCTGCTCCATGCAGACTGTTAGCTTTTACCTTAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTTCTCGAAGTCCAGTATCCAGAGTTTGGTTTTTGAACATAGCAATGCCTGTGAAAAA GAAACTGAATACCTAAGATTCTGTCTGGGGTTTTTGGTGCATGCA
EST35879 9	--	--	---	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCCTCCCAATCTTGTCGTTCCACCGATG GAACTGCCGGCAATCTGACACGTTGTCACCCAGGCTGACCCCAATAGGTGAACATGCTTCTGAG AGAGTTGAACAGATTCTTGAAGACAGCAGCGGGATGGGGCAGGAGAGCTGCCTGGATGAA
EST68308 5	--	--	---	---	---	GGAAGAGATTTAAGAAGCTTGATTTGGACAAATCTGTTCTTTGAGTGTGGAAGATTCATGTCTCT GCCTGAGTTACAAACAGATCCTTTAGTACAGCAGTAATAGATATATTCGACACAGATGGGAATGGA GAAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
EST54045 6	--	--	---	---	---	GGAATATTAAATATTTAAATACCTCCATTTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATGTGATGTTGGCAATTTGTTCTTACAAATCGGATGGGAATCT GTTAAGTAAGTACTGTTTGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
EST52908 0	--	--	---	---	---	ATCACAGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGGATGGTCTGCAAGCCCTTTGG CAATGTGAGATTGATG
EST19590 0	--	--	---	---	---	AGGAGAACTGAGGAGGGGAAGAGACAAAGATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAATATGAC
EST76136 6	--	--	---	---	---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCCGGCTACATCCTTATCTATAGCCTTCCCC TAGGCTCT
EST58607 0	--	--	---	---	---	CTCTGGATGGTTACAGGTGGCAGGCACAGCCAGTCCATCTCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCTCACTGGAGAACAGGACAGCCACATGGCGGGATGGCCGGCGGAGTCTGGT TGCGGCAACGGCTGTGGCTCTGTTGTAACGGTAGCCTTTGCGGTTCGATGCTTAAACCTTTGTTCT TGCCCAAGGAGGGGGGTGCCATGCCTGAGATGATGAGTGGCC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer
6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining
comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.

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(21) International Application Number: PCT/US98/12442 (22) International Filing Date: 11 June 1998 (11.06.98) (30) Priority Data: 60/049,612 13 June 1997 (13.06.97) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/049,612 (CIP) Filed on 13 June 1997 (13.06.97) (71) Applicant (for all designated States except US): AFFYMETRIX, INC. [US/US]; 3380 Central Expressway, Santa Clara, CA 95051 (US). (72) Inventor; and (75) Inventor/Applicant (for US only): CHEE, Mark [AU/US]; 3199 Waverly Street, Palo Alto, CA 94306 (US). (74) Agents: LIEBESCHUETZ, Joe et al.; Townsend and Townsend and Crew LLP, 8th floor, Two Embarcadero Center, San Francisco, CA 94111-3834 (US).		(81) Designated States: JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i>
(54) Title: METHOD TO DETECT GENE POLYMORPHISMS AND MONITOR ALLELIC EXPRESSION EMPLOYING A PROBE ARRAY (57) Abstract The invention provides methods of monitoring expression levels of different polymorphic forms of a gene. Such methods entail analyzing genomic DNA from an individual to determine the presence of heterozygous polymorphic forms at a polymorphic site within a transcribed sequence of a gene of interest. RNA from a tissue of the individual in which the gene is expressed is then analyzed to determine relative proportions of polymorphic forms in transcript of the gene. Having identified alleles of a gene that are expressed at different levels, the alleles can be further analyzed to locate a second polymorphism that has a causative role in the different expression levels. The methods are amenable to analyzing large collections of genes simultaneously using arrays of immobilized probes.		

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METHOD TO DETECT GENE POLYMORPHISMS AND MONITOR ALLELIC EXPRESSION EMPLOYING A PROBE ARRAY

5

CROSS-REFERENCE TO RELATED APPLICATIONS

The present application derives priority from USSN 60/049,612 filed June 13, 1997, which is incorporated by
10 reference in its entirety for all purposes.

BACKGROUND

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution
15 generating variant forms of progenitor sequences (Gusella, Ann. Rev. Biochem. 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not
20 transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both
25 progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP)
30 means a variation in DNA sequence that alters the length of a restriction fragment as described in Botstein et al., Am. J.

Hum. Genet. 32, 314-331 (1980). Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. Some polymorphisms take the form of single nucleotide variations between
5 individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Single nucleotide polymorphisms can occur anywhere in protein-coding sequences, intronic sequences, regulatory sequences, or intergenomic regions.

10 Many polymorphisms probably have little or no phenotypic effect. Some polymorphisms, principally those occurring within coding sequences, are known to be the direct cause of serious genetic diseases, such as sickle cell anemia. Polymorphisms occurring within a coding sequence typically
15 exert their phenotypic effect by leading to a truncated or altered expression product. Still other polymorphisms, particularly those in promoter regions and other regulatory sequences, may influence a range of disease-susceptibility, behavioral and other phenotypic traits through their effect on
20 gene expression levels. That is, such polymorphisms may lead to increased or decreased levels of gene expression without necessarily affecting the nature of the expression product.

SUMMARY OF THE INVENTION

25 The invention provides methods of monitoring expression levels of different polymorphic forms of a gene. Such methods entail analyzing genomic DNA from an individual to determine the presence of heterozygous polymorphic forms at a polymorphic site within a transcribed sequence of a gene of
30 interest. RNA from a tissue of the individual in which the gene is expressed is then analyzed to determine relative proportions of polymorphic forms in transcript of the gene.

In some methods, genomic DNA is analyzed by amplifying a segment of genomic DNA from a sample and hybridizing the amplified genomic DNA to an array of immobilized probes. In some methods the array used for
5 analyzing genomic DNA comprises a first probe group comprising one or more probes exactly complementary to a first polymorphic form of the gene and a second probe group comprising one or more probes exactly complementary to a second polymorphic form of the gene. In some methods, RNA is
10 analyzed by reverse transcribing and amplifying mRNA expressed from the gene to produce an amplified nucleic acid and hybridizing the amplified nucleic acid to an array of immobilized probes. In some such methods, the amplified nucleic acid is cDNA. In some methods, the array of
15 immobilized probes for analyzing RNA comprises a first probe group comprising one or more probes exactly complementary to a first polymorphic form of the gene, a second probe group comprising one or more probes exactly complementary to a second polymorphic form of the gene.

20 In some method, genomic DNA and the RNA are analyzed by hybridizing the genomic DNA or an amplification product thereof, and the RNA or an amplification product thereof, to the same array of immobilized probes comprising a first probe group comprising one or more probes exactly complementary to a
25 first polymorphic form of the gene, and a second probe group comprising one or more probes exactly complementary to a second polymorphic form of the gene.

In some methods, the genomic DNA, or amplification product, and the RNA, or amplification product, bear different labels
30 and are hybridized simultaneously to the array.

Some methods further comprise comparing a genomic DNA hybridization intensity of the first probe group to the

subset to identify a further polymorphism in a promoter, enhancer or intronic sequence of the gene.

5

DEFINITIONS

A nucleic acid is a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated.

10

An oligonucleotide is a single-stranded nucleic acid ranging in length from 2 to about 500 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides.

15

A probe is an oligonucleotide capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation.

20

Oligonucleotide probes are often 10-50 or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, oligonucleotide probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

25

30

Specific hybridization refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. Stringent conditions are conditions under which a probe will hybridize to its target subsequence,

but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances.

Longer sequences hybridize specifically at higher

temperatures. Generally, stringent conditions are selected to

5 be about 5°C lower than the thermal melting point (T_m) for the

specific sequence at a defined ionic strength and pH. The T_m

is the temperature (under defined ionic strength, pH, and

nucleic acid concentration) at which 50% of the probes

complementary to the target sequence hybridize to the target

10 sequence at equilibrium. (As the target sequences are

generally present in excess, at T_m , 50% of the probes are

occupied at equilibrium). Typically, stringent conditions

include a salt concentration of at least about 0.01 to 1.0 M

Na ion concentration (or other salts) at pH 7.0 to 8.3 and the

15 temperature is at least about 30°C for short probes (e.g., 10

to 50 nucleotides). Stringent conditions can also be achieved

with the addition of destabilizing agents such as formamide.

For example, conditions of 5X SSPE (750 mM NaCl, 50 mM

NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C

20 are suitable for allele-specific probe hybridizations.

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion

(subsequence) of the target sequence. The term "mismatch

25 probe" refer to probes whose sequence is deliberately selected not to be perfectly complementary to a particular target

sequence. Although the mismatch(s) may be located anywhere in

the mismatch probe, terminal mismatches are less desirable as

a terminal mismatch is less likely to prevent hybridization of

30 the target sequence. Thus, probes are often designed to have

the mismatch located at or near the center of the probe such

that the mismatch is most likely to destabilize the duplex

with the target sequence under the test hybridization conditions.

Transcriptions levels can be quantified absolutely or relatively. Absolute quantification can be accomplished by inclusion of known concentration(s) of one or more target nucleic acids (e.g. control nucleic acids such as Bio B or with known amounts the target nucleic acids themselves) and referencing the hybridization intensity of unknowns with the known target nucleic acids (e.g. through generation of a standard curve). Alternatively, relative quantification can be accomplished by comparison of hybridization signals between two or more polymorphic forms of a transcript.

A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as a the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two forms. A triallelic polymorphism has three forms.

A single nucleotide polymorphism (SNP) occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is

usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

5 A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms
10 can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele.

DESCRIPTION

I. General

15 A substantial number of polymorphic sites in humans and other species have been described in the published literature, and many other polymorphic sites in human genomic DNA are described in commonly owned copending patent applications, such as PCT/US98/04571, filed March 5, 1998
20 (incorporated by reference in their entirety for all purposes). The genomic locations of these sites are known, as is the nature of the polymorphic forms occurring at the sites. Many of the known polymorphic sites occur within so-called expressed sequence tags and are therefore represented in the
25 transcript of genomic DNA, as well as genomic DNA itself. The present invention uses polymorphisms within the transcribed region of a gene as a means to monitor the relative expression of different allelic forms of the gene. Having identified alleles of a gene that are expressed at different levels, the
30 alleles can be further analyzed to locate a second polymorphism that has a causative role in the different expression levels. Often, the causative polymorphism is found

outside the coding sequence of a gene; for example, in a promoter, other regulatory sequence or an intronic sequence.

In the present methods, nucleic acid samples from individuals are characterized at both the genomic and transcriptional levels. The genomic analysis screens genomic DNA from an individual to identify one or more genes that are heterozygous for a polymorphism occurring within a transcribed region of a gene. RNA from the individual is then analyzed to determine the relative levels of polymorphic forms in the transcript of the heterozygous genes identified by the genomic analysis. If the levels of polymorphic forms in the transcript of a gene differ significantly from each other, further analysis is performed to identify the cause of the different levels. It is possible that the polymorphism within the transcript that is used for monitoring expression levels may itself affect expression levels. However, it is more likely that the difference in expression levels stems from another polymorphic difference between the alleles. Such polymorphisms are particularly likely to reside in promoter sequences, enhancers, intronic splice sites, or other regulatory sequences.

II. Analyzing Polymorphic Forms at the Genomic Level

Strategies for identification and detection of polymorphisms are described in commonly owned USSN 08/831,159, EP 730,663, EP 717,113, and PCT US97/02102, filed February 7, 1997 (incorporated by reference in their entirety for all purposes). The present methods usually employ precharacterized polymorphisms. That is, the genotyping required by the present methods is usually performed after the location and nature of polymorphic forms present at a site have already been determined. The availability of this

information allows sets of probes to be designed for specific identification of the known polymorphic forms.

In the simplest form of analysis, a biallelic polymorphism forms can be characterized using a pair of allele specific probes respectively hybridizing to the two polymorphic forms. However, analysis is more accurate using specialized arrays of probes tiled based on the respective polymorphic forms. Tiling refers to the use of groups of related immobilized probes, some of which show perfect complementarity to a reference sequence and others of which show mismatches from the reference sequence (see EP 730,663). A typically array for analyzing a known biallelic single nucleotide polymorphism contains two group of probes tiled based on two reference sequences constituting the respective polymorphic forms.

The first group of probes includes at least a first set of one or more probes which span the polymorphic site and are exactly complementary to one of the polymorphic forms. The group of probes can also contain second, third and fourth additional sets of probes, which contain probes identical to probes in the first probe set except at one position referred to as an interrogation position. When such a probe group is hybridized with the polymorphic form constituting the reference sequence, all probes in the first probe show perfect hybridization and all of the probes in the other probe sets show background hybridization levels due to mismatches.

When such a probe group is hybridized with the other polymorphic form, a different pattern is obtained. That is, all but one probes in the array show a mismatch to the target and produce only background hybridization. The one probe that shows perfect hybridization is a probe from the second, third or fourth probe sets whose interrogation position aligns with

the polymorphic site and is occupied by a base complementary to the other polymorphic form.

When the probe group is hybridized with a heterozygous sample in which both polymorphic forms are present, the patterns for the homozygous polymorphic forms are superimposed. Thus, the probe group shows distinct and characteristic hybridization patterns depending on which polymorphic forms are present and whether an individual is homozygous or heterozygous.

Typically, an array also contains a second group of probes tiled using the same principles as the first group but with a reference sequence constituting the other polymorphic form. That is, the first probe set in the second group spans the polymorphic site and shows perfect complementary to the other polymorphic form. Hybridization of the second probe group to homozygous or heterozygous target sequences yields a mirror image of hybridization patterns from the first group. By analyzing the hybridization patterns from both probe groups, one can determine with a high accuracy which polymorphic form(s) are present in an individual.

The principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

Arrays can also be designed to analyze many different polymorphisms in many different genes simultaneously

simply by including multiple subarrays of probes. Each subarray has first and second groups of probes designed for analyzing a particular polymorphism according to the strategy described above.

5 For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. Genomic DNA is typically amplified before analysis.

10 Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. The target is usually labelled in the course of amplification. The amplification product can be RNA or DNA, single stranded

15 or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with

20 DNase-free RNase.

III. Expression Monitoring

 The invention monitors the levels of RNA transcripts expressed from genes of interest. The RNA transcript can be

25 nuclear RNA, mRNA, rRNA or tRNA. Nuclear RNA contains intronic sequences that have been spliced out of mRNA. Analysis of nuclear RNA can be useful in analyzing the effects on expression of polymorphisms occurring within intronic regions. In some methods, RNA is monitored directly and in

30 other methods RNA is monitored indirectly via an amplification product, such as cDNA or cRNA.

Strategies for analysis and quantification of transcript are described in detail in commonly owned WO 96/14839 and WO 97/01603. In general, the same probe arrays that are used for analyzing polymorphic forms in genomic DNA can be used for analyzing polymorphic forms of transcript. The hybridization patterns of the probe arrays can be analyzed in the same manner for genomic and RNA (or RNA-derived) targets. Comparison of the hybridization intensities of the first probe group that are perfectly matched with one polymorphic form to the hybridization intensities of the second probe group that are perfectly matched with the second polymorphic form indicates approximately the relative proportions of the polymorphic forms in the transcript.

In some instances, it can be useful to compare the ratio of hybridization intensities of perfectly matched probes from the first and second probe groups for genomic DNA and RNA targets (or amplification products thereof). Preferably, the comparison is performed between like forms of amplification products (i.e., both DNA or both RNA). In genomic DNA from a diploid individual, the polymorphic forms at a heterozygous gene are expected to be present in equal molar ratio. However, in practice, the ratio of hybridization intensities may differ somewhat from the expected molar ratio due to, for example, base-composition effects on hybridization intensity. By comparing the ratios of hybridization intensities for genomic DNA and RNA (or amplification products thereof) to the same groups of probes, factors other than molar ratio of polymorphic forms that might influence hybridization intensities can largely be eliminated from the analysis. If the ratio of hybridization intensities differs significantly for the genomic and RNA targets (or amplification products

thereof), then it can be concluded that the polymorphic forms are differently expressed in the transcript.

Some arrays contain additional probes for measuring the level of transcript of a gene without distinguishing between the polymorphic forms. These probes exhibit perfect complementarity to a segment of the gene distal from the polymorphism used to distinguish polymorphic forms. The presence and level of the transcript can be inferred from the hybridization intensities of these probes, optionally relative to control probes lacking complementarity to the target and designed to measure the background level of hybridization intensity.

RNA transcript for analysis is isolated from a biological sample obtained from a biological tissue or fluid in which the gene of interest is expressed. Samples include sputum, blood, blood cells (e.g., white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom. Biological samples may also include sections of tissues such as frozen sections taken for histological purposes.

Methods of isolating total mRNA are described in Chapter 3 of *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation*, P. Tijssen, ed. Elsevier, N.Y. (1993) and Chapter 3 of *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation*, P. Tijssen, ed. Elsevier, N.Y. (1993)).

Frequently, it is desirable to amplify RNA prior to hybridization. The amplification product can be RNA or DNA, single-stranded, or double-stranded. In one procedure, mRNA can be reverse transcribed with a reverse transcriptase and a

primer consisting of oligo dT and a sequence encoding the phage T7 promoter to provide single stranded DNA template. The second DNA strand is polymerized using a DNA polymerase. After synthesis of double-stranded cDNA, T7 RNA polymerase is added and RNA is transcribed from the cDNA template. Successive rounds of transcription from each single cDNA template result in amplified RNA. Alternatively, cDNA can be amplified to generate double stranded amplicon, and one strand of the amplicon can be isolated, i.e., using a biotinylated primer that allows capture of the undesired strand on streptavidin beads. Alternatively, asymmetric PCR can be used to generate a single-stranded target.

Typically, amplification product is labelled either in the course of amplification or subsequently. If RNA amplification product is to be hybridized simultaneously with genomic DNA, or an amplification product thereof, to an array, then the two targets are differentially labelled. A variety of different fluorescent labels are available. For example, one sample can be labelled with fluorescein and the other with biotin, which can be stained with phycoerythrin-streptavidin after hybridization. Two target samples can be diluted, if desired, prior to hybridization to equalize fluorescence intensities.

Detailed protocols for PCR are provided in *PCR Protocols, A Guide to Methods and Applications*, Innis et al., Academic Press, Inc. N.Y., (1990). Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics*, 4: 560 (1989), Landegren, et al., *Science*, 241: 1077 (1988) and Barringer, et al., *Gene*, 89: 117 (1990), transcription amplification (Kwoh, et al., *Proc. Natl. Acad. Sci. USA*, 86: 1173 (1989)), and self-sustained sequence replication (Guatelli, et al., *Proc. Nat.*

Acad. Sci. USA, 87: 1874 (1990)). In some methods, a known quantity of a control sequence is co-amplified using the same primers to provide an internal standard that may be used to calibrate the PCR reaction to ensure that the amplification products are produced in approximately the same molar ratio as the starting ratio of templates. The probe array then includes probes specific to the internal standard for quantification of the amplified nucleic acid.

IV. Correlation of Genotype with Expression Levels

Having identified alleles of a gene that are expressed at different levels, the alleles can be further analyzed to identify a difference between them that accounts for the different expression levels. The difference may reside in the same polymorphism that was used to distinguish the different allelic forms in the analyses described above. However, more typically, the difference in expression levels resides in a second polymorphism located in a promoter, enhancer or other regulatory regions. Such polymorphisms can be identified by sequencing the regulatory regions of the differentially expressed alleles and identifying sequence differences between the alleles.

A possible causative role of a polymorphism within a regulatory sequence in differential expression of alleles can be analyzed by both molecular biological and genetic approaches. For example, if differentially expressed alleles differ from each other at a polymorphic site within a promoter, the different forms of the promoter can be cloned and placed in operable linkage with a reporter gene. If the reporter gene is expressed at different levels from the two forms of the promoter, it is likely that the polymorphism within the promoter has a causative role in the observed

differential expression levels of allelic forms of the gene with which it is naturally associated. Similar reporter assays can be devised to assess the effect of polymorphisms in other regulatory sequences.

5 Polymorphisms within promoters and other regulatory sequences can also be characterized by association analysis. Association analysis identifies correlations between polymorphic forms and a population of individuals who have been tested for the presence or absence of a phenotypic trait
10 of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a polymorphism is determined for a set of the individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of the polymorphism are then reviewed to
15 determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods such as a χ^2 -squared test and statistically significant correlations between a polymorphic form and phenotypic characteristics are
20 noted.

V. Alternative Method of Correlating Expression Levels with Genotype

25 In an alternative or additional approach, a population of individuals is genotyped at one or more polymorphic sites within a gene including flanking sequences. Expression levels of the gene transcript are then determined in individuals without distinguishing between the polymorphic forms. Optionally expression levels from different
30 individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such that isolates in a given cluster tend to be similar and isolates in

different clusters tend to be dissimilar. See commonly owned
USSN 08/797,812, filed February 7, 1997 (incorporated by
reference in its entirety for all purposes). The population
of individuals on which the analysis is performed should
5 preferably be matched for characteristics that might have
indirect affects on expression levels such as age, sex and
ethnicity, and expression levels should be determined from the
same tissue type. The genotype of an individual with respect
to one or more polymorphisms within the gene is then
10 correlated with the expression level of gene transcript in the
same individual throughout the population. Polymorphic forms
showing strong correlation with expression levels of
transcript may have a causative role in determining the
expression level. This role can be further investigated using
15 the molecular biological and genetic approaches described
above.

VI. Association Analysis

Phenotypic traits suitable for association analysis
20 include diseases that have known but hitherto unmapped genetic
components (e.g., agammaglobulinemia, diabetes insipidus,
Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
syndrome, Fabry's disease, familial hypercholesterolemia,
polycystic kidney disease, hereditary spherocytosis, von
25 Willebrand's disease, tuberous sclerosis, hereditary
hemorrhagic telangiectasia, familial colonic polyposis,
Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute
intermittent porphyria). Phenotypic traits also include
symptoms of, or susceptibility to, multifactorial diseases of
30 which a component is or may be genetic, such as autoimmune
diseases, inflammation, cancer, diseases of the nervous
system, and infection by pathogenic microorganisms. Some

examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Such correlations can be exploited in several ways. In the case of a strong correlation between a polymorphic form and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of

several treatment regimes for a disease indicates that this treatment regime should be followed.

VII. Probe Array Design and Construction

5 VLSIPS™ technology provides methods for synthesizing arrays of many different oligonucleotide probes that occupy a very small surface area. See US 5,143,854 and WO 90/15070. For example, high density arrays can be produced which comprise greater than about 100, preferably greater than about
10 1000, 16,000, 65,000, 250,000 or 1,000,000 different oligonucleotide probes. The oligonucleotide probes range from about 5 to about 50 or about 5 to about 45 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length.
15 In some embodiments, the oligonucleotide probes are 20 or 25 nucleotides in length. The oligonucleotide probes are usually less than 50 nucleotides in length, generally less than 46 nucleotides, more generally less than 41 nucleotides, most generally less than 36 nucleotides, preferably less than 31
20 nucleotides, more preferably less than 26 nucleotides, and most preferably less than 21 nucleotides in length. The probes can also be less than 16 nucleotides or less than even 11 nucleotides in length.

The location and sequence of each different
25 oligonucleotide probe sequence in the array are generally known. Moreover, the large number of different probes can occupy a relatively small area providing a high density array having a probe density of generally greater than about 60, 100, 600, 1000, 5,000, 10,000, 40,000, 100,000, or 400,000
30 different oligonucleotide probes per cm². The small surface area of the array (often less than about 10 cm², preferably less than about 5 cm² more preferably less than about 2 cm²,

and most preferably less than about 1.6 cm²) permits uniform hybridization conditions, such as temperature regulation and salt content.

5 Finally, because of the small area occupied by the high density arrays, hybridization may be carried out in extremely small fluid volumes (e.g., 250 μ l or less, more preferably 100 μ l or less, and most preferably 10 μ l or less). In small volumes, hybridization may proceed very rapidly. In addition, hybridization conditions are extremely uniform
10 throughout the sample, and the hybridization format is amenable to automated processing.

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication
15 or patent application were specifically and individually indicated to be so incorporated by reference. Although the present invention has been described in some detail by way of illustration and example for purposes of clarity and understanding, it will be apparent that certain changes and
20 modifications may be practiced within the scope of the appended claims.

What is claimed is:

3 1. A method of monitoring expression levels of
4 different polymorphic forms of a gene, comprising:
5 analyzing genomic DNA from an individual to
6 determine the presence of heterozygous polymorphic forms at a
7 polymorphic site within a transcribed sequence of a gene of
8 interest;
9 analyzing RNA from a tissue of the individual in
10 which the gene is expressed to determine relative proportions
11 of polymorphic forms in transcript of the gene.

1 2. The method of claim 1, wherein analyzing genomic
2 DNA comprises amplifying a segment of genomic DNA from a
3 sample and hybridizing the amplified genomic DNA to an array
4 of immobilized probes.

1 3. The method of claim 2, wherein the array of
2 immobilized probes comprises a first probe group comprising
3 one or more probes exactly complementary to a first
4 polymorphic form of the gene and a second probe group
5 comprising one or more probes exactly complementary to a
6 second polymorphic form of the gene.

1 4. The method of claim 1, wherein analyzing the
2 RNA, comprises reverse transcribing and amplifying mRNA
3 expressed from the gene to produce an amplified nucleic acid
4 and hybridizing the amplified nucleic acid to an array of
5 immobilized probes.

1 5. The method of claim 4, wherein the amplified
2 nucleic acid is cDNA.

1 6. The method of claim 4, wherein the array of
2 immobilized probes comprises a first probe group comprising
3 one or more probes exactly complementary to a first
4 polymorphic form of the gene, a second probe group comprising
5 one or more probes exactly complementary to a second
6 polymorphic form of the gene.

1 7. The method of claim 1, wherein the genomic DNA
2 and the RNA are analyzed by hybridizing the genomic DNA or an
3 amplification product thereof, and the RNA or an amplification
4 product thereof, to the same array of immobilized probes
5 comprising a first probe group comprising one or more probes
6 exactly complementary to a first polymorphic form of the gene,
7 and a second probe group comprising one or more probes exactly
8 complementary to a second polymorphic form of the gene.

1 8. The method of claim 7, wherein the genomic DNA,
2 or amplification product, and the RNA, or amplification
3 product, bear different labels and are hybridized
4 simultaneously to the array.

1 9. The method of claim 7, further comprising
2 comparing a genomic DNA hybridization intensity of the first
3 probe group to the second group to determine a genomic
4 hybridization ratio, and comparing an RNA hybridization
5 intensity of the first group to the second group to determine
6 an RNA hybridization ratio, whereby a difference in the
7 genomic DNA and RNA ratios indicates that the polymorphic
8 forms of the gene are expressed at different levels in the
9 individual.

1 10. The method of claim 1, further comprising
2 sequencing a nontranscribed region of the gene to identify a
3 second polymorphic site in a promoter or enhancer region of
4 the gene.

1 11. A method of monitoring expression levels of
2 different polymorphic forms of a collection of genes,
3 comprising:
4 hybridizing genomic DNA, or an amplification product
5 thereof, from an individual to an array of immobilized probes
6 comprising a subarray of probes for each gene in the
7 collection, wherein each subarray comprises a first group of
8 one or more probes exactly complementary to a first
9 polymorphic form of the gene and a second group of one or more
10 probes exactly complementary to a second polymorphic form of
11 the gene;
12 analyzing the relative hybridization of the first
13 and second group of probes to the genomic DNA or amplification
14 product thereof for each subarray to identify heterozygous
15 genes in the individual;
16 hybridization RNA or an amplification product
17 thereof from the individual to the array of immobilized
18 probes;
19 comparing the hybridization intensities of the first
20 and second groups of probes to the RNA or amplification
21 product to identify a subset of the heterozygous genes for
22 which different polymorphic forms are expressed at different
23 levels.

1 12. The method of claim 11, wherein the collection
2 of genes comprises at least 100 genes.

1 13. The method of claim 11, wherein the collection
2 of genes comprises at least 1000 genes.

1 14. The method of claim 11, wherein the collection
2 of genes comprises at least 100,000 genes.

1 15. The method of claim 11, further comprising
2 sequencing a nontranscribed region of a gene in the subset to
3 identify a further polymorphism in a promoter, enhancer or
4 intronic sequence of the gene.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/12442

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12Q 1/68; C12P 19/34; C07H 21/04, 21/00

US CL : 435/6, 91.1, 91.2; 536/24.3, 24.31, 25.32

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1, 91.2; 536/24.3, 24.31, 25.32

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GUO, Z. Direct fluorescence analysis of genetic polymorphisms by hybridization with oligonucleotide arrays on glass supports. Nucleic Acids Research. 1994, Vol. 22, No. 24, pages 5456-5464, especially page 5456.	1-7
Y	SOUTHERN, E.M. Analyzing and Comparing Nucleic Acid Sequences by Hybridization to Arrays of Oligonucleotides: Evaluation Using Experimental Models. Genomics. 1992, Vol. 13, pages 1008-1017, especially pages 1008 & 1011.	1-15
Y	US 5,567,809 A (APPLE et al) 22 October 1996, see entire document, especially column 53.	1-15



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

26 AUGUST 1998

Date of mailing of the international search report

28 SEP 1998

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks

Authorized officer



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/12442

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,503,980 A (CANTOR) 02 April 1996, see entire document, especially column 7, lines 19-61.	1-15
Y	US 5,631,134 A (CANTOR) 20 May 1997, see entire document, especially column 2, lines 64-67.	1-15
A,E	US 5,795,714 A (CANTOR et al) 18 August 1998, see entire document.	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/12442

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, STN CAPLUS, MEDLINE, BIOSIS, WPIDS, GENBANK, SCISEARCH, EMBASE, CANCERLIT, JAPIO,
LIFESCI, DISSABS, TOXLINE, AIDSLINE, BIOTECHDS, DGENE, PHIC, PHIN, TOXLIT,
NTIS, BIOBUSINESS

SEARCH TERMS: PROBE, OLIGONUCLEOTIDE, ARRAY, CHIP, CARRIER, SUPPORT
IMMOBILIZED, BOUND OR BIND, DETECT RNA, RIBONUCLEO?, POLYMORPH?
MONITOR, EXPRESS?, different or heterogeneous label

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C07H 21/04, C12Q 1/68, C12N 15/63, 15/85, C12P 21/02	A1	(11) International Publication Number: WO 98/14466 (43) International Publication Date: 9 April 1998 (09.04.98)
(21) International Application Number: PCT/US97/17658 (22) International Filing Date: 30 September 1997 (30.09.97) (30) Priority Data: 08/724,394 1 October 1996 (01.10.96) US 08/852,495 7 May 1997 (07.05.97) US (71) Applicant: PROGENITOR, INC. [US/US]; 4040 Campbell Avenue, Menlo Park, CA 94025 (US). (72) Inventors: FEDER, John, N.; 1450 Chestnut Street, San Carlos, CA 94070 (US). KRONMAL, Gregory, S.; 277 Gateway Drive #131, Pacifica, CA 94044 (US). LAUER, Peter, M.; 128 Randall Street, San Francisco, CA 94131 (US). RUDDY, David, A.; 885 Greenwich Street, San Francisco, CA 94133 (US). THOMAS, Winston, J.; 40 White Plains Court, San Mateo, CA 94402 (US). TSUCHIHASHI, Zenta; 9 Light Way, Menlo Park, CA 94025 (US). WOLFF, Roger, K.; 41 Eugene Street, Mill Valley, CA 94941 (US). (74) Agents: FITTS, Renee, A. et al.; Townsend and Townsend and Crew LLP, 8th floor, Two Embarcadero Center, San Francisco, CA 94111-3834 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>

(54) Title: POLYMORPHISMS AND NEW GENES IN THE REGION OF THE HUMAN HEMOCHROMATOSIS GENE**(57) Abstract**

Polymorphic sites in the region surrounding the HFE gene are provided. These polymorphisms are useful as surrogate markers in diagnostic assays for hemochromatosis. Additionally, a fine structure map of the 1 megabase region surrounding the HFE gene is provided, along with 235 kb of DNA sequence and 8 loci corresponding to candidate genes within the 1 megabase region, and in the purification of related proteins.

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Polymorphisms and New Genes in the Region of the Human Hemochromatosis Gene

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BACKGROUND OF THE INVENTION

Hereditary hemochromatosis (HH) is an inherited disorder of iron metabolism wherein the body accumulates excess iron. In symptomatic individuals, this excess iron leads to deleterious effects by being deposited in a variety of organs leading to their failure, and resulting in cirrhosis, diabetes, sterility, and other serious illnesses. The gene which is defective in this disease was disclosed in copending U.S.S.N. 08/652,265.

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Fine structure mapping of the region to which the gene responsible for HH, HFE (denoted HH or HFE in some publications), was mapped makes possible the identification of candidate sequences comprising the HFE gene, along with structural elements for regulation and expression and neighboring genes.

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A variety of techniques is available for fine structure mapping, including direct cDNA selection, exon-trapping, and genomic sample sequencing. The direct selection approach (Lovett *et al.* Proc. Natl. Acad. Sci. U.S.A. 88:9628-9623 (1991)) involves the hybridization of cDNA fragments to genomic DNA. This technique is extremely sensitive and capable of isolating portions of rare transcripts. Exon-trapping (Church *et al.* Nature Genetics 6:98-105 (1994)) recovers spliced introns from *in vivo* expressed genomic DNA clones and produces candidate exons without requiring any prior knowledge of the target's gene expression. High-throughput genomic DNA sequencing with comparison of the sequence data to databases of expressed sequences has also been used, such as in the positional cloning of the Werner syndrome gene (Yu *et al.* Science 277:258-262 (1996)) and in cloning by homology of the second Alzheimer's disease gene on chromosome 1 (Levy-Lahad *et al.* Science 269:973-977 (1995)).

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HH is typically inherited as a recessive trait; in the current state of knowledge, homozygotes carrying two defective copies of the gene are most frequently affected by the disease. In addition, heterozygotes for the HFE gene are more susceptible to sporadic porphyria cutanea tarda and potentially other disorders (Roberts *et al.*, Lancet 349:321-323 (1997)). It is estimated that approximately 10-15% of Caucasians carry one copy of the HFE gene mutation and that there are about one million homozygotes in the United States. HH, thus, represents one of the most common genetic disease mutations in Caucasian individuals. Although ultimately HH produces debilitating symptoms, the majority of homozygotes and heterozygotes have not been diagnosed.

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The need for such diagnostics is documented, for example, in Barton, J.C. *et al.* Nature Medicine 2:394-395 (1996); Finch, C.A. West J Med 153:323-325 (1990); McCusick, V. Mendelian Inheritance in Man pp. 1882-1887, 11th ed., (Johns Hopkins University Press, Baltimore (1994)); Report of a Joint World Health Organization/Hemochromatosis Foundation/French Hemochromatosis Association Meeting on the Prevention and Control of Hemochromatosis (1993); Edwards, C.Q. *et al.* New Engl J Med 328:1616-1620 (1993); Bacon, B.R. New Engl J Med 326:126-

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127 (1992); Balan, V. et al. Gastroenterology 107:453-459 (1994); Phatak, P.D. et al. Arch Int Med 154:769-776 (1994).

A single mutation in the HFE gene, designated 24d1 in copending U.S.S.N. 08/630,912, gave rise to the majority of disease-causing chromosomes present in the population today.

5 This is referred to herein as the "common" or "ancestral" or "common ancestral" mutation. These terms are used interchangeably. It appears that about 80% to 90% of all HH patients carry at least one copy of the common ancestral mutation which is closely linked to specific alleles of certain genetic markers close to this ancestral HFE gene defect. These markers are, as a first approximation, in the allelic form in which they were present at the time the ancestral HFE mutation occurred. See, for
10 example, Simon, M. et al. Am J Hum Genet 41:89-105 (1987); Jazwinska, E.C. et al. Am J Hum Genet 53:242-257 (1993); Jazwinska, E.C. et al. Am J Hum Genet 56:428-433 (1995); Worwood, M. et al. Brit J Hematol 86:863-866 (1994); Summers, K.M. et al. Am J Hum Genet 45:41-48 (1989).

Several polymorphic markers in the HFE region have been described and shown to have alleles that are associated with HH disease. These markers include the published microsatellite
15 markers D6S258, D6S306 (Gyapay, G. et al. Nature Genetics 7:246-339 (1994)), D6S265 (Worwood, M. et al. Brit J Hematol 86:833-846 (1994)), D6S105 (Jazwinska, E.C. et al. Am J Hum Genet 53:242-257 (1993); Jazwinska, E.C. et al. Am J Hum Genet 56:428-433 (1995)), D6S1001 (Stone, C. et al. Hum Molec Genet 3:2043-2046 (1994)), D6S1260 (Raha-Chowdhury et al. Hum Molec Genet 4:1869-1874 (1995)) as well as additional microsatellite and single-nucleotide-polymorphism markers
20 disclosed in co-pending PCT application WO 96/06583, the disclosure of which is hereby incorporated by reference in its entirety. Additionally, copending U.S.S.N. 08/630,912 disclosed additional markers 24d2 and 24d7.

The symptoms of HH are often similar to those of other conditions, and the severe effects of the disease often do not appear immediately. Accordingly, it would be desirable to provide a
25 method to identify persons who may be destined to become symptomatic in order to intervene in time to prevent excessive tissue damage associated with iron overload. One reason for the lack of early diagnosis is the inadequacy of presently available diagnostic methods to ascertain which individuals are at risk, especially while such individuals are presymptomatic.

Although blood iron parameters can be used as a screening tool, a confirmed
30 diagnosis often employs liver biopsy which is undesirably invasive, costly, and carries a risk of mortality. Thus, there is a clear need for the development of an inexpensive and noninvasive diagnostic test for detection of homozygotes and heterozygotes in order to facilitate diagnosis in symptomatic individuals, provide presymptomatic detection to guide intervention in order to prevent organ damage, and for identification of heterozygote carriers.

35 Furthermore, a need exists for both methods for fine structure mapping and a fine structure map of the region of the chromosome to which the HH locus maps. This and other needs are addressed by the present invention.

SUMMARY OF THE INVENTION

One aspect of the invention is an oligonucleotide comprising at least 8 to about 100 consecutive bases from the sequence of Figure 9, or the complement of the sequence, wherein the at least 8 to about 100 consecutive bases includes at least one polymorphic site of Table 1.

Another aspect of the invention is an oligonucleotide pair selected from the sequence of Figure 9 or its complement for amplification of a polymorphic site of Table 1.

Another aspect of the invention is an isolated nucleic acid molecule comprising about 100 consecutive bases to about 235 kb substantially identical to the sequence of Figure 9, wherein the DNA molecule comprises at least one polymorphic site of Table 1.

Another aspect of the invention is a method to determine the presence or absence of the common hereditary hemochromatosis (HFE) gene mutation in an individual comprising:

providing DNA or RNA from the individual; and

assessing the DNA or RNA for the presence or absence of a haplotype of

Table 1,

wherein, as a result, the absence of a haplotype of Table 1 indicates the likely absence of the HFE gene mutation in the genome of the individual and the presence of the haplotype indicates the likely presence of the HFE gene mutation in the genome of the individual.

Another aspect of the invention is a method to determine the presence or absence of the common hereditary hemochromatosis (HFE) gene mutation in an individual comprising:

providing DNA or RNA from the individual; and

assessing the DNA or RNA for the presence or absence of a genotype

defined by a polymorphic allele of Table 1,

wherein, as a result, the absence of a genotype defined by a polymorphic allele of Table 1 indicates the likely absence of the HFE gene mutation in the genome of the individual and the presence of the genotype indicates the likely presence of the HFE gene mutation in the genome of the individual.

Another aspect of the invention is a culture of lymphoblastoid cells having the designation ATCC CRL-12371.

One aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF1.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF2.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF3.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF4.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to BTF5.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to NPT3.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to NPT4.

A further aspect of the invention is an isolated nucleic acid sequence comprising a nucleic acid sequence substantially identical to RoRet.

5 Additional aspects of the invention include nucleic acid sequences that are cDNAs, polypeptides encoded by the nucleic acids of the invention and antibodies specifically immunoreactive thereto, vectors comprising the nucleic acid sequences of the invention, and host cells stably transfected with the nucleic acids of the invention.

10 A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF1.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF2.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF3.

15 A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF4.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of BTF5.

20 A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of NPT3.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of NPT4.

A further aspect of the invention is an isolated nucleic acid sequence comprising at least 18 contiguous nucleotides substantially identical to at least 18 contiguous nucleotides of RoRet.

25 **BRIEF DESCRIPTION OF THE DRAWINGS**

Figure 1 depicts a combination genetic, physical and transcription map of the HFE gene region. The first line shows the relative positions of selected genetic markers that define the HFE region. The heavy bar below represents the YAC clone used in the direct selection experiment. The order and positions of the bacterial clones employed in the exon-trapping and sample sequencing is indicated under the YAC. The thin bar under the bacterial clones represents the approximate locations of a subset of the expressed sequence fragments mapped to the contig. The thicker bars show the location of the cDNAs cloned. Two regions are bracketed; the butyrophilin family of genes (BTF), and the region where complete genomic sequencing was carried out.

35 Figure 2 is a schematic of the 250 kb of genomic sequence including the HFE gene. Both the structure of the overall cDNA (top) and that corresponding to the coding regions (bottom), as well as the direction of transcription are shown. The positions of the histone genes, the zinc α -2 glycoprotein pseudogene, and the ESTs are also shown.

40 Figure 3 depicts an alignment of the predicted amino acid sequence of the BTF proteins. Sequences were aligned in a pair-wise fashion using CLUSTAL W (Thompson *et al.* Nucl. Acids Res. 22:4673-4680) to deduce the most parsimonious arrangement. The asterisks under the

alignment represent amino acids conserved in all 6 proteins; the "dots" represent conserved amino acids substitutions. Boxed are the regions within the proteins which correspond to three conserved motifs: 1) the B-G domain, 2) the transmembrane domain (TM), and 3) the B30-2 exon domain.

Figure 4, panel (A) depicts a Northern blot analysis of representative members of the two groups of BTF proteins, BTF1 and BTF5. BTF1 hybridized to all tissues on the blot as a major transcript at 2.9 kb and a minor one at 5.0 kb. BTF5 hybridized to several transcripts ranging between 4.0 and 3.1 kb and as a similar expression profile to BTF1. Autoradiography was for 24 hours. The β -actin hybridization demonstrated the variation in poly (A)+ RNA between the lanes. Autoradiography was for 1 hour. In panel (B), RT-PCR analysis demonstrated that the expression of both genes was widespread. Included in the (+) lane are cDNA 21 and 44 as positive controls; the (-) lane represents the no-DNA control. Amplification using primers for the RFP gene (Isomura *et al.* Nucleic Acid Res. 20:5305-5310 (1992)) controlled for the integrity of the cDNA. All first strand cDNAs were checked for contaminating genomic DNA amplification by carrying out an identical experiment excluding the reverse transcriptase. In all cases, no amplification was obtained (data not shown).

Figure 5(A) depicts an alignment of the predicted amino acid sequence of the RoRet gene to the 52 kD Ro/SSA auto-antigen protein. The asterisks under the alignment represent conserved amino acids; the "dots" represent conserved amino acids substitutions. The putative DNA binding cysteine-rich domain and the B30-2 exon domain are boxed. Figure 5(B) depicts an alignment of the predicted amino acid sequence of the two novel putative sodium phosphate transport proteins to that of the NPT1.

Figure 6, panel (A) depicts a Northern blot analysis of the RoRet gene. The RoRet cDNA hybridized to 4 different transcripts, ranging from 7.1 kb to 2.2 kb. Autoradiography was performed for 4 days. The re-hybridization of the blot with a β -actin probe showed the variation in poly (A)+ RNA between the lanes. Autoradiography was for 1 hour. Panel (B) depicts RT-PCR analysis of the RoRet gene. Included in the (+) lane was a cDNA 27 positive control. Weak amplification of the correct size was observed in the small intestine, kidney and liver. The other tissues were negative as was the no DNA control lane (-). The RFP primers demonstrated the integrity of the cDNA. Panel (C) depicts Northern blot analysis of NPT3 and NPT4. NPT3 was expressed at high abundance in the heart and muscle as a single 7.2 kb transcript. Lesser amounts were found in the other tissues. The expression pattern of NPT4 was more restricted, being found only in the liver and kidney as a smear of transcripts ranging from 2.8 to 1.7 kb. Panel (D) depicts RT-PCR analysis of the NPT3 and NPT4 genes. Included in the (+) lane were the respective cDNA22E and 22B positive controls. The NPT3 gene was expressed as the proper size PCR fragment in kidney, liver, spleen and testis. A smaller fragment was detected in all tissues with the exception of the liver. The no DNA control lane (-) was negative. NPT4 was expressed as the proper size fragment in the small intestine, kidney, liver and testis. Larger and smaller size fragments were found in all other tissues with the exception of the brain. For both genes these different size fragments may indicate alternative splice events. The no DNA control lane (-) was negative. The RFP primers demonstrated the integrity of the cDNA.

Figure 7 depicts the sequences of cDNA 21 (BTF1), cDNA 29 (BTF3), cDNA 23 (BTF4), cDNA 44 (BTF5), cDNA 32 (BTF2), cDNA 27 (RoRet), cDNA 22B (NPT3), cDNA22E (NPT4).

Figure 8 depicts the nucleotide sequence of approximately 235 kb in the HFE subregion from an unaffected individual.

Figure 9 depicts the nucleotide sequence of approximately 235 kb in the HFE subregion from an HH affected individual. Polymorphic sites in the HH affected individual determined by comparing a sequence of the corresponding region from an HH unaffected individual are listed and described in Table I.

DETAILED DESCRIPTION

A. Definitions

Abbreviations for the twenty naturally occurring amino acids follow conventional usage. In the polypeptide notation used herein, the left-hand direction is the amino terminal direction and the right-hand direction is the carboxyl-terminal direction, in accordance with standard usage and convention. Similarly, unless specified otherwise, the left hand end of single-stranded polynucleotide sequences is the 5' end; the left hand direction of double-stranded polynucleotide sequences is referred to as the 5' direction. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are 5' to the 5' end of the RNA transcript are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are 3' to the 3' end of the RNA transcript are referred to as "downstream sequences".

The term "nucleic acids", as used herein, refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. It includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence.

"Nucleic acid probes" may be DNA or RNA fragments. DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR, or synthesized by either the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett. 22:1859-1862 (1981), or by the triester method according to Matteucci, *et al.*, J. Am. Chem. Soc. 103:3185 (1981), both incorporated herein by reference. A double stranded fragment may then be obtained, if desired, by annealing the chemically synthesized single strands together under appropriate conditions or by synthesizing the complementary strand using DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The phrase "selectively hybridizing to" refers to a nucleic acid probe that hybridizes, duplexes or binds only to a particular target DNA or RNA sequence when the target sequences are present in a preparation of total cellular DNA or RNA. "Complementary" or "target" nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe's length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For

discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook *et al.*, Molecular Cloning: a Laboratory Manual (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989) or Current Protocols in Molecular Biology, F. Ausubel *et al.*, ed. Greene Publishing and Wiley-Interscience, New York (1987).

5 The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein or peptide. The nucleic acid sequence includes both the DNA strand sequence that is transcribed into RNA and the sequence translated into protein. The nucleic acid sequences include both full length sequences derived from the full length sequence as well as non-full length sequences derived from the full length sequence that the sequence includes the degenerate codons of the native sequence be introduced to provide codon preference in a specific host cell.

10 The phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell.

15 The phrase "expression cassette" refers to nucleotide sequences which are capable of affecting expression of a structural gene in hosts compatible with such sequences. Such cassettes include at least promoters and optionally, transcription termination signals. Additional factors necessary or helpful in effecting expression may also be used as described herein.

20 The term "operably linked" as used herein refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence.

25 The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids. Where a recombinant microorganism or cell culture is described as hosting an "expression vector," this includes both extrachromosomal circular DNA and DNA that has been incorporated into the host chromosome(s). Where a vector is being maintained by a host cell, the vector may either be stably replicated by the cells during mitosis as an autonomous structure, or is incorporated within the host's genome.

30 The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, and termination regions. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

35 The term "plasmid" refers to an autonomous circular DNA molecule capable of replication in a cell, and includes both the expression and nonexpression types. Where a recombinant microorganism or cell culture is described as hosting an "expression plasmid", this includes both extrachromosomal circular DNA molecules and DNA that has been incorporated into the host chromosome(s). Where a plasmid is being maintained by a host cell, the plasmid is either being stably replicated by the cells during mitosis as an autonomous structure or is incorporated within the host's genome.

The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence.

Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 85:2444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

The terms "substantial identity" or "substantial sequence identity" as applied to nucleic acid sequences and as used herein and denote a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 85 percent sequence identity, preferably at least 90 to 95 percent sequence identity, and more preferably at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 20 nucleotide positions, frequently over a window of at least 25-50 nucleotides, wherein the percentage of sequence identity is calculated by comparing the reference sequence to the polynucleotide sequence which may include deletions or additions which total 20 percent or less of the reference sequence over the window of comparison. The reference sequence may be a subset of a larger sequence.

As applied to polypeptides, the terms "substantial identity" or "substantial sequence identity" mean that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 80 percent sequence identity, preferably at least 90 percent sequence identity, more preferably at least 95 percent sequence identity or more.

"Percentage amino acid identity" or "percentage amino acid sequence identity" refers to a comparison of the amino acids of two polypeptides which, when optimally aligned, have approximately the designated percentage of the same amino acids. For example, "95% amino acid identity" refers to a comparison of the amino acids of two polypeptides which when optimally aligned have 95% amino acid identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. For example, the substitution of amino acids having similar chemical properties such as charge or polarity are not likely to effect the properties of a protein. Examples include glutamine for asparagine or glutamic acid for aspartic acid.

The phrase "substantially purified" or "isolated" when referring to a peptide or protein, means a chemical composition which is essentially free of other cellular components. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein which is the predominant species present in a preparation is substantially purified. Generally, a substantially purified or isolated protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the protein is purified to represent greater than 90% of all macromolecular species present. More preferably the protein is purified to greater than 95%, and most preferably the protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional techniques.

The phrase "specifically binds to an antibody" or "specifically immunoreactive with", when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologies. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) Antibodies, a Laboratory Manual, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

As used herein, "EST" or "Expressed Sequence Tag" refers to a partial DNA or cDNA sequence of about 150 to 500, more preferably about 300, sequential nucleotides of a longer sequence obtained from a genomic or cDNA library prepared from a selected cell, cell type, tissue or tissue type, or organisms which longer sequence corresponds to an mRNA or a gene found in that library. An EST is generally DNA. One or more libraries made from a single tissue type typically provide at least 3000 different (i.e. unique) EST's and potentially the full complement of all possible EST's representing all possible cDNAs, e.g., 50,000 - 100,000 in an animal such as a human. (See, for example, Adams *et al.* Science 252:1651-1656 (1991)).

"Stringent" as used herein refers to hybridization and wash conditions of 50% formamide at 42°C. Other stringent hybridization conditions may also be selected. Generally, stringent conditions are selected to be about 5° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is at least about 0.02 molar at pH 7 and the temperature is at least about 60°C. As other factors may significantly affect the stringency of hybridization, including, among others, base composition and size of the complementary strands, the presence of organic solvents and the extent of base mismatching, the combination of parameters is more important than the absolute measure of any one.

B. Transcript Map and New Genes near HH

The instant invention provides a fine structure map of the 1 megabase region surrounding the HFE gene. As part of that map the instant invention provides approximately 250 kb of DNA sequence of which about 235 kb are provided in Figure 8 and eight loci of particular interest corresponding to candidate genes within the 1 megabase region. These loci are useful as genetic and physical markers for further mapping studies. Additionally, the eight cDNA sequences corresponding to those loci are useful, for example, for the isolation of other genes in putative gene families, the identification of homologs from other species, and as probes for diagnostic assays. In particular, isolated nucleic acid sequences of at least 18 nucleotides substantially identical to contiguous nucleotides of a cDNA of the invention are useful as PCR primers. Typically, the PCR primer will be used as part of a pair of primers in a PCR reaction. Isolated nucleic acid sequences preferably comprising about 18-100 nucleotides, more preferably at least 18 nucleotides, substantially identical to contiguous nucleotides in a cDNA of the invention are useful in the design of PCR primers and probes for hybridization assays. Additionally, the proteins encoded by those cDNAs are useful in the generation of antibodies for analysis of gene expression and in diagnostic assays, and in the purification of related proteins.

Thus, in one embodiment of the invention, a 235 kb sequence is provided for the HFE subregion within the 1 megabase region mapped. This sequence can serve as a reference in genetic or physical analysis of deletions, substitutions, and insertions in that region. Additionally, the sequence information provides a resource for the further identification of new genes in that region. Thus, nucleic acid sequences substantially identical to the 235 kb sequence are also included in the scope of this invention.

In a further embodiment of the invention, a family of five genes, BTF1-5, is provided which are related by sequence homology to the milk protein butyrophilin (BT) (Figures 1, 3, and 7). The predicted amino acid sequences of the proteins encoded by these genes are provided in Figure 3. These cDNAs are useful for the identification of further members of the BT family and to study regulation of expression of this family of genes. The proteins encoded by these cDNAs can be useful in the identification and isolation of ligands for the BT protein, and in the generation of agonists or antagonists of BT function. Nucleic acid sequences substantially identical to BTF1-5 and the proteins encoded by them are also included in the scope of this invention, including allelic forms.

In a further embodiment of the invention, a novel gene RoRet is provided, which is related by sequence homology to the 52 kD Ro/SSA Lupus and Sjogren's syndrome autoantigen. This sequence is especially useful in the identification of other genes that may be involved in Lupus or Sjogren's syndrome. The protein encoded by this cDNA can be useful in the identification and isolation of ligands for the autoantigen, and in the generation of agonists or antagonists of the antigen. Nucleic acid sequences substantially identical to RoRet and the proteins encoded by them are also included in the scope of this invention.

In a further embodiment of the invention, two genes, NPT3 and NPT4, with structural homology to a type 1 sodium transport gene are provided. These cDNAs and the proteins expressed by them are useful in determining the etiology of hypophosphatemia, along with being useful as probes

in the identification and isolation of further members of the gene family. Nucleic acid sequences substantially identically to the NPT1-like sequences and the proteins encoded by them are also included in the scope of this invention.

C. Polymorphic Markers

The invention provides 397 new polymorphic sites in the region of the HFE gene. These polymorphisms are listed in Table 1. As described below, these polymorphisms were identified by comparison of the DNA sequence of an affected individual homozygous for the common ancestral HH mutation with that of an unaffected individual disclosed in copending U.S. 08/724,394.

Table 1. Polymorphic Sites in the HH Region

Base Location	Difference	Base Location	Difference
35-36	AC DEL	19755	G-A
841	T-C	19949	C-T
2662-2663	TT DEL	20085	C-T
3767	T-C	20366-20367	A INS
3829	C-G	20463	C-A
4925-4928	TAAA DEL	20841	A-T
5691	C-T	21059	A-T
5839	T-C	21117	A-G
6011	G-A	21837	A-C
6047	C-G	22293	A-C
6231	G-A	22786	C-A
6643	A DEL	23009	G-A
6698	T-C	24143	T-A
7186	T-C	26175	G-C
7273	G-A	26667	C-A
7545-7558	TCACACACCGATTGG DEL	26994	T-C
7672	G DEL	27838	G-T
7933	T-C	27861	T DEL
8746	T-G	28132	G-A
9115	G-A	29100	G-A
9823	G-A	29454-29457	TTTT DEL
10027	G-A	29787	T-G
10214	C-T	29825	A-C
10828	A-G	30009	T-C
10918	C-G	30177	A-G
10955	A-G	30400	A-G
11524	C-A	31059	T-A
11674	A-G	31280	C-T
11955	T-C	31749	C-T
12173-12175	TTT DEL	32040	C-G
13304	G-A	32556-32559	TGTG DEL
13455	G-A	33017	T-G
14416-14417	A INS	33026	T DEL
14998	C-T	34434	C-T
15564	T-C	35179	A-C
15887	A-G	35695	G-A
15904-15919	CCAACTGATCTTTGA DEL	35702	G-A
16019	T DEL	35983	A-G
16211	A-T	37411	A-G
17461	A-G	38526	C-T

	Base Location	Difference	Base Location	Difference
	40431	C-A	72688	C-G
	42054-42055	TT DEL	75323-75324	T INS
	43783-43784	TTTT INS	75887	G-C
5	45120	C DEL	77519	T-C
	45567	A-C	77749	G-A
	46601	A-T	77908	T-C
	47255	C-G	78385	C-G
	47758	C-A	78592-78593	AG INS
	47994	G-C	80189	T-G
10	48440	G-A	80279	T DEL
	48650	T-G	80989-80990	A INS
	48680	A-G	81193	T-C
	50240	C-T	81273	A DEL
	50553	G-A	82166	G-A
15	50586	G-T	83847	T DEL
	51322	G-C	84161-84162	CA-GG
	51747	A-G	84533	A-G
	52474	C-G	84638	T-G
	52733	C-A	85526	T-G
20	52875	G-A	85705	G-T
	53631-53637	TTTTTTT DEL	86984	T-C
	53707	G-A	87655	T-C
	54819	A-G	87713	A-C
	55913	T-C	87892	C-T
25	56225	A-C	88192	T DEL
	56510	T-C	88528	A-G
	56566	G-A	89645	A-T
	56618	A-T	89728	A-G
	57815	A-G	90088	T-C
30	58011	T DEL	91193-91194	2209bp INS
	58247-58248	T INS	91373	T-C
	58926	C-G	91433-91434	A INS
	59406	C-G	91747	G-A
	59422	G-C	93625	T DEL
35	60221-60222	A INS	95116-95117	T INS
	60656-60657	CA DEL	96315	G-A
	61162	G-A	97981	A-G
	61465	G-A	98351	T DEL
	61607	A DEL	99249	C-T
40	61653	T-C	100094-100095	T INS
	61794-61795	T INS	100647-100648	TTC INS
	62061	G-C	100951	C-T
	62362	T-G	101610	C-G
	62732	C-G	102589	C-T
45	63364	G-A	103076-103077	TATATATATATA INS
	63430-63431	GT INS	103747	T-C
	63754	C-T	105638	A-C
	63785	A-C	107024	C-T
	63870-63871	A INS	107322	C-T
50	64788	A-G	107858	C-G
	64962	G-A	109019	A DEL
	65891	C-T	109579	T DEL
	66675	G-C	110021	C-A
	67186-67187	ATT INS	111251	C-A
55	67746-67747	TT INS	111425	G-A
	68259	T-C	112644	T-A
	68836	T-C	113001	G-C
	68976	C-G	113130	C-T
	72508	T-G	114026	G-A

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	Base Location	Difference	Base Location	Difference
	114250	A DEL	176222	T-C
	115217	C-G	176524	A-T
	117995	G-A	176684	G-A
5	118874	A-G	176815	T-C
	119470	T-C	177049	T-C
	119646	G-T	177065	G-T
	120853	C-T	178285	T-C
	121582	G-A	178551-178552	CTTTTTTTTTTTT INS
10	123576	A-C	179114-179115	A INS
	125581	C-T	179260	C-G
	125970	G-T	179281	C-G
	126197	A-G	180023	G-C
	126672	A DEL	180430	T-C
	126672	G-C	180773	T-C
15	128220-128221	A INS	180824	T-C
	132569	C-T	181097	C-T
	133572	A-C	181183	A-T
	134064	T-G	182351	C-T
	136999	G-A	183197	G-A
20	137784	C-T	183623	A-T
	138903	G-A	183653	G-T
	139159-139160	A INS	183657	T-G
	140359	G-A	183795-183796	A INS
	140898	C-T	184060	G-A
25	141313	C DEL	184993	G-A
	141343	T-C	185918	A-G
	142148	T-C	186036	T-C
	142178	C-A	186506-186507	TAAC INS
	142433-142434	ATAGA INS	186561-186568	TATTTATT DEL
30	143783	C-T	186690	G DEL
	144090	C-T	186751	T-A
	144220-144221	A INS	187221	A-G
	144725	A-C	187260	A-G
	145732-145733	AAAAAAAAAAAAA INS	187444-187447	CTCT DEL
35	147016-147017	CG DEL	187831-187832	C INS
	147021	G-T	188638	G-A
	147536	T-G	188642	C-T
	148936	T-A	189246	T-C
	149061	T-C	190340	A-C
40	154341	A-T	190354	A-G
	154588	G-A	190762	A-G
	155464	G-A	191260	G-T
	158574	C-G	193018-193019	AGAT INS
	160007	C-T	193147	T-G
45	164348	A-T	193196-193197	C INS
	164499	C-G	193499	C-T
	166677-166678	AAAG INS	193738	C-G
	167389	G-A	193984-193985	ACACACAC INS
	168506-168507	AGGATGGTCT INS	194064	C-G
50	168515	T-C	194504	A DEL
	169413-169414	AA INS	194734	G-A
	170300-170301	TTGTTGTTGTTG INS	194890	A-C
	170491	G-A	195404	G-A
	173428	T-C	195693	A-T
55	173642	G-A	196205	G-A
	173948	T-G	197424	C-T
	175330	T-C	197513	C-T
	175836	T-C	197670	G-A
	176200	G-C	198055	C-A

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Base Location	Difference	Base Location	Difference
198401	C-T	215947	C-A
198692	A-G	216232	A-G
198780	T DEL	217478	G-A
199030	T-G	219052	T-C
199933	C-T	219082-219083	ATATATATATATATATAT INS
200027	G-A	219314	C-A
200439	T-A	219327	G-A
200452	A-G	219560	C-T
200472-200483	AATAATAATAAT DEL	219660	C-T
200559	A-T	219889	G-A
200745	A-G	220198	G-T
200919	T-A	220384	G-A
201816	C-T	220451-220452	CAAAAA INS
201861-201862	42bp INS	221363	G-A
202682	T-C	221645	G-A
202880	T-C	222119	T-C
204341	C-T	222358	A-G
204768	A-T	222367	A-C
205284	T-G	222686	A-G
207400	C-A	222959	T-C
208634	T-C	223270-223271	TT DEL
208718	T DEL	223283	T-C
208862	A-C	224964	T-C
209419-209420	TT DEL	225232	A-C
209802	G-A	225366-225367	TTTT INS
209944	C-G	225416	G-C
210299	A-G	225486	T-C
211142	G-A	226088	A-G
212072	G-A	228421	A-G
212146	T-C	230047	G-A
212379	G-A	230109	G-C
212637-212639	TCT DEL	230376	C-G
212696	T-C	230394	A-G
213042	T-A	231226	A-G
214182	A-G	231447	G-A
214529-214530	TTTTTTTTTTT INS	231835	A-G
214549	T-C	232400-232402	AAA DEL
214795	C-T	232402-232403	G INS
214908	T-G	232515	T-C
214977	A-G	232703	G-T
215769	C-T	232750	A-G

* D6S2238 occurs at base 1. 24d1 occurs at base 41316. D6S2239 occurs at base 84841. D6S2241 occurs at base 235032

Table 2. Polymorphic Allele Frequencies

Location	Frequency of ancestral variant in random chromosomes	Frequency of unaffected variant in random chromosomes
232703	53%	47%
231835	53%	47%
230394	85%	15%
230376	25%	75%
230109	53%	47%
225486	45%	55%
225416	75%	25%
220198	43%	57%
219660	58%	42%

	Location	Frequency of ancestral variant in random chromosomes	Frequency of unaffected variant in random chromosomes
	219560	53%	47%
	214977	65%	35%
	214908	50%	50%
	214795	24%	76%
5	214549	53%	47%
	214192	65%	35%
	210299	53%	47%
	208862	80%	20%
	208634	48%	52%
10	207400	25%	75%
	205284	50%	50%
	204341	53%	47%
	202880	58%	42%
	202662	98%	2%
15	200027	25%	75%
	199030	58%	42%
	198692	55%	45%
	198401	55%	45%
	198055	55%	45%
20	195693	60%	40%
	195404	25%	75%
	194890	55%	45%
	175330	53%	47%
	173948	83%	17%
25	173642	55%	45%
	173428	80%	20%
	168515	80%	20%
	160007	18%	82%
	149061	58%	42%
30	148936	82%	18%
	147536	100%	0%
	147021	46%	54%
	141343	55%	45%
	140359	55%	45%
35	138903	55%	45%
	132569	81%	19%
	125581	18%	82%
	121582	80%	20%
	120853	18%	82%
40	118874	85%	15%
	115217	50%	50%
	113130	40%	60%
	113001	48%	52%
	107858	48%	52%
45	103747	50%	50%
	96315	25%	75%
	91194	80%	20%
	90088	75%	25%
	89728	50%	50%
50	89845	50%	50%
	88528	63%	37%
	87892	75%	25%
	87713	60%	40%
	87655	50%	50%
55	86984	79%	21%
	85705	50%	50%
	85526	50%	50%

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Location	Frequency of ancestral variant in random chromosomes	Frequency of unaffected variant in random chromosomes
84638	50%	50%
84533	50%	50%
82166	78%	22%
81193	58%	42%
80189	50%	50%
78385	80%	20%
77908	88%	12%
68976	50%	50%
68259	51%	49%
66675	80%	20%
62732	50%	50%
62362	40%	60%
61653	48%	52%
61465	5%	95%
61162	60%	40%
53707	100%	0%
52875	50%	50%
52733	74%	26%
52474	47%	53%
50588	50%	50%
50553	50%	50%
50240	50%	50%
48680	53%	47%
48650	63%	37%
48440	50%	50%
47255	50%	50%
46601	53%	47%
45567	49%	51%
41316	5%	95%
40431	20%	80%
38526	23%	77%
37411	70%	30%
35983	5%	95%

These polymorphisms provide surrogate markers for use in diagnostic assays to detect the likely presence of the mutations 24d1 and/or 24d2, in preferably 24d1, in homozygotes or heterozygotes. Thus, for example, DNA or RNA from an individual is assessed for the presence or absence of a genotype defined by a polymorphic allele of Table 1, wherein, as a result, the absence of a genotype defined by a polymorphic allele of Table 1 indicates the likely absence of the HFE gene mutation in the genome of the individual and the presence of the genotype indicates the likely presence of the HFE gene mutation in the genome of the individual.

These markers may be used singly, in combination with each other, or with other polymorphic markers (such as those disclosed in co-pending PCT application WO 96/06583) in diagnostic assays for the likely presence of the HFE gene mutation in an individual. For example, any of the markers defined by the polymorphic sites of Table 1 can be used in diagnostic assays in combination with 24d1 or 24d2, or at least one of polymorphisms HHP-1, HHP-19, or HHP-29, or microsatellite repeat alleles 19D9:205; 18B4:235; 1A2:239; 1E4:271; 24E2:245; 2B8:206; 3321-1:98; 4073-1:182; 4440-1:180; 4440-2:139; 731-1:177; 5091-1:148; 3216-1:221; 4072-2:170; 950-1:142; 950-2:164; 950-3:165; 950-4:128; 950-6:151; 950-8:137; 63-1:151; 63-2:113; 63-3:169; 65-1:206; 65-

2:159; 68-1:167; 241-5:108; 241-29:113; 373-8:151; and 373-29:113, D6S258:199, D6S265:122, D6S105:124; D6S306:238; D6S464:206; and D6S1001:180.

Table 2 lists the frequency of about 100 of the alleles defined by the polymorphic sites of the invention in the general population. As is evident from the Table, certain of these alleles are present rarely in the general population. These polymorphisms are thus preferred as surrogate markers in diagnostic assays for the presence of a mutant HFE allele ("gene mutation") such as 24d1 or 24d2. Preferably, the frequency of the polymorphic allele used in the diagnostic assay in the general population is less than about 50%, more preferably less than about 25%, and most preferably less than about 5%. Thus, of the genotypes defined by the alleles listed in Table 2, polymorphisms occurring at base 35983 and base 61465 of Figure 1 are preferred.

It will be understood by those of skill in the art that because they were identified in an ancestral HH homozygote, the haplotypes defined by the polymorphic sites of Table 1 are predictive of the likely presence of the HFE gene mutation 24d1. Thus, for example, the likelihood of any affected individual having at least two or more of any of the polymorphic alleles defined by Table 1 is greater than that for any unaffected individual. Similarly, the likelihood of any affected individual having at least three or more of any of the polymorphic alleles defined by Table 1 is greater than that for any unaffected individual.

Thus, for example, in a diagnostic assay for the likely presence of the HFE gene mutation in the genome of the individual, DNA or RNA from the individual is assessed for the presence or absence of a haplotype of Table 1, wherein, as a result, the absence of a haplotype of Table 1 indicates the likely absence of the HFE gene mutation in the genome of the individual and the presence of the haplotype indicates the likely presence of the HFE gene mutation in the genome of the individual.

The markers defined by the polymorphic sites of Table 1 are additionally useful as markers for genetic analysis of the inheritance of certain HFE alleles and other genes which occur within the chromosomal region corresponding to the sequence of Figure 9 which include, for example, those disclosed in copending U.S.S.N. 08/724,394.

As the entire nucleotide sequence of the region is provided in Figure 9, it will be evident to those of ordinary skill in the art which sequences to use as primers or probes for detecting each polymorphism of interest. Thus, in some embodiments of the invention, the nucleotide sequences of the invention include at least one oligonucleotide pair selected from the sequence of Figure 9 or its complement for amplification of a polymorphic site of Table 1. Furthermore, in some embodiments of the invention a preferred hybridization probe is an oligonucleotide comprising at least 8 to about 100 consecutive bases from the sequence of Figure 9, or the complement of the sequence, wherein the at least 8 to about 100 consecutive bases includes at least one polymorphic site of Table 1. In some embodiments the polymorphic site is at base 35983 or base 61465.

It will also be appreciated that the nucleic acid sequences of the invention include isolated nucleic acid molecules comprising about 100 consecutive bases to about 235 kb substantially identical to the sequence of Figure 9, wherein the DNA molecule comprises at least one polymorphic

site of Table 1. Such isolated DNA sequences are useful as primers, probes, or as the component of a kit in diagnostic assays for detecting the likely presence of the HFE gene mutation in an individual.

D. Nucleic Acid Based Screening

Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. The genomic DNA used for the diagnosis may be obtained from body cells, such as those present in peripheral blood, urine, saliva, bucca, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically *in vitro* through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other *in vitro* amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods Appl. 1:25-33 (1992)), prior to mutation analysis. The methodology for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art.

The detection of polymorphisms in specific DNA sequences, such as in the region of the HFE gene, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl Acids Res 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. U.S.A. 86:6230-6234 (1989)) or oligonucleotide arrays (Maskos and Southern Nucl Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995)), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. Proc. Natl. Acad. Sci. U.S.A. 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. Acad. Sci. U.S.A. 85:4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvänen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. Nucl Acids Res 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-193 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., Nucl. Acids Res. 21:5332-5356 (1993); Thiede et al., Nucl. Acids Res. 24:983-984 (1996)).

In addition to the genotypes defined by the polymorphisms of the invention, as described in co-pending PCT application WO 96/35802 published November 14, 1996, genotypes characterized by the presence of the alleles 19D9:205; 18B4:235; 1A2:239; 1E4:271; 24E2:245; 2B8:206; 3321-1:98 (denoted 3321-1:197 therein); 4073-1:182; 4440-1:180; 4440-2:139; 731-1:177; 5091-1:148; 3216-1:221; 4072-2:170 (denoted 4072-2:148 therein); 950-1:142; 950-2:164; 950-3:165; 950-4:128; 950-6:151; 950-8:137; 83-1:151; 63-2:113; 63-3:169; 65-1:206; 65-2:159; 68-1:167; 241-

5:108; 241-29:113; 373-8:151; and 373-29:113, alleles D6S258:199, D6S265:122, D6S105:124, D6S306:238, D6S464:206; and D6S1001:180, and/or alleles associates with the HHP-1, the HHP-19 or HHP-29 single base-pair polymorphisms can also be used to assist in the identification of an individual whose genome contains 24d1 and/or 24d2. For example, the assessing step can be performed by a process which comprises subjecting the DNA or RNA to amplification using oligonucleotide primers flanking a polymorphism of Table 1, and oligonucleotides flanking 24d1 and/or 24d2, oligonucleotide primers flanking at least one of the base-pair polymorphisms HHP-1, HHP-19, and HHP-29, oligonucleotide primers flanking at least one of the microsatellite repeat alleles, or oligonucleotide primers for any combination of polymorphisms or microsatellite repeat alleles thereof.

Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides. Such oligonucleotides can be derived from either the genomic DNA of Figure 8 or 9, or cDNA sequences derived therefrom, or may be synthesized.

Additionally, the proteins encoded by such cDNAs are useful in the generation of antibodies for analysis of gene expression and in diagnostic assays, and in the purification of related proteins.

E. General Methods

The nucleic acid compositions of this invention, whether RNA, cDNA, genomic DNA, or a hybrid of the various combinations, may be isolated from natural sources, including cloned DNA, or may be synthesized *in vitro*. The nucleic acids claimed may be present in transformed or transfected whole cells, in a transformed or transfected cell lysate, or in a partially purified or substantially pure form.

Techniques for nucleic acid manipulation of the nucleic acid sequences of the invention such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like are described generally in Sambrook *et al.*, Molecular Cloning - a Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook *et al.*"

There are various methods of isolating the nucleic acid sequences of the invention. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences complementary to the sequences disclosed herein. Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known. See Gubler, U. and Hoffman, B.J. Gene 25:263-269 (1983) and Sambrook *et al.*

For a genomic library, for example, the DNA is extracted from tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments

are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, *et al.* Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, Science 196:180-182 (1977). Colony hybridization is carried out as generally described in
5 M. Grunstein *et al.* Proc. Natl. Acad. Sci. USA, 72:3961-3965 (1975).

DNA of interest is identified in either cDNA or genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, *et al.*

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of
10 the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired.

15 PCR can be used in a variety of protocols to isolate cDNA's encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from sequence obtained.

20 Oligonucleotides for use as primers or probes are chemically synthesized according to the solid phase phosphoramidite triester method first described by Beaucage, S.L. and Carruthers, M.H., Tetrahedron Lett., 22(20):1859-1862 (1981) using an automated synthesizer, as described in Needham-VanDevanter, D.R., *et al.*, Nucleic Acids Res., 12:6159-6168 (1984). Purification of oligonucleotides is by either native acrylamide gel electrophoresis or by anion-exchange HPLC as
25 described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). The sequence of the synthetic oligonucleotide can be verified using the chemical degradation method of Maxam, A.M. and Gilbert, W., in Grossman, L. and Moldave, D., eds. Academic Press, New York, Methods in Enzymology 65:499-560 (1980).

1. Expression

30 Once DNA encoding a sequence of interest is isolated and cloned, one can express the encoded proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

35 In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain transcription and translation terminators, initiation sequences, and
40 promoters useful for regulation of the expression of polynucleotide sequence of interest. To obtain

high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, *i.e.*, shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook *et al.* Examples of expression of ATP-sensitive potassium channel proteins in both prokaryotic and eukaryotic systems are described below.

a. Expression in Prokaryotes

A variety of procaryotic expression systems may be used to express the proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacteriol. 158:1018-1024 (1984) and the leftward promoter of phage lambda (P_{λ}) as described by Herskowitz, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol. See Sambrook *et al.* for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503.

Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

b. Expression in Eukaryotes

A variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, are known to those of skill in the art. As explained briefly below, a sequence of interest may be expressed in these eukaryotic systems.

Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., *et al.*, Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast.

Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, *et al.*, Gene 8:17-24 (1979); Broach, *et al.*, Gene 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glucylase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, *Nature* (London) 275:104-109 (1978); and Hinnen, a., *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., *et al.*, *J. Bact.* 153:163-168 (1983)).

The proteins of the invention, once expressed, can be isolated from yeast by lysing the cells and applying standard protein isolation techniques to the lysates. The monitoring of the purification process can be accomplished by using Western blot techniques or radioimmunoassay or other standard immunoassay techniques.

The sequences encoding the proteins of the invention can also be ligated to various expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen *et al.* *Immunol. Rev.* 89:49 (1986)), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences. Other animal cells useful for production of ATP-sensitive potassium channel proteins are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)).

Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from the SF9 baculovirus. Suitable insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider *J. Embryol. Exp. Morphol.* 27:353-365 (1987)).

As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences.

As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 Intron from SV40 (Sprague, J. *et al.*, *J. Virol.* 45: 773-781 (1983)).

Additionally, gene sequences to control replication in the host cell may be incorporated into the vector such as those found in bovine papilloma virus type-vectors.

Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238.

The host cells are competent or rendered competent for transformation by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

2. Purification

The proteins produced by recombinant DNA technology may be purified by standard techniques well known to those of skill in the art. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide.

The polypeptides of this invention may be purified to substantial purity by standard techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, Protein Purification: Principles and Practice, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

3. Antibodies

As mentioned above, antibodies can also be used for the screening of polypeptide products encoded by the polymorphic nucleic acids of the invention. In addition, antibodies are useful in a variety of other contexts in accordance with the present invention. Such antibodies can be utilized for the diagnosis of HH and, in certain applications, targeting of affected tissues.

Thus, in accordance with another aspect of the present invention a kit is provided that is suitable for use in screening and assaying for the presence of polypeptide products encoded by the polymorphic nucleic acids of the invention by an immunoassay through use of an antibody which specifically binds to polypeptide products encoded by the polymorphic nucleic acids of the invention in combination with a reagent for detecting the binding of the antibody to the gene product.

Once hybridoma cell lines are prepared, monoclonal antibodies can be made through conventional techniques of priming mice with pristane and interperitoneally injecting such mice with the hybrid cells to enable harvesting of the monoclonal antibodies from ascites fluid.

In connection with synthetic and semi-synthetic antibodies, such terms are intended to cover antibody fragments, isotype switched antibodies, humanized antibodies (mouse-human, human-

mouse, and the like), hybrids, antibodies having plural specificities, fully synthetic antibody-like molecules, and the like.

This invention also embraces diagnostic kits for detecting DNA or RNA comprising a polymorphism of Table 1 in tissue or blood samples which comprise nucleic acid probes as described herein and instructional material. The kit may also contain additional components such as labeled compounds, as described herein, for identification of duplexed nucleic acids.

The following examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims.

10 F. EXPERIMENTAL EXAMPLES

1. Megabase transcript map

In these studies direct selection, exon-trapping, and genomic sample sequencing were used to generate a transcript map of a 1 megabase region approximately 8.5 megabases telomeric to HLA-A in the vicinity of HFE. This region 6p21.3 was flanked by the genetic markers D6S2242 and D6S2241. The starting material for these experiments was a 1 megabase YAC labeled y899g1 and a bacterial clone contig of this region (Feder *et al.* Nature Genetics 13:399-408 (1996)). These techniques and other methods used in the study are outlined below.

a. Direct Selection (DS)

Poly A⁺ RNA from human fetal brain, liver and small intestine (Clontech, Palo Alto, CA) were converted into cDNA using random primers and a Superscript cDNA synthesis kit (Life Technologies, Gaithersburg, MD). The cDNA was digested with Mbo I and ligated to cDNA Mbo I linker-adaptors. Unligated linker-adaptor were removed by passage through cDNA spun columns (Pharmacia, Piscataway, NJ). The 5 ng of each of the ligated cDNAs were amplified using the cDNA Mbo I-S primer (5'-CCTGATGCTCGAGTGAATTC-3'). The amplified products were purified on S-400 spin columns (Pharmacia, Piscataway, NJ), ethanol precipitated and resuspended at 1mg/ml in TE. Gel-purified yac899g1 (Centre d'Etude du Polymorphisme Humain) was processed as described by Morgan *et al.* (Nucl. Acids Res. 20:5173-5179 (1992)). The cDNAs were mixed in equal molar amounts for a total of 3 mg, and blocked with a mixture of 4 mg Cot-1 DNA (Life Technologies, Gaithersburg, MD), and a cocktail of Sau 3A-digested ribosomal and five different histone DNAs. The blocked cDNAs were hybridized to biotinylated yac899g1 DNA and streptavidin capture was carried out as described by Morgan *et al.* (*ibid*). After the second round of selection, the eluted cDNAs were amplified using the cDNA Mbo I-S primer which included a (CUA)₄ repeat at the 5' end to facilitate cloning into a version of pSP72 (Promega, Madison, WI) constructed for use with uracil-DNA glycosylase cloning (UDG, Life Technologies, Gaithersburg, MD). Recombinants were transformed in DH5 α , 1000 clones picked into a 96 well format, and clones prepped for DNA sequencing using AGTC boiling 96-well mini-prep system (Advance Genetic Technologies, Gaithersburg, MD).

Four hundred and sixty five clones were sequenced and the resulting data searched by BLAST (Altschul *et al.* J. Mol. Biol. 215:403-410 (1990)). Those clones representing repetitive, bacterial, yeast, mitochondrial and histone sequences were eliminated from future considerations. The remaining sequences were then searched for overlaps and assembled into 108 unique DS contigs.

The number of clones per DS contig varied between 1 to 22 with the length of each contig ranging from 250bp to 850 bp. Small sequence-tag-sites PCR assays were developed for each DS contig and two experiments were carried out concomitantly; mapping each DS contig back to the bacterial clone contig of the region and testing for the presence of each DS contig in cDNA libraries. Overall, 86 or 80% of the DS contigs mapped back to the region and were found to be in cDNA libraries. The number of 80% mapping to the region was probably an underestimate of the fidelity of the direct-selection since PCR assays which cross exon-intron boundaries would be expected to fail or give larger size products, thereby being scored negative.

b. Exon-Trapping

CsCl-purified genomic P1 (Genome Systems), BAC (Research Genetics) and PAC (Genome Systems) DNAs were digested with BamHI, Bgl II, Pst I Sac I and Xho I and 125 ng of each digest ligated into 500 ng pSPL3 (Church *et al.* Nature Genetics 6:98-105 (1994)) (Life Technologies, Gaithersburg, MD) digested with the appropriate restriction enzyme and phosphatased with calf intestinal alkaline phosphatase (USB, Cleveland, OH). One tenth of the ligation was used to transform XL1-Blue MRF⁺ cells (Stratagene, La Jolla, CA) by electroporation. Nine tenths of the electroporation was used to inoculate 10 ml of LB + 100µg/ml of carbenicillin and after overnight growth, DNA was prepared using Qiagen Q-20 tips (Qiagen GmbH, Hilden Germany). The remaining one tenth was plated on LB + 100 µg/ml carbenicillin plates to evaluate the efficiency on cloning and to test individual clones for the presence of single inserts. COS-7 cells were seeded overnight at a density of 1.4×10^5 /well in 6 well dishes. One µg of DNA was transfected using 6ml of Lipofect-Ace. Cytoplasmic RNA was isolated 48 hr post-transfection. RT-PCR was carried out as described by Church *et al.* (*ibid*) using commercially available reagents Life Technologies, Gaithersburg, MD). The resulting CUA-tailed PCR fragments for each restriction digested bacterial clone were pooled and UDG cloned into pSP72-U (a derivative of pSP72). The DNA was transformed in DH5α and the cells plated onto nylon membranes. After overnight growth, duplicates were made and the DNA hybridized to ³²P end-labeled oligos designed to detect various background products associated with the pSPL3 vector. One set of filters was hybridized with the following gel-purified oligos in 6X SSC aqueous hybridization solution at 42° C:

vector-vector splicing	5'-CGACCCAGCAACCTGGAGAT-3'
cryptic donor-1021	5'-AGCTCGAGCGGCCGCTGCAG-3'
cryptic donor-1134	5'-AGACCCCAACCCACAAGAAG-3'

The filters were washed twice in 6X SSC, 10 mM sodium pyrophosphate (NaPPi) at 60°C, 30 mins.

After overnight autoradiography, non-hybridizing clones were picked and grown in 250 µl of LB + 100µg/ml of carbenicillin in 96 well mini-rack tubes. The samples were analyzed by PCR using the secondary PCR primers supplied in the kit (Life Technologies, Gaithersburg, MD) and those clones with inserts greater than 200 bp were selected for sequencing.

Ninety-six exon traps per bacterial clone were sequenced for a total of 768 reactions and the resulting data analyzed by BLAST. In addition, each potential exon was searched against a database of the 86 DS contigs to eliminate redundant sequences. PCR assays were developed for

each of the potential exons and they were tested for their presence in cDNA libraries. A total of 48 potential exons remained after these screening steps.

c. Sample Sequencing

A minimal set of bacterial clones chosen to cover y899g1 were prepped with the Qiagen Maxi-Prep system and purified on CsCl. Ten micrograms of DNA from each bacterial clone was sonicated in a Heat Systems Sonicator XL and end-repaired with Klenow (USB) and T4 polymerase (USB). The sheared fragments were size selected between three to four kilobases on a 0.7% agarose gel and then ligated to BstXI linkers (Invitrogen). The ligations were gel purified on a 0.7% agarose gel and cloned into a pSP72 derivative plasmid vector. The resulting plasmids were transformed into electrocompetent DH5 α cells and plated on LB-carbenicillin plates. A sufficient number of colonies was picked to achieve 15-fold clone coverage. The appropriate number of colonies was calculated by the following equation to generate a single-fold sequence coverage: Number of colonies = size of bacterial clone (in kb)/average sequence read length (0.4 kb). These colonies were prepped in the 96-well AGCT system and end-sequenced with oligo MAP1 using standard ABI Dye Terminator protocols. MAP1 was CGTTAGAACGCGGCTACAAT. The MAP1 sequences were screened locally with the BLAST algorithm against all available public databases. All sequence identities were catalogued and cross referenced to the DS and exon-trapped databases.

A total of 3794 end sequence reactions were run to achieve the theoretical 1X coverage. Eighty-five percent of these sequences contained non-bacterial non-vector inserts. An additional 1060 end sequence reactions were run from the opposite end of the cloning vector to augment the sequence coverage and to prepare for contigging across selected regions. BLAST searches to all publicly available databases identified 12 histone genes and 74 unique expressed sequence fragments (ESF). The ESF represent a collection of ESTs and other expressed sequence fragments that were selected due to their sequence identity over a significant portion of genomic DNA. The ESF were cross referenced against the DS and exon-trapped databases to eliminate redundancies. 58 unique ESF remained, representing 39 distinct clones. Included in these ESF are 5 sequences homologous to histone genes.

Table 3. EST's found by Sample Sequencing Large Insert Bacterial Clones

Clone name	Bacterial clone	Homology 5' blastx	Homology 3' blastx	Poly A + signal ¹	Genomic poly (A) _{cat}	cDNA Homology
EST03556	pc157c3	na ²	none ³	+	-	cDNA 28
ym33f11	pc157c3	ZNF	na	na	na	
EST04698	pc157c3	na	NSH ⁴	+	-	
EST04812	pc157c3	na	NSH	-	-	
yb89b08	pc157c3	NSH	na	na	na	
yd88g11	pc157c3	na	nsh	+	-	
yj49b01	pc157c3	NSH	na	na	na	
yv81d05	pc157c3	HG17 Human	NSH	+	-	cDNA 30
yg57h09	p196e20	BUTYBOVIN	NSH	+	-	cDNA 21
yq23d08	p196e20	BUTYBOVIN	NSH	+	-	cDNA 21

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30	Clone name	Bacterial clone	Homology 5' blastx	Homology 3' blastx	Poly A+ signal ¹	Genomic poly (A) _{on}	cDNA Homology
	yo65f06	p196e20	NSH	na	na	na	cDNA 29
	yv88c09	p196e20	BUTYBOVIN	na	na	na	cDNA 29
	yd17d06	p196e20	NSH	na	na	na	cDNA 23
	ye25g03	p196e20	BUTYBOVIN	NSH	na	na	cDNA 44
5	ys04h08	pc45p21	NSH	NSH	+	-	cDNA 44
	yn01c05	p196e20	BUTYBOVIN	na	na	na	cDNA 32
	YG78F10	PC45P21	NSH	NSH	na	na	
	yh54f11	p196e20	none	NSH	-	-	
	ys05b08	pc157c3	NSH	Alu	-	+	
10	yb12h11	b132a12	NSH	Histone H3.1	-	-	
	HSC2EE082	b132a12	na	NSH	+	-	
	HUM160h11b	b132a12	none	na	na	na	
	yg04f09	b132b12	Line element	Alu	-	+	
	yd37d11	b132a12	NSH	Alu	-	+	
15	ym29g03	b132a12	Histone H2A	NSH	+	-	cDNA 37
	yi77b02	b132a12	NSH	NSH	-	-	cDNA 37
	yh76b05	b132a12	NSH	Alu	-	-	
	yu98e02	b132a12	NSH	Alue	-	+	
	yd72h12	b132a12	Alu	NSH	+	+	
20	yd19d03	pc222k22	Histone H2B.1	NSH	+	-	
	ye98g01	b132a12	NSH	NSH	+	-	cDNA
	yi61f07	b132a12	NSH	NSH	-	+	
	ESTO5340	b3e17	na	Alu	-	+	
	yd35d05	pc222k22	NSH	NSH	-	+	
25	yc52a05	pc75L14	NSH	na	na	na	
	yd84a05	pc75L14	none	none	-	? ⁵	
	yr42a05	pc75L14	NaPi transport	none	+	-	cDNA 22B
	yd83h08	b20h20	NSH	none	+	-	
	ye38c09	b20h20	NSH	Alu	-	+	
30	yp74c05	b20h20	NaPi transport	Alu	? ⁶	na	

Bracketed area is the critical region

1	Signal of ATAAA or ATTAA	4	No Significant Homologies
2	Not available	5	3' splice that is not on contig
35	3 "NONE" reported by blast	6	Poor EST sequence

d. cDNA library screening

Superscript plasmid cDNA libraries, brain, liver and testis, were purchased from Life Technologies, Gaithersburg, MD. Colonies were plated on Hybond N filters (Amersham) using

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standard techniques. Insert probes from DS, exons and EST (I.M.A.G.E. clones; Genome Systems) were all isolated by PCR followed by purification in low-melting point agarose gels (Seakem). The DNAs were labeled in gel using the Prime-it II kit (Stratagene, La Jolla, CA). Small exon probes were labeled using their respective STS PCR primers instead of random primers. Up to 5 different probes were pooled in a hybridization. Filters were hybridized in duplicate using standard techniques. Putative positives were screened by PCR using the probe's STSs to identify clones. Inserts from positive clones were subcloned in pSP72 and sequenced.

e. Northern blots and RT-PCR analysis

Multiple tissue northern blots were purchased from Clontech and hybridized according to the manufacturer's instructions. RT-PCR was carried out on random primed first strand cDNA made from poly A+ RNA (Clontech) using AmpliTaq Gold (Perkin-Elmer). Control reactions were performed on RNA samples processed in the absence of reverse transcriptase to control for genomic DNA contamination.

f. Genomic Sequencing

The MAP1 sequences from the bacterial clones b132a2, 222K22, and 75L14 were assembled into contigs with the Staden package (available from Roger Staden, MRC). A minimal set of 3 kb clones was selected for sequencing with oligo labeled MAP2 that sits on the opposite end of the plasmid vector. The sequence of MAP2 was GCCGATTCATTAATGCAGGT. The MAP2 sequences were entered into the Staden database in conjunction with the MAP1 sequences to generate a tiling path of 3 kb clones across the region. These sequences were also screened with the BLAST algorithm and all novel sequence identities were noted. The plasmid 3 kb libraries were concurrently transformed in 96 well format into pox38UR (available from C. Martin, Lawrence Berkeley Laboratories). The transformants were subsequently mated with JGM (Strathman *et al.* P.N.A.S. 88:1247-1250 (1991) in 96 well format. All matings of the 3 kb clones within the tiling path were streaked on LB-carbenicillin-kanamycin plates and a random selection of 12 colonies per 3 kb clone was prepped in the AGCT system. The oligos -21: CTGTAAAACGACGGCCAGTC, and REV: GCAGGAAACAGCTATGACC were used to sequence off both ends of the transposon. Each 3 kb clone was assembled in conjunction with the end sequence information from all bacterial clones to generate complete sequence across the region. The genomic sequence was analyzed with the BLAST nucleotide and protein homology algorithms and the GRAIL 1.2 software to identify novel open reading frames (ORF) for gene finding.

g. Discussion

A compilation of 174 ESF led to the construction of an expressed sequence map of the region that served as the framework for the isolation of full-length cDNAs (Figure 1). (The map shows the subset of ESF that were actually mapped). Probes were developed for 82 best ESFs which appeared to be derived from the coding portions of cDNAs and the appropriate cDNA libraries were screened. This led to the isolation of 19 cDNAs, 17 of which represented novel sequences. 70 of the 174 ESF were included in the cDNAs isolated (40%). 36 probes failed to produce any clones even after repeated screening of several libraries. 51 ESF which were not accounted for in the cDNAs

cloned were not used in any screen. Therefore, it is possible that some additional genes within this 1 megabase region may have escaped detection.

A list of these cDNAs cloned and a comparison of the methods used to find them is presented in Table 4. Direct selection found 14 out of the 18 cDNAs contained within the boundaries of the YAC used in the experiment. Exon trapping found 15 out of the 19 cDNAs contained within the boundaries of the large insert bacterial clone contig. Sample sequencing identified 11 genes that had corresponding ESTs in the public database.

Table 4. Comparison of gene finding methods

	Bacterial Clone	CDNA #	Homology	EST	DS	Exon Trap
	157c	28	zinc finger	EST03556	2	1
	157c3	30	nonhistone	yv81d05	1	none
				yvh07a10		
	157c3	46	ORF	yd88g11	1	
15	157c3	20	BT	none	none	3
	p18696	21	BTF1	yn01G5	4	5
				yg23d08		
				yg57h09		
				yu15h03		
	45p21	32	BTF2	yg78f10	7	3
				yn01c05		
	45p21	29	BTF3	ye25g03	2	9
				yo65f06		
	45p21	23	BTF4	yd17d06	4	6
20	45p21	44	BTF5	ys04h08	2	4
	3e17	41	genomic?	none	none	1
	132a2	43	genomic?	none	none	3
	132a2	36	genomic?	none	1	none
	132a2	37	histone 2A	ym29g03	3	none
				yh87a03		
25	75114	24	MHC class I	ye98g01	1	2
	132a2	39	genomic?	none	none	4
	132a2	27	Ro/SSA	none	3	4
	132a2	22B	NPT1-like	yr42a05	1	7
				yf09g06		
	20h20	22E	NPT1-like	none	2	5
30	20h20	NPT1	NPT1	yp74c05	N/A	3

As a final approach, a tiling path with overlapping end sequences from the sample sequence database was generated. Each 3 kb clone within the path was shotgun-sequenced using transposable elements as platforms for dual end sequencing. These individual clones were assembled in conjunction with the end sequences from all bacterial clones in the region. The resulting sequence (Figure 2) was analyzed systematically with BLAST homology searches and the Grail 1.2 program to identify novel open reading frames (ORF) and other gene-like structures. The BLAST homology searches did not produce any probes that had not already been identified by sample sequencing. Grail predicted exons for all the genes in the region, but was only able to assemble the histones into any representative form. A detailed analysis of BLAST homology searches to protein databases identified an enticing homology to a zinc alpha 2 glycoprotein approximately 25 kb upstream of HFE, but the lack of a substantial ORF and the presence of a stop codon suggested that it was a pseudogene. Figure 2 shows the positions, the exon and intron structures, and the relative orientation of transcription of novel genes within this region. Also shown are the positions and transcriptional orientations of the histone genes. A total of 12 histone genes were identified in this study.

In an effort to account for the ESTs that did not associate with the characterized genes in the 250 kb region, the genomic sequence around the putative 3' ends were examined for polyadenylation signals to determine whether certain EST sequences may have originated from genomic DNA contamination in the normalized cDNA libraries used in EST generation. The positions of the 14 ESTs found in this region are indicated in Figure 2 to show those associated with the cDNAs cloned and those which did not associate with genomic DNA of obvious coding potential. Four ESTs corresponded to 3 of the 4 cDNAs cloned from the region (Table 2). One EST encoded a histone H2B.1 gene and another was a repetitive element. Of the remaining 8, 6 EST clones were used as probes of cDNA libraries with negative results. Those sequences representing putative 3' ends of cDNA were searched for the presence of poly (A)+ addition signals. Five of the 13 ESTs which had 3' end sequence, had the sequence ATAAA or ATTAA. Five of the remaining 8 ESTs that did not have a poly (A)+ addition signal had genomic encoded stretches of poly (A) near the end of EST sequence and, therefore, may have been created by oligo d(T) priming of contaminating genomic DNA. This analysis was expanded to include all ESTs in the large-insert bacterial contigs with definitive 3' ends. Of the remaining 26, 15 had 3' end sequence and, of these, 8 had poly (A)+ addition signals. Five of these 8 ESTs were associated with the cloned cDNAs. Of the remaining 7 which did not have poly (A)+ addition signals, 4 had genomic encoded stretches of poly (A).

i. Butyrophilin gene family

The human homolog of the bovine butyrophilin gene (BT) was cloned and mapped to approximately 480 kb centromeric to HFE (Figure 1). BT is a transmembrane protein of unknown function which constitutes 40% of the total protein associated with the fat globule of bovine milk (Jack *et al.* J. Biol. Chem. 265:14481-14486 (1990)). A human homolog of BT has recently been cloned by Tayloer *et al.* (Biochem Biophys Acta 1306:1-4 (1996)). The results in this study indicated that BT is a member of a gene family with at least five other members of the family residing in this region (Figure 1). A comparison of these proteins is shown in Figure 3. The proteins were aligned based on their descending order of relatedness and to minimized gaps in the sequence. Each of the five proteins

display varying degrees of homology to BT. BTF1 (cDNA 21), BTF2 (cDNA 32), BTF5 (cDNA 44), and BTF3 (cDNA 29) are 45%, 48%, 46%, and 49%, identical to BT, whereas BTF4 (cDNA 23), which is more similar to BTF3 (cDNA 29), is only 26% identical. This low degree of identity to BT is largely due to a truncation at the carboxyl terminus of the protein. The BTF family falls into two groups: BTF1 and 2 which are more related to each other than to BT or the other BTF members, and BTF5, 3 and 4, which appear to have a common evolutionary origin. The order of these genes on the chromosome suggests that the BT gene has duplicated two times, giving rise to BTF1 and BTF5. Subsequently, it appears likely these two genes experienced further duplication events to give rise to the other members in their groups.

The three major components of BT, the B-G immunoglobulin superfamily domain (containing the V consensus sequence) (Miller *et al.* Proc. Natl. Acad. Sci. U.S.A. 88:4377-4381 (1991)), the transmembrane region, and the B30-2 exon are found in all of these proteins (with the exception of BTF4 (cDNA 23) which lacks the B30-2 exon by virtue of the carboxyl terminal truncation). The exon B30-2 is a previously noted feature of the MHC class 1 region found approximately 200 kb centromeric to the HLA-A gene (Vernet *et al.*, J. Mol. Evol. 37:600-612 (1993)). In addition this exon is found in several genes of diverse function telomeric to HLA-A namely MOG (approximately 200 kb) and RFP (approximately 1 megabase) (Amadou *et al.* Genomics 26:9-20 (1995)).

The levels of the BTF mRNA were analyzed by northern blot analysis (Figure 4A). The expression of the BTF genes fell into two patterns. BTF1 and BTF2 were expressed as a single major transcript of 2.9 kb and one minor transcript of 5.0 kb. These genes were expressed at high levels in all the tissues tested with the exception of the kidney where the expression level was less. The two genes are 90% identical at the DNA sequence level, therefore, it is possible that the signal observed on the northern blots was the result of cross-hybridization and only one of the two genes was actually expressed. To address this possibility RT-PCR experiments were carried out on a panel of different tissues in order to detect possible tissue dependent expression that would suggest that both genes are expressed. Identical, and thus equivocal, results were obtained with both BTF1 and BTF2 amplification (Figure 4B).

The second group of genes, BTF3-5, are expressed as three (BTF5) (Figure 4A) and two (BTF3 and 4) transcripts ranging from 4.0 to 3.3 kb. BTF5 is expressed at moderate levels in all tissues tested with the exception of the kidney where the expression level is less. RT-PCR experiments showed that mRNA from the BTF5 gene can be found in all tissues tested, including the kidney (Figure 4B). Identical results were obtained with primers from the other genes of this group (data not shown). These genes are also 90% identical to each other at the DNA sequence level (but only 58% identical to BTF1 and 2), hence like BTF1 and BTF2, cross-hybridization could account for the similarity in size and patterns on the northern blots and RT-PCR. This might be particularly true for BTF4 which lacks the B30-2 exon but still hybridizes to larger size transcripts like BTF5 and BTF3.

ii. A gene with similarity to 52 kD Ro/SSA auto-antigen

Located approximately 120 kb telomeric to the HFE gene is a gene, RoRet, that has 58% amino acid similarity to the 52 kD Ro/SSA protein, an auto-antigen of unknown function that is frequently recognized by antibodies in patients with systemic lupus and Sjogren's syndrome (Anderson

et al. Lancet 2:456-560 (1961); Clark *et al. J. Immunol.* 102:117-122 (1969)) (Figures 1 and 2).

Alignment of the predicted amino acid sequence of this cDNA with that of 52 kD Ro/SSA indicated two features associated with the 52 kD Ro/SSA protein: a putative DNA binding cysteine rich motif (C-X-(I,V)-C-X(11-30)-C-X-H-X-(F,I,L)-C-X(2)-C-(I,L,M)-X(10-18)-C-P-X-C) found at the N terminus (Freemont *et al. Cell* 64: 483-484 (1991)) and the B30-2 exon found near the carboxyl terminus, are both conserved in RoRet (Figure 5). Northern blot analysis indicated the RoRet gene was expressed as two major transcripts of 2.8 and 2.2 kb and two minor transcripts of 7.1 and 4.4 kb in all of the tissues on the blot at levels reflective of the RNA amounts as determined by β -actin probing (Figure 6A). Using RT-PCR, expression can also be detected in small intestine, kidney liver, and spleen (Figure 6B).

iii. Two genes with homology to a sodium phosphate transporter

A cDNA for a sodium phosphate transport protein (NPT1) was previously cloned and mapped to 6p21.3 using a somatic cell hybrid panel (Chong *et al. Genomics* 18:355-359 (1993)). NPT1 maps 320 kb telomeric to the HFE gene (Figures 1 and 2). Two additional cDNAs were cloned which show appreciable homology to NPT1 (Figure 5). These genes, NPT3 and NPT4, mapped 1.5 megabases and 1.3 megabases centromeric to the NPT1 gene (Figure 1). Like NPT1, the gene products of NPT3 and NPT4 were extremely hydrophobic, which may reflect a membrane location. Both proteins gave hydrophilicity profiles which were indistinguishable from NPT1 in this study (data not shown). Northern blot analysis indicated that the two genes have different patterns of expression (Figure 6C). NPT3 was expressed at high levels as a 7.2 kb transcript predominately in muscle and heart. Lesser amount of the mRNA were also found in brain, placenta, lung, liver and pancreas. RT-PCR analysis indicated that expression of the proper size PCR fragment for NPT3 was clearly absent in fetal brain, bone marrow and small intestine (Figure 6D). A smaller size fragment was detectable in all tissues with the exception of the liver, which may represent evidence for alternative splicing. Although expression was apparently absent from the kidney by northern blot analysis, it was detectable by RT-PCR. Expression was also noted in the mammary gland, spleen and testis. NPT4, on the other hand, was expressed only in the liver and the kidney as a smear of transcripts approximately 2.6 - 1.7 kb (Figure 6C). RT-PCR confirmed these results, although a small amount of the proper size PCR fragment was also found in the small intestine and testis (Figure 6D). Other tissues showed amplification, but the fragments were of larger and smaller size than that produced by the cDNA 22E positive control. Hence, these two genes which apparently have the structural characteristics of a sodium phosphate transporter, appeared to be under the control of different regulatory mechanism that lead to differential patterns of expression.

2. Sequencing of 235 kb from a Homozygous Ancestral (Affected) Individual

In these studies the entire genomic sequence was determined from an HH affected individual for a region corresponding to a 235,033 bp region surrounding the HFE gene between the flanking markers D6S2238 and D6S2241. The sequence was derived from a human lymphoblastoid cell line, HC14, that is homozygous for the ancestral HH mutation and region. The sequence from the ancestral chromosome (Figure 9) was compared to the sequence of the region in an unaffected individual (Figure 8) disclosed in copending U.S.S.N. 08/724,394 to identify polymorphic sites. A

subset of the polymorphic alleles so defined were further studied to determine their frequency in a collection of random individuals.

The cell line HC14 was deposited with the ATCC on June 25, 1997, and is designated ATCC CRL-12371.

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a. Cosmid Library Screening

The strategy and methodology for sequencing the genomic DNA for the affected individual was essentially as described in copending U.S.S.N. 08/724,394, hereby incorporated by reference in its entirety. Basically, a cosmid library was constructed using high molecular weight DNA from HC14 cells. The library was constructed in the supercos vector (Stratagene, La Jolla, CA).

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Colonies were replicated onto Biotrans nylon filters (ICN) using standard techniques. Probes from genomic subclones used in the generation of the sequence of the unaffected sequence disclosed in 08/724,394 were isolated by gel electrophoresis and electroporation. Subclones were chosen at a spacing of approximately 20 kb throughout the 235 kb region. The DNA was labeled by incorporation of ³²P dCTP by the random primer labeling approach. Positively hybridizing clones were isolated to purity by a secondary screening step. Cosmid insert ends were sequenced to determine whether full coverage had been obtained, and which clones formed a minimal path of cosmids through the 235 kb region.

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b. Sample Sequencing

A minimal set of cosmid clones chosen to cover the 235 kb region were prepped with the Qiagen Maxi-Prep system. Ten micrograms of DNA from each cosmid preparation were sonicated in a Heat Systems Sonicator XL and end-repaired with Klenow (USB) and T4 DNA polymerase (USB). The sheared fragments were size selected between three to four kilobases on a 0.7% agarose gel and then ligated to BstXI linkers (Invitrogen). The ligations were gel purified on a 0.7% agarose gel and cloned into a pSP72 derivative plasmid vector. The resulting plasmids were transformed into electrocompetent DH5α cells and plated on LB-carbenicillin plates. A sufficient number of colonies was picked to achieve 15-fold clone coverage. The appropriate number of colonies was calculated by the following equation to generate a single-fold sequence coverage: Number of colonies = size of bacterial clone (in kb)/average sequence read length (0.4 kb). These colonies were prepped in the 96-well Qiagen REAL, and the 5' to 3' DNA Prep Kit, and AGCT end-sequenced with oligo MAP1 using standard ABI Dye Terminator protocols. MAP1 was CGTTAGAACGCGGCTACAAT.

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c. Genomic Sequencing

The MAP1 sequences from the cosmid clones HC182, HC187, HC189, HC195, HC199, HC200, HC201, HC206, HC207, and HC212 were assembled into contigs with the Staden package (available from Roger Staden, MRC). A minimal set of 3 kb clones was selected for sequencing with oligo labeled MAP2 that sits on the opposite end of the plasmid vector. The sequence of MAP2 was GCCGATTCATTAATGCAGGT. The MAP2 sequences were entered into the Staden database in conjunction with the MAP1 sequences to generate a tiling path of 3 kb clones across the region. The plasmid 3 kb libraries were concurrently transformed in 96 well format into pox38UR (available from C. Martin, Lawrence Berkeley Laboratories). The transformants were subsequently mated with JGM (Strathman et al. P.N.A.S. 88:1247-1250 (1991) in 96 well format. All matings of the

35

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3 kb clones within the tiling path were streaked on LB-carbenicillin-kanamycin plates and a random selection of 12 colonies per 3 kb clone was prepped in the AGCT system. The oligos -21: CTGTAAAACGACGGCCAGTC, and REV: GCAGGAAACAGCTATGACC were used to sequence off both ends of the transposon. Each 3 kb clone was assembled in conjunction with the end sequence information from all cosmid clones in the region.

In some regions, the coverage of the genomic sequence by cosmids was incomplete. Any gaps in the sequence were filled by using standard PCR techniques to amplify genomic DNA in those regions and standard ABI dye terminator chemistry to sequence the amplification products.

d. Identification of Polymorphic Sites

The assembled sequence of the cosmid clones in connection with the PCR amplified genomic DNA was compared to the genomic sequence of the unaffected individual using the FASTA algorithm. Numeric values were assigned to the sequenced regions of 1 to 235,303, wherein base 1 refers to the first C in the CA repeat of D6S2238 and base 235,303 is the last T in the GT repeat of D6S2241 of the unaffected sequence (Figure 8). Table 1 lists the differences between the two compared sequences. Note that previously disclosed (Feder et al., Nature Genetics 13:399-408 (1996)) polymorphic sites D6S2238 (base 1), D6S2241 (base 235,032), 24d1 (base 41316), and D6S2239 (base 84841) are not included in the list of new polymorphisms, although they are provided for reference in a footnote to the Table and were observed in the ancestral sequence. In the Table, a single base change such as C-T refers to a C in the unaffected sequence at the indicated base position that occurred as a T in the corresponding position in the affected sequence. Similarly, an insertion of one or more bases, such as TTT in the affected sequence, is represented as "TTT INS" between the indicated bases of the unaffected sequence. A deletion of one or more bases occurring in the affected sequence, such as AAA DEL, is represented as the deletion of the indicated bases in the unaffected sequence.

e. Characterization of Rare Polymorphisms

In this study about 100 of the polymorphisms of Table 1 were arbitrarily chosen for further characterization. Allele frequencies in the general population were estimated by OLA analysis using a population of random DNAs (the "CEPH" collection, J. Dausset et al., Genomics 6(3):575-577 (1990)). These results are provided in Table 2.

One single base pair difference, occurring at base 35983 and designated C182.1G7T/C (an A to G change on the opposite strand) was present in the ancestral chromosome and rare in the random DNAs. This change occurred in a noncoding region of the hemochromatosis gene near exon 7 approximately 5.3 kb from the 24d1 (Cys282Tyr) mutation. OLA was used to genotype 90 hemochromatosis patients for the C182.1G7T/C base pair change. The frequency for C occurring at this position in the patients was 79.4% as compared to 5% in the random DNAs. Eighty-five of the 90 patients assayed contained identical 24d1 and C182.1G7T/C genotypes. Four of the remaining 5 patients were homozygous at 24d1 and heterozygous at C182.1G7T/C; one was heterozygous at 24d1 and homozygous at C182.1G7T/C. The primers used for this analysis were as follows.

PCR primers for detection:

182.1G7.F 5'-GCATCAGCGATTAACCTTCTAC -3'

182.1G7.R 5'-TTGCATTGTGGTGAAATCAGGG -3'

For the detection assay, the biotinylated primers used were as follows.

5 182.1G7.C 5' (b)CTGAGTAATTGTTTAAGGTGC -3'

182.1G7.T 5' (b)CTGAGTAATTGTTTAAGGTGT -3'

The phosphorylated digoxigenin-labeled primer used was:

182.1G7.D 5' (p)AGAAGAGATAGATATGGTGG -3'

10 A further rare single base pair change was detected at 61,465bp. The inheritance pattern of this polymorphism, C195.1H5C/T (a G to A change on the opposite strand), is identical to that of 24d1. The frequency of T occurring at that position (C195.1H5T) observed in a set of 76 patients was 78.5% as compared to 5% in random individuals.

15 PCR primers for detection:

1951H5.3F 5'-GAATGTGACCGTCCCATGAG-3'

1951H5.3R 5'-CAACTGAATATGCAGAAAAAAGTACACC-3'

For the detection assay, the biotinylated primers used were:

1951H5.3.4 5' (b)AGTAGCTGGGACTCACGGTGT-3'

20 1957H5.3.5 5' (b)AGTAGCTGGGACTCACGGTGC-3'

The phosphorylated digoxigenin-labeled primer used was:

1951H5.3.6 5' (p)GCGCCACCACTCCCAGCTCAT-3'

25 These rare alleles are thus preferred surrogate markers for 24d1 and are especially useful in screening assays for the likely presence of 24d1 and/or 24d2.

All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety.

WHAT IS CLAIMED IS:

- 1 1. An oligonucleotide comprising at least 8 to about 100 consecutive bases from the
2 sequence of Figure 9, or the complement of the sequence, wherein the at least 8 to about 100
3 consecutive bases includes at least one polymorphic site of Table 1.
- 1 2. The oligonucleotide of claim 1, wherein the polymorphic site is selected from the
2 group consisting of base 35983 or base 61465.
- 1 3. An oligonucleotide pair selected from the sequence of Figure 9 or its complement for
2 amplification of a polymorphic site of Table 1.
- 1 4. An isolated nucleic acid molecule comprising about 100 consecutive bases to about
2 235 kb substantially identical to the sequence of Figure 9, wherein the DNA molecule comprises at
3 least one polymorphic site of Table 1.
- 1 5. The isolated nucleic acid molecule of claim 4, wherein the polymorphic site is selected
2 from the group consisting of base 35983 or base 61465.
- 1 6. The isolated nucleic acid molecule of claim 4, wherein the nucleic acid is selected
2 from the group consisting of cDNA, RNA, or genomic DNA.
- 1 7. A polypeptide encoded by the nucleic acid molecule of claim 4.
- 1 8. An antibody which specifically recognizes the polypeptide of claim 7.
- 1 9. A method to determine the presence or absence of the common hereditary
2 hemochromatosis (HFE) gene mutation in an individual comprising:
3 providing DNA or RNA from the individual; and
4 assessing the DNA or RNA for the presence or absence of a haplotype of Table 1,
5 wherein, as a result, the absence of a haplotype of Table 1 indicates the likely absence of the
6 HFE gene mutation in the genome of the individual and the presence of the haplotype indicates the
7 likely presence of the HFE gene mutation in the genome of the individual.
- 1 10. The method of claim 9, wherein the method further comprises assessing the RNA or
2 DNA for the presence of at least one of the polymorphisms 24d1, 24d2, HHP-1, HHP-19, or HHP-29;
3 or microsatellite repeat alleles 19D9:205, 18B4:235, 1A2:239, 1E4:271, 24E2:245, 2B8:206, 3321-
4 1:98, 4073-1:182, 4440-1:180, 4440-2:139, 731-1:177, 5091-1:148, 3216-1:221, 4072-2:170, 950-
5 1:142, 950-2:164, 950-3:165, 950-4:128, 950-6:151, 950-8:137, 63-1:151, 63-2:113, 63-3:169, 65-

6 1:206, 65-2:159, 68-1:167, 241-5:108, 241-29:113, 373-8:151, 373-29:113, D6S258:199, D6S265:122,
7 D6S105:124, D6S306:238, D6S464:206, or D6S1001:180.

1 11. The method of claim 9, wherein the haplotype comprises at least two polymorphic
2 sites of Table 1.

1 12. The method of claim 11, wherein one of the at least two polymorphic sites of Table 1
2 is at base 35983 or 61465.

1 13. The method of claim 11, wherein the haplotype comprises at least three polymorphic
2 sites of Table 1.

1 14. A method to determine the presence or absence of the common hereditary
2 hemochromatosis (HFE) gene mutation in an individual comprising:
3 providing DNA or RNA from the individual; and
4 assessing the DNA or RNA for the presence or absence of a genotype defined by a
5 polymorphic allele of Table 1,
6 wherein, as a result, the absence of a genotype defined by a polymorphic allele of Table 1
7 indicates the likely absence of the HFE gene mutation in the genome of the individual and the
8 presence of the genotype indicates the likely presence of the HFE gene mutation in the genome of the
9 individual.

1 15. The method of claim 15, wherein the polymorphic allele occurs in less than about 50%
2 of a random population of individuals.

1 16. The method of claim 15, wherein the polymorphic allele occurs in less than about 25%
2 of a random population of individuals.

1 17. The method of claim 15, wherein the polymorphic allele occurs in less than about 5%
2 of a random population of individuals.

1 18. The method of claim 15, wherein the genotype is C182.1G7C or C195.1H5T.

1 19. A kit comprising one or more oligonucleotides of claim 1.

1 20. A kit comprising at least one oligonucleotide pair of claim 3.

1 21. A culture of lymphoblastoid cells having the designation ATCC CRL-12371.

- 1 22. An isolated nucleic acid sequence comprising a sequence substantially identical to
2 BTF1.
- 1 23. The isolated nucleic acid sequence of claim 23, wherein the nucleic acid is cDNA.
- 1 24. The polypeptide encoded by the isolated nucleic acid sequence of claim 23.
- 1 25. A vector comprising the nucleic acid sequence of claim 23.
- 1 26. A host cell stably transfected with the nucleic acid sequence of claim 23.
- 1 27. An antibody that is specifically immunoreactive with the polypeptide of claim 24.
- 1 28. An isolated nucleic acid sequence comprising a sequence substantially identical to
2 BTF2.
- 1 29. The isolated nucleic acid sequence of claim 28, wherein the nucleic acid is cDNA.
- 1 30. The polypeptide encoded by the isolated nucleic acid sequence of claim 28.
- 1 31. A vector comprising the nucleic acid sequence of claim 28.
- 1 32. A host cell stably transfected with the nucleic acid sequence of claim 28.
- 1 33. An antibody that is specifically immunoreactive with the polypeptide of claim 30.
- 1 34. An isolated nucleic acid sequence comprising a sequence substantially identical to
2 BTF3.
- 1 35. The isolated nucleic acid sequence of claim 34, wherein the nucleic acid is cDNA.
- 1 36. The polypeptide encoded by the isolated nucleic acid sequence of claim 34.
- 1 37. A vector comprising the nucleic acid sequence of claim 34.
- 1 38. A host cell stably transfected with the nucleic acid sequence of claim 34.
- 1 39. An antibody that is specifically immunoreactive with the polypeptide of claim 36.

- 1 40. An isolated nucleic acid sequence comprising a sequence substantially identical to
2 BTF4.
- 1 41. The isolated nucleic acid sequence of claim 40, wherein the nucleic acid is cDNA.
- 1 42. The polypeptide encoded by the isolated nucleic acid sequence of claim 40.
- 1 43. A vector comprising the nucleic acid sequence of claim 40.
- 1 44. A host cell stably transfected with the nucleic acid sequence of claim 40.
- 1 45. An antibody that is specifically immunoreactive with the polypeptide of claim 42.
- 1 46. An isolated nucleic acid sequence comprising a sequence substantially identical to
2 BTF5.
- 1 47. The isolated nucleic acid sequence of claim 46, wherein the nucleic acid is cDNA.
- 1 48. The polypeptide encoded by the isolated nucleic acid sequence of claim 46.
- 1 49. A vector comprising the nucleic acid sequence of claim 46.
- 1 50. A host cell stably transfected with the nucleic acid sequence of claim 46.
- 1 51. An antibody that is specifically immunoreactive with the polypeptide of claim 48.
- 1 52. An isolated nucleic acid sequence comprising a sequence substantially identical to
2 NTP-3.
- 1 53. The isolated nucleic acid sequence of claim 52, wherein the nucleic acid is cDNA.
- 1 54. The polypeptide encoded by the isolated nucleic acid sequence of claim 52.
- 1 55. A vector comprising the nucleic acid sequence of claim 52.
- 1 56. A host cell stably transfected with the nucleic acid sequence of claim 52.
- 1 57. An antibody that is specifically immunoreactive with the polypeptide of claim 54.

1 58. An isolated nucleic acid sequence comprising a sequence substantially identical to
2 NTP-4.

1 59. The isolated nucleic acid sequence of claim 58, wherein the nucleic acid is cDNA.

1 60. The polypeptide encoded by the isolated nucleic acid sequence of claim 58.

1 61. A vector comprising the nucleic acid sequence of claim 58.

1 62. A host cell stably transfected with the nucleic acid sequence of claim 58.

1 63. An antibody that is specifically immunoreactive with the polypeptide of claim 60.

1 64. An isolated nucleic acid sequence comprising a sequence substantially identical to
2 RoRet.

1 65. The isolated nucleic acid sequence of claim 64, wherein the nucleic acid is cDNA.

1 66. The polypeptide encoded by the isolated nucleic acid sequence of claim 64.

1 67. A vector comprising the nucleic acid sequence of claim 64.

1 68. A host cell stably transfected with the nucleic acid sequence of claim 64.

1 69. An antibody that is specifically immunoreactive with the polypeptide of claim 66.

1 70. An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides
2 substantially identical to 18 contiguous nucleotides of BTF1.

1 71. An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides
2 substantially identical to 18 contiguous nucleotides of BTF2.

1 72. An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides
2 substantially identical to 18 contiguous nucleotides of BTF3.

1 73. An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides
2 substantially identical to 18 contiguous nucleotides of BTF4.

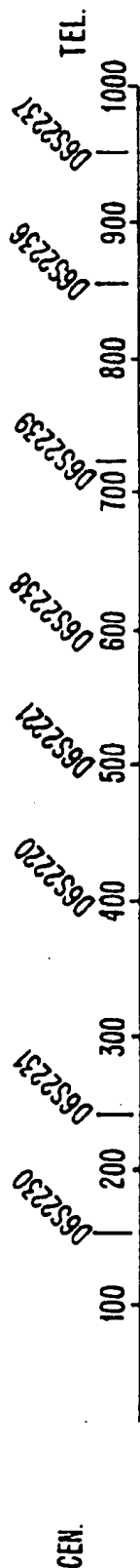
1 74. An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides
2 substantially identical to 18 contiguous nucleotides of BTF5.

1 75. An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides
2 substantially identical to 18 contiguous nucleotides of NPT3.

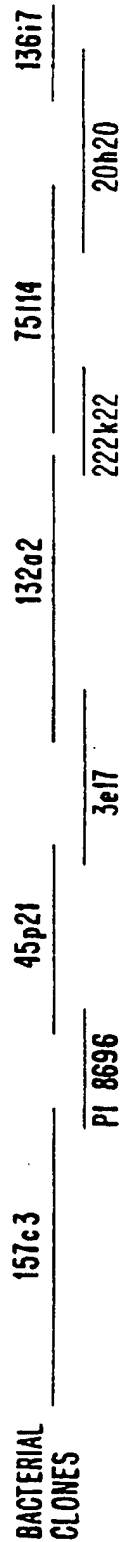
1 76. An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides
2 substantially identical to 18 contiguous nucleotides of NPT4.

1 77. An isolated nucleic acid sequence comprising at least 18 contiguous nucleotides
2 substantially identical to 18 contiguous nucleotides of RoRet.

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YAC



EXPRESSED
SEQUENCE
FRAGMENTS



ZNF
NON-HISTONE
HISTONE
HLA-H
RoRet
NPT3
NPT4
NPT1

SEQUENCED REGION

FIG. 1.

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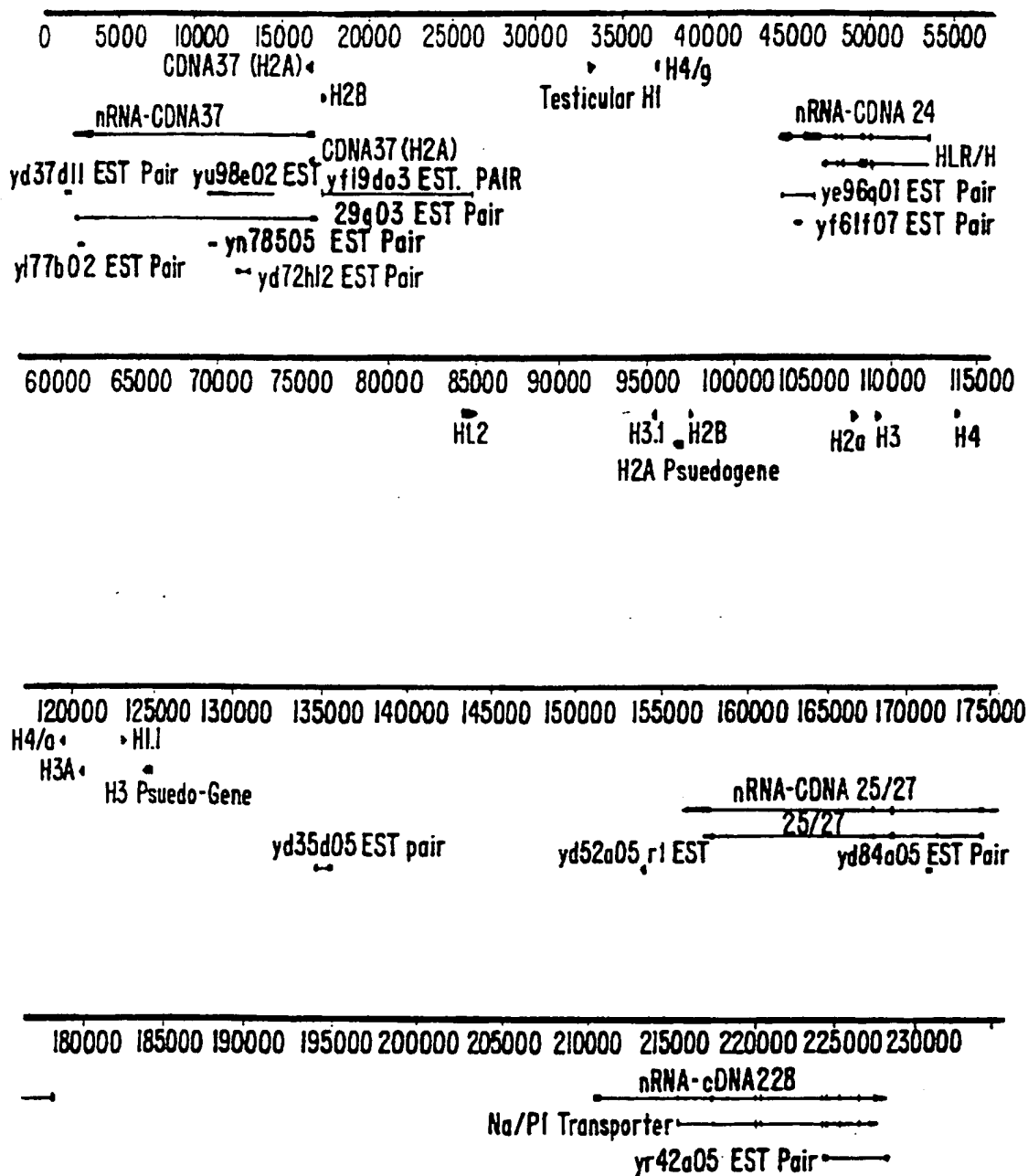


FIG. 2.

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BT      --MAVFPSSGLPRCL---LTLILLQLPKLDSAPFDVIGPPEPILAVVGEDAELPCRISP
BTf1    MESAAALHFSRPAS----LLLLLLSLCALVSAQFIVVGPTDPILATVGENTTLRCHLSPE
BTf2    MEPAAALHFSLPASLLLLLLLLLLLLSLCALVSAQFTVVGPANPILAMVGENTTLRCHLSPE
BTf5    MKMASFLAFLLLNFR---VCLLLQLLMPHSAQFSVLGPGSGPILAMVGEDADLPCHLFPT
BTf3    MKMASSLAFLLLNFH---VSLFLVQLLTPCSAQFSVLGPGSGPILAMVGEDADLPCHLFPT
BTf4    MKMASSLAFLLLNFH---VSLLLVQLLTPCSAQFSVLGPGSGPILAMVGEDADLPCHLFPT
      *      * * * * * * * * * * * * * * * *

BT      ASAEHLELRWFRKKVSPAVLVHRDGREQAEQMPEYRGRATLVQDGIAGRVALRIRGVR
BTf1    KNAEDMEVRWFRSQFSAPVAVFYKGGRRERTEEQMEEYRGRITFVSKDISRGSVALVIHNIT
BTf2    KNAEDMEVRWFRSQFSAPVAVFYKGGRRERTEEQMEEYRGRITFVSKDINRGSVALVIHNVT
BTf5    MSAETMELKWVSSSLRQVVNVYADGKEVEDRQSAPYRGRITSILRDGITAGKAALRIHNVT
BTf3    MSAETMELKWVSSSLRQVVNVYADGKEVEDRQSAPYRGRITSILRDGITAGKAALRIHNVT
BTf4    MSAETMELKWVSSSLRQVVNVYADGKEVEDRQSAPYRGRITSILRDGITAGKAALRIHNVT
      * * * * * * * * * * * * * * * *

BT      VSDDGEYTCFFREDGSYEEALVHLKVAALGSDPHISMVQENGEICLECTSVGWYPEPQV
BTf1    AQENGTYRCYFQEGRSYDEAILHLVVAGLGSKPLISMRGHEDGGIRLECISRGWYPKPLT
BTf2    AQENGIYRCYFQEGRSYDEAILRLVVAGLGSKPLIEIKAQEDGSIWLECISGGWYPEPLT
BTf5    ASDSGKYLICYFQDGDIFYEKALVELKVAALGSDLHVDVKGYKDGGIHLECRSTGWYPQPI
BTf3    ASDSGKYLICYFQDGDIFYEKALVELKVAALGSDLHIEVKGYEDGGIHLECRSTGWYPQPI
BTf4    ASDSGKYLICYFQDGDIFYEKALVELKVAALGSLNHVEVKGYEDGGIHLECRSTGWYPQPI
      * * * * * * * * * * * * * * * *

BT      QWRTSKGEKFPSTSESERNPDEEGLFTVAASVIIRDSTTKNVSCYIQNLLLGQEKKEVEISI
BTf1    VWRDPYGGVAPALKEVSMPPDADGLFMVTTAVIIRDKSVRNMSCSINNTLLGQKKESVIFI
BTf2    VWRDPYGEVVPALKEVSIADADGLFMVTTAVIIRDKYVRNVSCSVNNTLLGQEKETVIFI
BTf5    QWSNNKGENIPTVEAPVVADGVGLYAVAASVIMRGSSGEGVSCITRSSLLGLEKTASISI
BTf3    KWSDTKGENIPAVEAPVVADGVGLYAVAASVIMRGSSGGGVSCIIRNSLLGLEKTASISI
BTf4    QWSNAKGENIPAVEAPVVADGVGLYAVAASVIMRGSSGEGVSCIIRNSLLGLEKTASISI
      * * * * * * * * * * * * * * * *

BT      PASSLPRLTPWIVAVAV-----ILMVLGLLTIGSIFFTWRLYNER-----
BTf1    PESFMPSVSPCAVALP-----IIVVILMPIAVCIYWNKLQKEKKILSGEK
BTf2    PESFMPSASPWMVALAVILTASPWMVSMTVILAVFIIFMAVSICCIKKLQREKKILSGEK
BTf5    ADPFFRSAQRWIAALAR-----TLPVLLLLLLGGAGYFLWQQQEEKKTQFRKK
BTf3    ADPFFRSAQPWIAALAG-----TLPISLLLLLAGASYFLWRQQKEKIALSRET
BTf4    ADPFFRSAQPWIAALAG-----TLPILLLLLLAGASYFLWRQQKEITALSSEI
      *      *      *      *      *      *      *

BT      PRER-----RNEFS-----SKERLLEELKWKATLHA-----
BTf1    EFERETREIALKELEKERVQKEELQVKEKLQEELRWRRTFLHA-----
BTf2    KVEQE-----EKE-----IAQQLQEELRWRRTFLHA-----
BTf5    KREQELREMAWSTMKQEQS-----TRVKLLEELRWRSIQYASRGERHSAYNEWKKALF
BTf3    EREREMKEMGYAATEQEIS-----LREKLQEELKWRKIQYMARGEKSLAYHEWKMALE
BTf4    ESEQEMKEMGYAATEREIS-----LRESLQEELKRKKSST-----
      *      *      *      *      *      *

BT      --VDVTLDPDTAHPHFLYEDSKSVRLSDSRQK---LPEKTERFDSWPCVLGRETFTSGR
BTf1    --VDVLDLPDTAHPDLFLSEDRRSVRRCPFRHLGESVPDNPERFDSQPCVLGRESFASGK
BTf2    --ADVLDLPDTAHPDLFLSEDRRSVRRGPYRQR---VPDNPERFDSQPCVLGWESFASGK
BTf5    KPADVILDPKTANPILLVSEDQRSVQRAKEPDQ---LPDNPERFNWHYCVLGCESFISGR
BTf3    KPADVILDPDTANAILLVSEDQRSVQRAEPRD---LPDNPERFEWRYCVLGCENFTSGR
BTf4    -----

BT      HYWEVEVGDRTDWAIGVCRENVMKK-GFDPMTPENGFWAVELY-GNGYWALTPLRTPLPL
BTf1    HYWEVEVENVIEWTVGVCRDVERK-GEVLLIPONGFWTLEMH-KGQYRAVSSPDRILPL
BTf2    HYWEVEVENVMVTVGVCRHSVERK-GEVLLIPONGFWTLEMF-GNQYRALSSPERILPL
BTf5    HYWEVEVGDRKEWHIGVCSKNVQRK-GWVKMTPENGFWTMGLTDGNKYRTLTEPRTNLKL
BTf3    HYWEVEVGDRKEWHIGVCSKNVERKKGWVKMTPENGYWTMGLTDGNKYRALTEPRTNLKL
BTf4    -----

```

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BT	AGPPRRVGIFLDYESGDISFYNMNDGSDIYTFSNVTFSGLRPPFFCLWSSGKKPLTICPI
BTF1	KESLCRVGVFLDYEAGDVSFYNMRRSHIYTCPRSAFSVPVRPFFRLGC-EDSPIFICPA
BTF2	KESLCRVGVFLDYEAGDVSFYNMRRSHIYTCPRSAFTVPVRPFFRLGS-DDSPIFICPA
BTF5	PKPPKKVGVFLDYETGDISFYNAVDGSHIHTFLDVSFSEALYPVFRILTLEPTALSICPA
BTF3	PEPPRKVGIFLDYETGEISFYNATDGSHIYTFPHASFSEPLYPVFRILTLEPTALTICPI
BTF4	-----
BT	ADGPERVTVIANAQDLSKEIPLSPMGEEAPRDADTLHSLIPTQPSQGAP-----
BTF1	LTGANGVTVP-----EEGLTLHRVGTHQSL-----
BTF2	LTGASGVMVP-----EEGLKLHRVGTHQSL-----
BTF5	-----
BTF3	PKEVESSPDPLVPDHSLETPLTPGLANESGEPQAEVTSLLLPAHPGAEVSPSATTNQNH
BTF4	-----
BT	-----
BTF1	-----
BTF2	-----
BTF5	-----
BTF3	KLQARTEALY
BTF4	-----

Figure 3 (Page 2 of 2)

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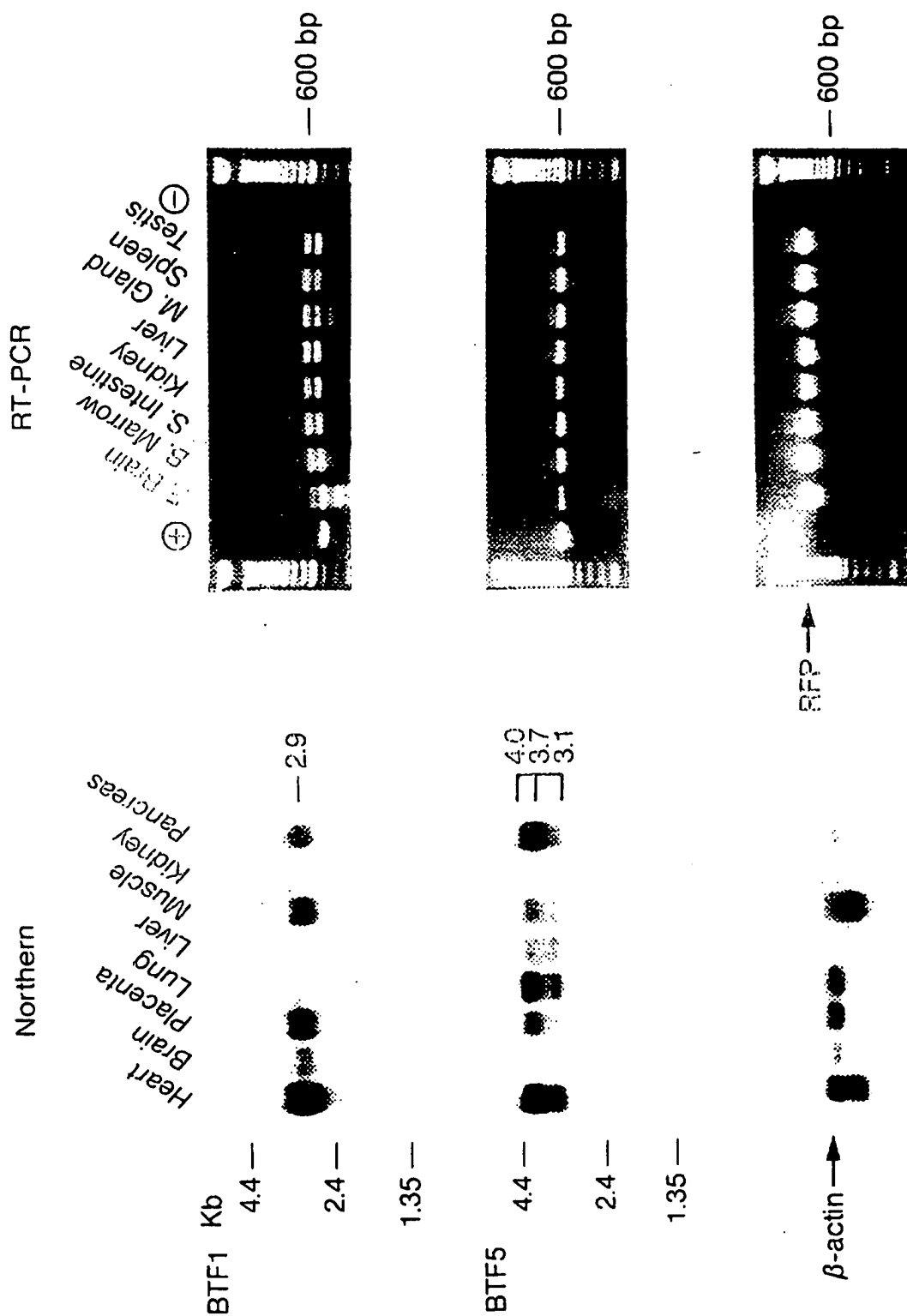


FIG. 4A.

FIG. 4B.

		CYSTEINE-RICH DOMAIN																			
52 kD	Ro	MASAARLTMMWEEVTCPICLDPFVEPVSVIECGHSFCQECISQVGKGGG	-----	VCPVCRQRFLLKNLRPNRQLAMMVN																	
RoRet		MASTTSTKKMMEEATCSICLSLMTNPVSINCGHSYCHLCITDFFKNPSQQLRQETFCPCQCRAPFHMDSL RPNKQLGSLIE																			
		***	*	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**
52 kD	Ro	NLKKISQEAAREGTQGERCAVHGERLHLFCEKDGKALCWVCAQSKKHRDHAMVPLEEAAQYQEKQLQVALGELRRKQELAEKL																			
RoRet		ALKKTDQEM-----	SCEEHGEQFHLFCEDEGQLICWRCERAPQHKGHTT	TALVEDVCQGYKEKQLQKAVTKLKQLEDRCTEQ																	
		***	**	*	***	***	*	**	*	*	*	*	*	*	*	*	*	*	*	*	*
52 kD	Ro	EVEIAIKRADWKKTVETQKSRIHAEFVQQNFLVEEEQRLQLEKDEREQRLILGEKEAKLAQQSQALQELISELDRRCHS																			
RoRet		KLSTAMRITKWKEKVQIQORQKIRSDFKNLQCFLHEEEKSYLWRLEKEEQOTLSRLRDYEAGLGLKSNELKSHILELEKCKQG																			
		*	**	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
52 kD	Ro	SALELLQEVIIVLERSESNLKDLDITSPELRSVCHVP	----	GLKKMLRTCAVHITLDPDTANPWLILSEDRRQVRLGDTQQ																	
RoRet		SAQKLLQNVDNLTLSRSWAVKLETSEAVSLELHTMCNVSKLYFDVKKMLRSHQVSVTLDPDTAHHELILSEDRRQVTRGYTQE																			
		**	***	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
52 kD	Ro	SIPGNEERFDSYPMVLGAQHFGHSGKHYWEVDVTGKEAWDLGVCRDVSRRKGHFLSSKSGFWT IWLWNKQKYEAGTYPQTPL																			
RoRet		NQDTSSRRFTAFPCVLGCEGFTSGRRRYFEVDVGEGTGWDLGVCMENVQVGTGMKQEPQSGFWTLRLCKKKGYVALTSPPTSL																			
		**	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
52 kD	Ro	HLQVPPCQVGIFLDYEAGMVSFYNITDHGSLIYSFSECAFTGPLRPF																			
RoRet		HLHEQPLLVGIFLDYEAGVVSFYNG-NTGCHIFTEPKASFSDTLRPFYQVYQYS-----																			
		**	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*

FIG. 5A.

NP1 -PMYNWSPDIQFIILSSTSYGVIIIQVPVGYFSGIYSTKKMIGFALCLSSVLSSLIPPAAGIGVAVVVCRAVQGAQAQIGIVA
 NP3 ASVYQWSPETQGIIFSSINYGIILTLIPSGYLAGIFGAKKMLGAGLLISSLLTLFTPLAADFGVILVIMVRTVQGMAGQMAW
 NP4 -----VLPVDSFGGLSKAPKSLP-----AKSSIL*

NNPT1 TAQFEIYVKWAPPLERGRLTSMSTGFLLGPFIVLLVTGVICESLGWPMVFIYFGACGCAVCLLWFVLFYDDPKDHPCCISIS
 NNPT3 TGQFTIWAKWAPPLERSKLTITAGSGSAGFSFIILCVGGLISQALSWPFFIFYIFGSTGCVCLLWFTVIYDDPMHHPCISVR
 NNPT4 GGQFAIWEKGWPPQERSRLCSIALSGMLLGCFTAILIGGFISETLGWPFVFIYFGVGVCVCLLWFWVIYDDPFSEYPWISTS

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EKEYIISLKKQVGSKKQPLPIKAMLRSLPIWSICLGCFSHQWLVTMVVYIPTYISSVYHVNI RD NGLLSALPFI VAWVIG

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FIG. 5B.

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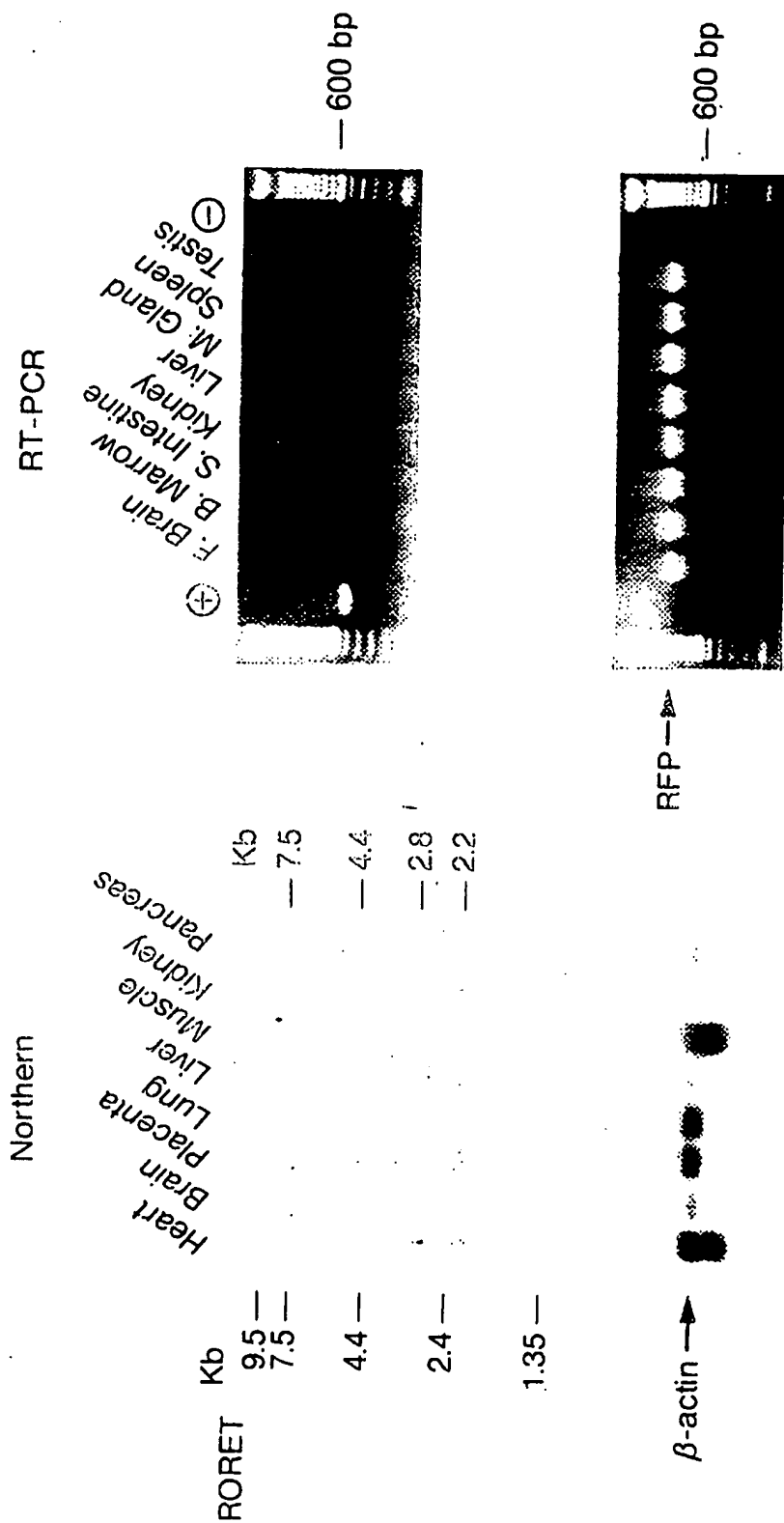


FIG. 6B.

FIG. 6A.

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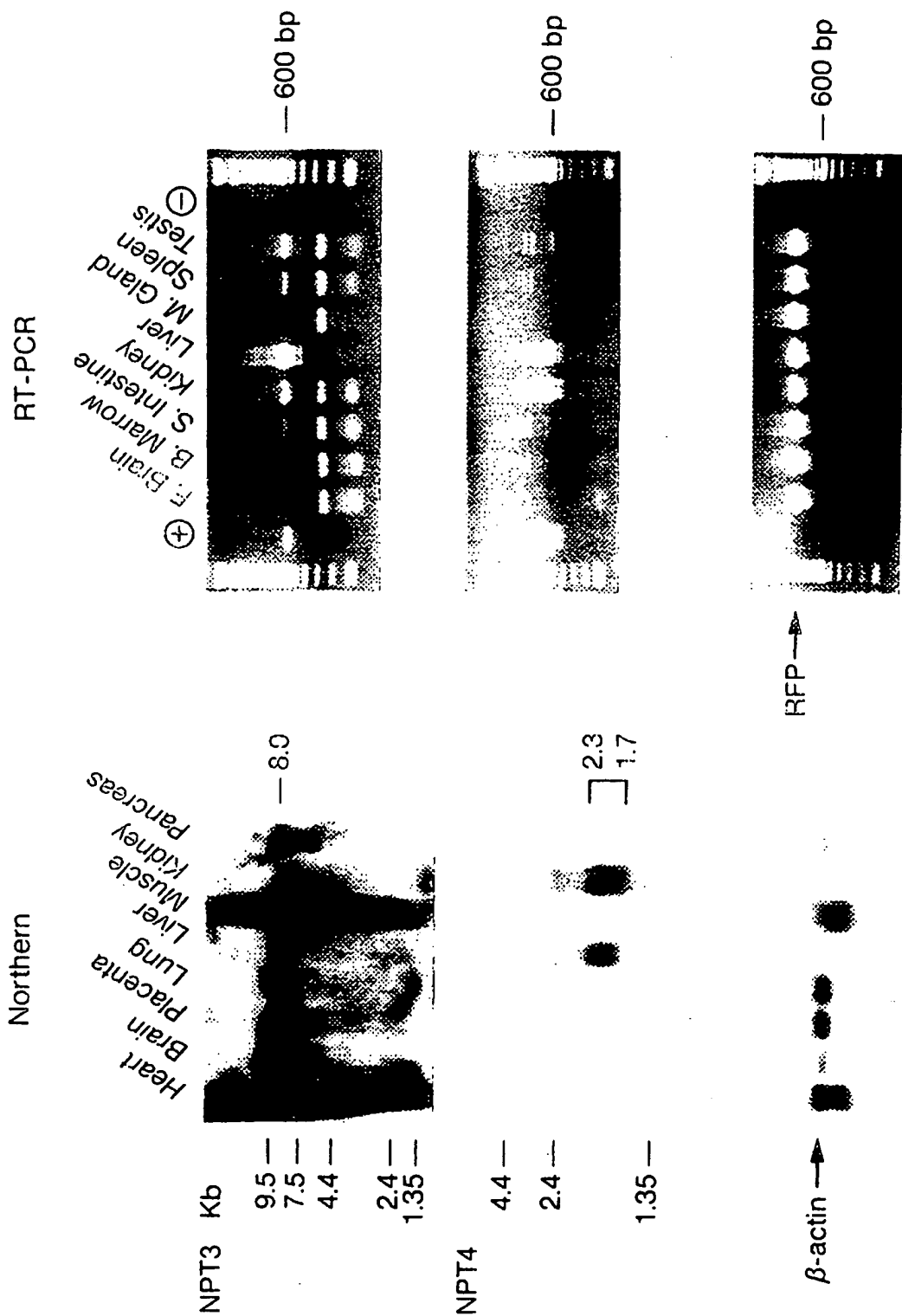


FIG. 6D.

FIG. 6C.

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SUBSTITUTE SHEET (RULE 26)

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3781   TGACCTTCTG ATCCGCCTGC CTGGCTTCC CAAAGTGCTG GGATTACACG TGTGAGCCAC
3841   CATGCCCCGC TGGGATGGAA TAAATTTATC TTGTATGGGA GAAGGACATA CATTTTGGCA
3901   GGTCAAGGAC AGAATGTTAT GGACTAAACT GTGTCCCCCA AAATTCATTT ATTAAACCC
3961   TAAACCCAG TGTGACTGCA TTTGGACATA GAGCCTTTAG GGGGTACATA AACTTAAAGA
4021   TCACAGGATA GGGCCCTAAT CCCATTGGGG CTGGTGTCTT TACAGAAGAT GAGACACTTA
4081   GAGCTCTCTC TCCACGCAGG CACCAAGGAA ACACCATAA AACACACAGT GAGATGGCAG
4141   CCATCTGTTA GCCAGGAACA GATTCTCACC ATAAACTATG TTGGCACCTT GATCTTAAAC
4201   TTCCAGGCTC CAAAACTGTG AGAAAATGAA TTTCTGTTCC AAGCCTCTTA GATATGAAAA
4261   AAAAGATTCT GTTGTTTAAG CCATCCAGTC TCTGGTATTT TGTTATGGCA GCCTGAGTAG
4321   GCTAAGACAA TGAAGGATGT GGTAAAACCT TACGTCCCAA CCACATACCA AAGAGGCTGG
4381   AATTTAGCAT GCTTTCTTCT TTCAACTGTA GGCAATGTGC ACAAGTTCTA AATCCTAAGA
4441   CATGTTGGCT CCTTTACTCT GCCCAAACCT CAACTCAAAC AAACAACGTG AATATAATAA
4501   CATCCAATGA AGTTCTGACA TTTCTTCAAC ATGAGTACAG TAATTCAATG CCAGAGAATT
4561   CATTTTATTT TGAAATCTAC ATGCCATATT CCAATTTCTG TTGAAGATGC AATGGTTATA
4621   TTTATTCTTT TTAATATAGA TTTATCAGAC TGGGCGCGGT GGCTCATACC TGTAATCCTA
4681   GCATTGAGAG GGCTGAGGTG GGCATATCAC CTGAGGTCAG GAGTTTGAGA CCAGGCTGGC
4741   CAACATGGTG AAACCCTGTC TCTACTATAA ATATAAAAAT TAGCTGGGTG TGGTGGTGCA
4801   TGCCTGTAGT CCCAGTTACT AGGGAGGCTG AGGTAGAATT GCTTGAACCT GGGAGCAGGA
4861   GGTGCAATG AGTGGAATC GCACCACTAC ACTCCAGCCT GGATGACAGA GCAAAATAAT
4921   AAATAAATAC ATAAATAGA TTTATCAGTT TATCAATAAT ATAGTTTTCT TTTCTAGGTG
4981   TAAATATAGG TAATGACTGT CCTTTAGTAC ATTTTCTCAT GATGCTCCTC TTACTTGGTT
5041   TGGTACAATA TTAAGTATTG AAATAAATA GAGAATCCTG TCGCTACACA TGAGCACTTA
5101   TTCCATTGTC TCATCTCCAA TATGCACGGG AAATTCTCAA ATTGCTAATA ATCTTGTAAC
5161   ACACATGCAT TATATTCAAC AGGAATATAT AAATTTATAA TTATAATTTA GGATCAACAG
5221   ATGACAAACC TTTAGAAGGT TTGTATTTAA CCTTAAATA TAATTTTTTA AAAATTGGTT
5281   ATAAATTTT TAATACTTTC TTTTTTGTA CCTCAAGGGG AAAATATAAT TCTTATAAAA
5341   GTTCAAATGA TTTACAGAAT ACAAAAAGTG AATAGAGATG ATGAATGAAT TAAAGGAAAG
5401   GATATTGCTA CATAGATTG GAAATTTAAA AAGGGAAATT ACGATTGTTG ATTTTGTGTT
5461   AAAGTATCT GCTTTGTTCA AGATACTTA TGTACCAAAA AATGATTTTA TCTCAGCCTC
5521   ATATCTCAGT AAATTCCTGA GACAACTTT AGTCCCTGGT GCCCAGGTGC CTTTGGTAAT
5581   TGGGAGACCT CTAGTTTAG CATCCTCATC CACTCGCCCC AATTTAAATA GTCCTCCCCA
5641   GGGCCATTCA GGCAAGGGAG ATGAAAACCT GCTCAAGAGT TGGAATCCAA CTGAAGCTAC
5701   CGAAATTCAT TGCTCAATAG ATAATTTTCC CTGGAAGTAA CTAGGGCTTT TGAATATAAT
5761   AGTGGGCATT TCAAAGTAGA AGGTAAAGTA TTTTGGAGAT GAGGAGACAG GACAGAGCTA
5821   CGAGGAATGT CCTTGCTTA GGGACTAGGC TCTTAGCAGT ACCTCTTAGG TAAGAAGCTGG
5881   TTAACCTGGCA CCTTCTGTGT TTCTCTGAAG CTCCCTTTGC TTAGGGACTA GGCTCTTAGC
5941   AGTACCTCTT AGGTAAAGAC TGGTTAACTG ACACCTTCTA TGTGTCTGAA GCTCCCAGAA
6001   CAACTGCCA GTGAAATTTG GATTTTGGGA ATATAGTTTC TTTTTTCTTG TTACTTTTTG
6061   TTTTGTGTT TTTTTTTGAG AGTCTCACTC TCACTGCAAC CTCCCCCTCC TATATTCAAG
6121   TGATTCTCTT GCCTCAGCCT CCCGAGTAGC TGGGACTACA GGCCTGCACT AGCATGCCCA
6181   GCTAATTTTT GTATTTTTTA GTAGAGATGG GGTGTTTGT TTTTGTAGAC GGAGTTTCAC
6241   TTTGTGCCCC AGGCTGGAGT GCAGTGGCAC GATCTGGCT CACTACAACC TCCACCTCCC
6301   GGGGTTCAAG TGATTCTTCT GCCTCAGTCT CCTGAGTAGC TGGGACTACA GGCCTTACA
6361   GTTGAACACC GCCACACCTG ACTAATTTGT GTAGTTTTAT TAGAGATGGG GTTTCGCCAT
6421   GTTGGCCAGG CTGGTCTCAA ACTCTGACC TCAGGTGATC TACCCACCTC AGCCTCCCCA

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6481 AGTGCTGGGA TTACAGATGT GAGACACCAG ATCAGCCTCA GAAGACATTT TCTATTGGAA
6541 AGAGAAAACA CTATTAGCAA CCTATTAGTC TAATATTTAA TACTTAATGT CTTCCTTAGT
6601 AATAAACCAA CTCTCTACAA CAAAGTGCTT CCTGGCTGCC TAAGTCATTG ATTCATTGAG
6661 TTCAACATTT TCTCAATGCC CAACAGCCAA GTGTCTCTTG TATGCCAAGT TCTATGCTGA
6721 TTATCAGTAT TTGAATAAGA GGGGGTCTAC ATCTTAAGTA CTGCTTAAGA TGAAAGCCTC
6781 TAGGTTAACA AACTTAACAC AATGTATCAT TCACTACTAA ATAGACCGAA TACAAAATCT
6841 TGTTATTGGA GCCCAGAGAG AAGAATTGAA ATTCAAGTTT TCTCTCTCTC CTTTTCTCAC
6901 TCACCACAAT AAGTCAGTTG CACCAAGTCT TGTAGCTCTT TACTGAGCCA TGTTTTCACG
6961 TGTCCCTTTG TTTTATTTGC CACACCCTAA ATAAAAATTG TACTGGCTTT TTTTCCCTGG
7021 GTTTACAGTA TTAATACATT GTCAAGATTT ACCTCTTCGT GTAGATTCCC TGGGGAAAAT
7081 TACCTTTCCT CCTTCCCTTA AATTCTTCAG AGGTTAGAAA GCCATTAGTA ACATTCTGGT
7141 ATGTGGACAA AGTTTACCCA TTATGTATGG ATGTTTTACT CTTTCTATTT TTCTGACAAT
7201 AATCTCTTAA GGAGGTGTGG TTATAGAATA GTCAGCTGTT ATAAGTACTG TTTTCTGGC
7261 CTTACAACCT AAGTCTTTTA AGCTGTTTCT TAGTTTGCTC ATCTCAAAAT TCGGAATAAG
7321 GATAAACCTT ATCTCTTAGA TTGTTGGATT AAATGAATTA ACATACTGGA AGCTCATGAA
7381 ATGTGCCTGG CACACAGTAG TGCCTAATAA ACCATCTCTC TTATTCAGCC TGTTTTCTGA
7441 TTTCAGAATC TACACTTGCT GAGCCAGGTT CTTTTCATTT CAAGGTGAGC AAAAGCATAC
7501 AAGGAAGAGA TGGAGGTAGG AAGAGATTAA GCCCTAGGCC AAGGTCACAC ACCGATTGGG
7561 AGCTGGAATC AAAGGCAATT TGGTCAGTGA ATAAAAAGGA TTCCAAGGCC CATAAGGCCAA
7621 TTCTAACCTT AGGATCGAAA TTCTCGGACA TACAGGAAAT GCTGGGGGGG GAAAATCCGG
7681 TCTTCTCAGC CCAAGAGCCA TGTGAAACCA GACCTTCAA TCTGATGATT CTCAGCCCAG
7741 CTGCCCATTA GAATCGTTGT AATTTAAAAA TACCCTCGGA AAATTCTAAT ATGTGGCTAT
7801 CAAAGGTGAT CATTTGCTTT TATGCCACTT TGTTTTCCACC CAAATGGGAC ATCCAACCCT
7861 TTTCTTTTGA GAGTAGTTGT AGGGAAGGA GGGGGTGGAG GGAGGGAAGA GCGGAAAAGG
7921 CTGGATCCGC CCTGAGCCGG TGTCAATATC TGGGAAGTGG GAGGCGCGTC AGCAGTAAAC
7981 AGCTTCTGCT AGGATTATTA TCTCCTGCCA CACACTCGGA TTTGAAGGCT CCAAACGAAA
8041 CAATGCAAAA CGCTTCAGTG GAGTTCAGTA AGCGTTAGAC TAAACGACTG GGTATGTTTG
8101 GCCAGTCTGA GCAGCTGGGC GCAGATGCAT AGGCAAGACT TAGCCCGCCT AGACTTTTCT
8161 GCCCACTTAA TTCCGATCAA AGCAGAAACC GGCCGGGCGC GGTGGCTCAC GCCTGTAATC
8221 CCAGCACTTT GGTAGGCAGA GGCTGGCGGA TCACCTGAGG TCAGGAGTTC GAGACCAGCC
8281 CGGCTAACCT GGTGAAACTC CGTTTCTACT GGTGGCGGGC GCTTGTATAT CCATCTACTA
8341 GGGAGGCTGA GGCCGGAGAG TCGTCTGAAC CCGGGAGGCG GAGTTTGTAT GCAGTGAGCC
8401 GAGATCGCGC CACTGCATT CAGCTTGGGC AACAGGAGCA AAACCTCCGT TCAAAAAAGC
8461 AAGCAACAA AAAAAAAT GCAGAAACCG AGATCCGGA GAAACCTCG GCGAGATTCA
8521 CAGAATCCAG GAAATAGGT CTCTAGAAAT TTGTCCATGG TCCCAGATCT CCATTCTCTG
8581 TGGGTGGGGC AGCTGTTACC AGATCCCTAG AAGCAAAGGT TTTTTGGGG GACCGTGTCT
8641 CACTGTTGCC CAGGCTGGAG GGCAGTGGCA CGATCTCGGC TTACTACAAC CTCGCCCTCC
8701 CAGGCTCAAG CGACTCTCCT GCGTCAGCTT CAAGAGTAGC TGGGATTACA AGGTATGTGC
8761 CACCACGCCC AACTTATTTT TTTATTTATT ATTTTATTT AGTAGAGAGG TGTTCACCA
8821 GTTGGCCAG GTTAGTGTG AAGTCGTGAC CTCAGGTGAT CAGCCCCCTC GGCCTCCCAA
8881 AGTGGTAGGA TTAGAGGGGT GAGCAGAAAG CAAAGGTTTT TGAGTGGCCA CAGCCCCAC
8941 TCTATTTCTT TTTCTGCCTG TAATGGCAAC CTAGACGCTT GAGCTTCTTA AAATACAAGA
9001 GTAAGTTGCA TGTGAGGCAC CGTCTACAT TAGGGACATT AGTCTGTTTT ACAGACACCT
9061 TTCAACTCCC TGGTTAACTT TTAGGTAATA TACTCTGCAC TTTAGCAGGA ATGGGACCTA
9121 TAACTCTCAC AGAATTAGGA AAGTGAGGCT GCCTACAGCC TAAATTGAGA AAAAAATAGA
9181 CGGGGGACTA GTCGGAGGAC CAAACAAGGT TACCAACAGC TTAGAGTTTT GCCTTCAATT
9241 TACATTTTTA AAGTAATCAC AACGAAGTGT TTAGATCACG AGGCATCCCT GCATGTAAAC
9301 TGTTAGGCAC TAACTATGGT CGATCTTACA AAGCATTAA TAGAATATTT CTTTAGAGTA
9361 TGATAGTACG TAACTGACCT ACTATTACAT ACAAACAGAC CAACCTTTAG TAACAGCGCT
9421 CCCCCAAAAC CGAAAAGCAG TAATACGCTT TGCTCAAGGT TGGCATAAAA TTAACCTACC
9481 TTAGTGCCTT TTTTCTTCT ACCTACAAGC AGTGAGGTTA GCTCTTCTT TGAAACGGTA
9541 GGGGGGCTCT GAAAAGAGCC TTGGGTTTT ATAGCGTTTC CGGGAGCTCA GATACCTGTC
9601 AAATCACTTG CCCTTGGCCT TGTGGTGA CTGGTCTTC TTAGGCAGAA GCACGGCCTG
9661 GATGTTAGGA AGGACGCCG CCTGAGCAAT GGTCACCCG CCTAGCAGTT TGTGAGCTC

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9721 CTCGTCGTTG CGGATGGCCA GCTGCAAGTG GCGCGGGATG ATGCGAGTCT TCTTGTGTGC
9781 GCGAGCCGCG TTGCCGGCCA GCTCCAGGAT CTCGGCGGTC AGGTACTCTA ACACCGCCGC
9841 CAGGTACACC GCGCGCCTG CCCCACCCG CTCTGCGTAG TTGCCTTTAC GGAGCAGGCG
9901 GTGCACTCGG CCCACCGGGA ACTGGAGACC AGCGCGAGAA GAGCGGGATT TCGCTTTGGC
9961 GCGAGCTTTG CCTCCTTGCT TACCACGTCC AGACATTGCA ATCAGACAAA AATCACCAAA
10021 ACCAGCGGCC TAAGCTCACG AGAAAACAAA CAAAATCAAG AAATATGTAA AACATGGCCG
10081 CTTTATAGG TAGTTCCTGG GGAGTAAATC CGACTTTTGG ATTGGTCGGT AGCAAATGCT
10141 AGTCAGATAG CCAATAGAAA AGCTGTACTT TCATACCTCA TTTGCATAGC TCTGCCACG
10201 GATGACAACT GTGCAGTTTG TCTTCCAATT AACTAAGAGG TACTCTCCAT CCCTCATTAG
10261 CATAAAAGCC CTATAAGTAG CAGAAATCCG CTCTTTACTT TCGACACATT TCTGGTGTCT
10321 TAAGATGCCT GAGCCAGCCA AGTCTGCTCC CGCCCCGAAG AAGGGCTCCA AGAAGGCAGT
10381 GACCAAAGCG CAGAAGAAAG ATGGCAAGAA GCGCAAGCGC AGCCGCAAGG AGAGTTACTC
10441 TGTGTACGTG TACAAGGTGC TGAACAGGT CCATCCCGAC ACTGGCATCT CTTCCAAGGC
10501 CATGGGCATC ATGAATTCTT TCGTTAACGA CATATTTGAG CGCATCGCGG GCGAGGCTTC
10561 CCGCCTGGCG CATTACAACA AGCGCTCGAC CATCACCTCC AGGGAGATCC AGACGGCCGT
10621 GCGCCTGCTG CTTCCCGGAG AGCTGGCCAA GCACGCCGTG TCGGAGGGCA CCAAGGCCGT
10681 CACCAAGTAC ACCAGCTCCA AGTAAACATT CCAAGTAAGC GTCTTAACAC CTAACCCCAA
10741 AGGCTCTTTT AAGAGCCACC CAGATACCCA CTAAGAGAGC TGTGGCCAGA CGCCAAATTT
10801 TATTTGGCGG CGGAGGGGTA TTAGAATATA GGAAGTGGAG AGGGGTGGGG ACAAGTGTG
10861 CAGCTTAGAG AGGGACAAAG GGTCTGAAC CCGAAAGAAG CCAGCCATTA AAAATGGCTT
10921 TGGGGTCAAT TCGTTGTGCT TAAATTTAAA ATGGAGACAA GCGGCCATTT TGCTAACTCG
10981 GCGTTCGCGG AAGAAAACGC AGGCTCGCTT AGGTTTCAGA CCCAGCTGTC TGTCCCTGTC
11041 TACGTCGCCA GGATCAACGG TTGCCGTAAT GTCATAATTT CGCCACCAGC TTCTAGCCAA
11101 TAGGCTGTCC TGTCATTTTA AATATTAACC AATCGAGGGA AAGCTGTTTT GAGACTCTGA
11161 TTTACATAGC GGACCGGAGT GGAACCTGG SCAGTAACTG CCTAAGGAAG GACTCCCCCT
11221 CTGTTTTTCG TCGGCACACC TTCGTAGTAT ACTGAAGGGT GTGTCTCCTG GGTTTCCAAC
11281 TGCCCCGGTA ATAGTCTTTT AACCTAATAT GCGTCAGTTT TGATAACAAC ACTAAGCCAG
11341 TACAGAACTA AAGATGTAAG CACTGCGCCA GATGTTGCTT CATACATCTT ATTCTATTCA
11401 ACTGGTTTAT TCAAGATTCA AATCAAATCA AATTTTGCTT GAATCCAGT GCTCAGTCAG
11461 CCATAAATGG TGTGTTGCCT GATTGAACT TAAAATCTCC GTAGGGGGCT TGTAACATGC
11521 AGACAAGTTT GAAAGTTGCT TTAGGAGAAG CCAACTCTTA ACTGCTGGGT AAATGACAA
11581 GCCTTCGAAC ACTGAACTGA AGGCCAGTAA GGACTAGGCG CTGGGTGGGG GAGAATGAAG
11641 AGGAGACGTC ATTAACTTA GCACATACAC TGTATCTCCT AGAGGACTCT CCCTTCCTAG
11701 ACAACTGCAG GCCGCTTTGT GGCCTGGGAA ATTCCACATT CCCTAAGTA TTTTACTCAT
11761 GGTCTTTTCC AGGTAAAGAT TTAAAGATGA AGGGTTAGAC GTAGTCTACC TATCTTTT
11821 TTCAAGTCTA GAACACGTTT TTAGCACCTA GAAGTTTGCT TTCTCCATTA AAAACCGGGA
11881 ATATACAATA AATAAAATTA GTGTTAAAGC AGATTTTAC AAACCTAAAT ACCATGTAAT
11941 TTAGGTTACA GTTATTTAAC ATAAGGACTG TGTGATCTTA AATCTGCAAT TTCTTTACA
12001 CCTGGGAAAT AACTAAGGC CTGTCTTTGG TGCCAGACAA GGCCTTATAC TTGAACACTG
12061 CTGTGCAATC ACAGGCTGCC TTGCCTAGAT AACTTATCTG AGAAATTCTG ATGAGAAATG
12121 AAATTTCCAG AGTCCCTCAC AAGTAAATTT TTTTTCTTT TTTTTTTTTT TTTTGGAGAC
12181 GAAGTTTCTC TCTTGTTTCC CAGGCTGGAG TGCAATGGCG CGATCTTGGC TCACAGCAAC
12241 CTCCGCCTCC CGGGTTCAAG CCATTCTCCT GCCTCAGCCT CCGGAGTAGC TGGGATTACA
12301 GGCATGCGCC ACGACACCCT GGCTAATTTT GTATTTTATG TAGAGACGAG GTTCTCTCAT
12361 GTCGGTCAGG CTGGTCTCGA ACTCCGGACA TCAGGTGATC TGCCCGCCTT GGCTCCCAA
12421 AGTCCTGGAT TACAGGCTTG AGCCACCGCG CCGGGCCTAA ATGGTTTTTT TTTTTCTAT
12481 GCCTCTAATG GACCTGGTCA CTTATTTCCA TTCAGACTGA CCGCTCTCCT ACCTGCCAAC
12541 TAACTAATCA GTGTAACCAA AATCTGCAAA CAAAATTCAG TATTCTTTCC CCGCCTTTTC
12601 CCCTTTCTCT TACATAGATT ATGTTTTTGC CTGTGTTAGA TGAAATAATT CTATTGCTTG
12661 TTCTCTCTTC TGTACAAGTA CCCAGTAAGC AAATTATTAA CTTCTTGGTC ATTTATTTCT
12721 GAATTTTCCA CCAAGACAGT GTTTATGTGA GTCATACAA AAGAACCAAC AGAAATGTGT
12781 GTCTTGGAAG CAGGTTGTCT ATCCCTGGAC CCTTTGAGTT TTCTGTTTAC TTTCTTTGG
12841 CTTTTGCATG CTAAGGTTT ATCGTCCGCG TTTGTTTGT TTTGTTTATC TAATTGGACT
12901 TGGCTGATTG GTTGCATATT GGTGGCAGTA GTAGAATTTG AATTCTGGTT TTCTGGTCAC

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12961 ATCATTAAGT GATTAGTCAG TGGAGAGGAC AGGAAATCTG GTTTATTTAT TAACCTTTTT
13021 TTGGGGTGTT TTTGTTTGAA GATGTTGATA TTCTCTGTGA GGACACAGGG TTAGAGTTGG
13081 TGTTTTCTT TCTGACTTTA CATGGGATTT GATGTTTTGT GCTTGTATGC CTCTTTCCAC
13141 CTTCAAAAC TTGCTTTTT TGAGTCCAAA TAGTTGTCGA TATCTGCAA ACCAGTATTC
13201 CTGTGTTAAG ATGATATGAA TATAAATGG CTGCCCTGTT ATAACCTTTG ACTTTAAGAA
13261 AGTGTTAGGA CTAACAGGAG ACAAAAAGGA AATCAAGGAA ACCGAATGTC TGGTCTCAAT
13321 AACTGCTATG GCAGAGGCTC TACAGCTTAT TATTAATTTT AGTAATTTCA CATTATTGCC
13381 CCTTCACGTT CTTAAGTAA GGTTAGAGGA CAGAAGAAAC ATAATGTTGT TACAAATTGG
13441 ACTATTGAGT CAGGGAAAAA AAAGAGTGCT TTCAATATCT GAATAAAACA AAGATTTAAT
13501 ATTTTCTAAA CCTAACGAG TTTATTGTAA GGGATGTGAT GCTGGAACT AGGAAACTAG
13561 AATTTTCTTC TAACTGAGA ATCAGAATTA TTCATATTCT CAGCAGTGGT GCCACCTGAG
13621 GGACTTCTGA TCTTAATTAC ATACTTTTAT TTCTTTAACT GATCAACATG CTAAATAGAT
13681 AACCTATGGC TCTGTTTTTA CCCACTTTAA ATTCTGTTCT ATTAGCACGG TTAGCTTTCC
13741 TAATTGGCAA TAAGATTGAG ACTATCTTTT TTTTTTTTTT GAGACAGAAT TTTGCTCTGT
13801 GGCCCAGGCT GGGGTGCAGT GGCACAATCT CGGCTCACTG CAACCTCTGC CTCCAGGGTT
13861 CTAGCAATTT TCCTGCCTCA GCCTCCCCAG TAGCTGGGAT TACAGGTGCA CCACCACGCC
13921 TGGCTAATTT GTGCATTTTT AGTAGAGATG GGGTTTCGCC ATGTTGGCCA AACTGGTCTC
13981 GAACTCAGGT GATCCACCTC GGCCTCCCAA AGTGATGAGA TTACAGGCGT GAGCCACCGT
14041 GCCCAGAAAA GACTATCTTA TTTTATGAAT TTAAATAATT GTGAAATTAT CCACCTAAGG
14101 GAATTAATAA ATTATAATGT AATCTTAAAT TTAGTTGGC TTACATAAAG ACTTAAATA
14161 CATCAATTTA AATAAAAACT CATTGTGCTA AAAAAAATC AAAAATTTTC CTTGTGCTTT
14221 AAATGTGCTA CCTCTTAAAG TTCTAATTAA GAGAAAAAAA GTTTAACTGT GAGTTTCATT
14281 AGTGGTCTTA GTTAACAGCT TAAAGTATTT TGTAATAAAA ATACTTCACA ATTTTAAAT
14341 AACTTAAAAA TATTAATACC TCTTTTATTA GGTTTTTTTA ATAAGGAAAA TATATAATAC
14401 ATCTAATCAA GATTTTTTTT GGACAAATTG GCTTAATAAT TTCATTTTAA AAATGGCTTC
14461 TTTATTCTTA TACTGTAAAA ATAATATTAG CAGAATATTA TAGTATACAC AAGTTTAGGG
14521 TTCATATTCT AAAAAACAAA AACAAAAGCT AATTTAACTT GCATTTACTA AATTTCTTCC
14581 ACTAGTTGTA CTGGTTACAT GAGTTAACAT CACTTTATTT ATTATTCTAA AATTGTAAAT
14641 TATTCATTGA ACCAAATTAA ATGATAATAG ATAATGTCAT TTTTAAAAAT GGAATTAAAT
14701 TTTATGTTAC TAATTATAAG GATTCAATGT GTGAGCTTAA GTACTGAGTT CACAGTGTAT
14761 GATAACTTTA AGAATTTAGG TGAATATTAT TAAATTGAGT AAATTAATTC TCAATCTTTG
14821 GATACCTGGA CAATTTCTAA ATTGGAGGGT ACAAATACA AATCACAAGA AACAGTGTAG
14881 TTTTATGCAA ATAACATTTT TACACAGTTT AGAATAACCA TTGATAAACA GATAAGAGAA
14941 CATATGATTG CCTTAGAATA GATACTGTTG CTTTCGCCAC TTTAGATTG TAAATCACGT
15001 ACTGTATACG TGTGGGCGTA GAGGACCATG CAGGTTTTGG ATGACTGCCT CTGTTTTCGT
15061 CATGCCTATG CGGGAACACA ATTGCCTGCT TTGTTTAAAG GCTATGGTTA ATCCAAACAG
15121 CTCTGACTCT ATCAAGTACT ATAGCTACAG AGAAACACAA GTAAGCATTG GAGATAATGA
15181 CTACCTTGAG CCTTTACTTA TTTAAAAAGT TGTTACTGTT TGTTAATGTG GTACATTCAA
15241 TTTACTATGG ATTGTCACTC TAAAATAAGA CTTCAATCTT TTTCTTATTT TTATATAGCC
15301 ATGATTTATA TTCATATCTT AATGTAATAA CCAATCTTCT CTGACAACAT TATAACAATG
15361 CTGGAACCTC CATTTTCAGT ACTTCAAACA ACAAATACTG CTTTTTACT TCAGAGCAGA
15421 TGGATATGTG CTTCCCAGTG TAAACACATT TGGAATCTCA CTGAGAAATA CACTATCACT
15481 AAAAATACAG TTCTGAGATT CATTAAAAGA CCTCCAGAA TCTGGAAGTA GGAAGTTTCC
15541 TCTTCAAAGT CTACAGAGGA AGATGAGGTC TGAAATAGAC AGCTTCTTCC TTCTTTTACC
15601 TGTGGTATTA TTCTGTTTTG TCCTTTTCTC CATTATCTGT CTTTCCAGTG ATGAAATTTT
15661 GATCTGGCCC TCCCAAGTAT TAAAAAACAA GCAAATAAAC AAATCTCAGT TATATTTTAC
15721 TAAGATATTG GCATGCTAAC TTTTTCAGG TTTGTAAACAA GGACCTTTAT AACTTGACTA
15781 AAAGTTCCTA AATAAGAATA TTTACTAGAA AATTTATTTC TGCCTGTGGC CCACATTGTA
15841 GTCAAAATAA TCAATTAGGA AAAATGAAC TGTTTAACTA AAGTTGACCA AACTGATCTT
15901 TGACCAAACT GATCTTTGAG ACCTATTTCAT CTAAGACAAG CCAATTAAT TCTTGGAGAC
15961 AATTTGTACT TTAAGGAATT CTTATAATAT TTGTAATTAC CCTCATACT TTTTTTTTTG
16021 CCCTACTTCT GTGCTTCTCT AATATGCAGA TTATTAAATG TTGTTACAAA GCCATTGTCA
16081 AAAAAACAAA AAACAAAAAA CTAAACAAC TCACATGGTT AGACTTGCTC CTTTATGAGA
16141 TATTTTTACC AAAAAATGGAG GAGTTGAAAA ACTCTGGTGC CAGAAATCGT GAAGACATGG

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16201 CCTACCTAAC ATGGAAATGT TGGTTGTCAG TGGAAAATAC TACACAGAGA TAGCCATAGT
16261 GCTGCACAGC CAATCTTAAG TGTTCCTAGA GAATCACTAA TTGTTTCTAG AGAATCACTA
16321 ATTGTTTTCT TTTAACATT C TGGTTTATA CAAGAAGAGA GTATCCATAC TAAACTCTTT
16381 TCTACTGAAA ATAATGTGCA AACATAACAT CCTATTCCTA GACAGTTTGT AGTTTTTTTC
16441 TCCCATTCT ATTTTATAAA TCATCTTTTT AAAATACTTT GTTGAGTGAA ATCAGTCCAT
16501 TGCTTGATAT ACCTTGAGCA CAAGTAAATA GTATGCCAAA AATTAAATGT CTTTCAGTCA
16561 CAGTTTGACA AACTCAACTA CCTGAGCCT ATAGAGTGGT AATAATTGCC CTAATCATAA
16621 AGATGGGGTG AAGATTAAAT GAAATAGCAC CTATAGAACA CTAGTTCAG ACGTGGTATC
16681 ATGCTAGTAA AATGGCTGCA CAGCACTGCT CAATGATGAC AAAAAAGTGAA GCTTCTGGAG
16741 ACAGACTCCA AGTTTGACTC CCAGATCACC ACATATAAGA TGTGGGACTC TGAGGCAGGT
16801 CATTTAATCT CTCTGTGCAT TAGTATCCTT CTCTATACCT TTACAGTGAT GGTAATAGCA
16861 CCTACCTTCT AGAAGTATGT GAAGATTAAA GATCCTTAAT GCATATAAAC CACTGTGTTT
16921 ACTGCTGTTT GACAAATTTT ATTTATAACC ATCTTTACGC TCCTAAAAGG ACTTGAAGCA
16981 GCTTATGACT GAAGACTTTG GTAGGAGTTG GCCTTCTATA AATTATAAGA ATTTCATAAA
17041 TTATTTGATA TGAAAATGCC AGTTGATCAT AGTATGTTTA CCGGGGTCCA ACAGGTTGAG
17101 AAAAAATACA CTTTTTTTCC CTGAACATAT GAAATTAGCT CTCTAGGCAT ATTCCTAAGG
17161 ACTTAAAGAA TGATAACTAT CATTTCTCTT AAATCTTCCA GATTTGGAAG GATATATATA
17221 TTCAGCACAT TGACAGACAA TCCCAGTAGT CCTAAATTAA AAGACATTAA AAATTAGTGA
17281 AACTTTTCCT ACCTTTAGCC TGTGTAATCC TGGATGACCA AGCATAAAAT TAAATTGAGT
17341 AGAGTATACC ACTGTAACAT TTCCTGAAAG GTATTCTAGG CTCTGAGTAA TTTCTTTGGG
17401 GTCTGAAGAT CAGTTTGACA TATCCTCAAG TATCATGAGT TCATTATAAT TAAGAAAAAG
17461 AGAGTAAATC TGGAGAATGA GCCACTTTCT TACTACTCCT TGACCTCAGT TCTTTTTTTC
17521 AGAGACAGGG TCTCACTTTG TTGCCCAGGC TGCCAGGCTG GAGTGTAGTG GCGCAATCGC
17581 ATCTCATGT AACCTCCACC TTCTGGGCTG AAGCCATCCT CCTGCCTCAG CATCCTGAGT
17641 ATCTGGAACC ACAGCAGGTG CACACCACCA TGCCAAGCTA ATTTTTTAAA AAGTTTTTTG
17701 TAGAGATGGG GTCTTACTAT GTTGCCCAGG CTGGTCTCAA ACTCCTGGGC TTAAGTGATC
17761 CTCCTGCCTC AGCCTCCCAA ATTGTTGGGA TTACTAGTGT GAGTCACTGT ACCCCGCCCC
17821 ACTTCAGTTC TGAGGAGGAA AAAATATGTA ATAATAATGG GACTTTGGTT TGCTGATTTA
17881 AAGATTCATG TAACCTTATC ATCCAATGCG CAATTTGTAG AATAATTAAT AGAGACATCT
17941 GGTCTCATGT TTCTACAGTT GCTCATGCCT TGATAGTAGA TCTCCTTGCT GCTGGCTCAG
18001 AAGGGTAAAA GAGCAGAAAT GATGGGGCTT CTCTCATCTT ATGAGGAAAT AGACCTATGT
18061 AGAGGAGGCT ACCTGTGGTA AAACCTTATC CTCATCACTT AAAATCTAG GCTTATTCTC
18121 TGACCATATC AAGTTTCAA ATGGTAAAAG AATTGGATT C AAGAGAAATA TGAATAAACT
18181 TTTGTTTCA CTTTTCTCCC TCCTCTCCCC CCATTCTCCC TTTCTTTATT TTCTTGCTCT
18241 TAGTTTTCTT TTCACTTTTT TGTCTACTAT TATTTGCCCA AACTCAACTG TAGGCTAGAA
18301 CAAAAAATAA TTGAAAATTA AAATGTGCCC CTTTTGTTGT TAGACTTGCT TAAACAATTG
18361 GGGTAATGAA CCTTGGACAC TAGATTTTAA AACACACACA TTTGAGCTTC AGTGCAGTGA
18421 AATAAATATA TTTTAAACAA TTAATAAATA AAATTGCATG TTTAAAAAAT CTGCAGAGAA
18481 CAATACACGT TGTGAGATCT TGAATGGAAG GAAAACCTGCT AGCCTCAAGA GTGGATCAAA
18541 GATGCTCAGC AGGCAACAGA GTAAGAGCAT GTTGAGGGGT TTAGAGAGTG TGCTCAGGGT
18601 TCTAGGCTCT AAAAAACAGA CAGTCCCCAC GGCCTGGCCT TCGTCGCTGT ATCTTCTTTA
18661 TGAAAAACAC TAAGTCTTTT TCCTCACTGG ATAAATTTTT ATCCTTCAAG TTTAGATCAA
18721 ATGGAACCTT AGGACACTGA CTAGGTTACA TTCATCTTTT AAGAGCGTAC AGACATTCAA
18781 GGGCTAGAGG ATGTGGGTTT ACTGCACAGG CTCATTATCC AACAGCTGTG CTACCTGGGA
18841 AACTTAACCT CTCTGTGCCT TAATTTCTCT ATCTATAACG CAGGGAGAAT GACAGTAGGT
18901 ATCTCATAAG GTTGTGGGAA CAACTAAATG CATTGGTATC TATTGTGTAA AGTGCTTAAA
18961 ACACTGCCTG GCACAGAGCA AACATCCAGT GAACCTTAGC CATCATCATT ATCATTGTTT
19021 TCAGAGTCAA ATACAATATC TCATATCTGA TAAATTACAG AAGTGAATCA ATCACTCTCT
19081 CTCTTTTCTC CAGGGGGAGA CAACAGCTTT TAGACATATC TTTCCAACA GTCGCTACTG
19141 CTGGACACTG TTTTATCTTG CAAATAAACC AATGAAAATG AGTGATCCTA GAAGAAGATA
19201 AATGGAGGTA TTTTGAACAA TCAAAGAAGG ACAAATGAAC ACCTGGCTGA GAAAAATTAG
19261 CTCTTTTTTTC TATGCATAAA ACTATTAAAA TATTCTTCAT AGAAATTTAT GACACAGGAA
19321 ACATAAAGAC AAAATTAAAA TAACTCCTAG TATCTCCTAT TCTTTTATA TGTATATTAT
19381 ATATACTCAT ATTCATATAT ACATATATCT CACATCATGT ATCATATATA AAATAAATTT

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19441 AGGTGTCATG ATATATATTT AGATAAATAT ACTTAGAAAC TTTTATATGG ATGTATAATT
19501 TATGGATATA TTGATAATTA TGTATTTGTT ATTGACTACT TCAATTGATT CCCATTTTTA
19561 TGCATTATAT TATAGATTAT ATAGCTCACA CATCTTTGTA CATAAATCTT TGTTCAAATA
19621 TTATTTCCCTA AGGATAGACT TCATGAAGTG GAAATACTAA ATCAAAAGTG AAAAACATTT
19681 TCTAAGGTTC TTAACATATA CATTGCCAAA TTGCTATTCA GGATCATACC AATTTATAAT
19741 CCCAAAATAA TATGGAAATT CCTGTTTTAT AGCACTCATA TTTACAATAA ATTTTAAAAA
19801 TCACTGTTAA CCTAATAGTC CTTCAAAAGA AAAAAAATTT GAAATTACAT TATTTTAATG
19861 ACTCTATTAG TGAGGGTCAT TCTTCCCATG TTTCTTGTTA GCCATGACCC TATAAGAAAT
19921 AAAGTCACT GCAAAATGAT AAACATGACA TCAATCATT CATGGGAAGG CACTATATAA
19981 AGAATAATAC CTTAGGTTAA GGCCACATAA ATATTTATCA GGTGCCTTTT CTGCGGAGGA
20041 CTCTGAAGGG ATACTAACT GCATTTAGCT GCATGCAACT GAAACTACTT TTACCTACAT
20101 TGTCTCTTAT AAACATTATA ACTACTCTTT GAGAAAGTGT TTACTATGGA CTGAATTGTC
20161 TCCCCATCCC CCCAAATTCA TATATTGAAG CCATAAACCC CAATATGACT CTATTCCTAG
20221 ACAGGACTTA TAAGAGGTAA TTAAGGTTAA ATGAGGTCAT TAGGATGGGT TCCTAACTGG
20281 ATAGGATTGG TGGCCTTATA AGAAGAGGAA GATTCTGCAC TTGGTCTTCC AAATTAATAA
20341 ATTTATTTAA AAGAAAAAAA AAAAAGAGGA AGAGAGGGAG CTCTGCACAT ATACTGAGGA
20401 AAGGCTATGT GAGCTCTCAC AGTGAGAAGG TAGCACTCTA CAAGCCAGCA AGAGAGCCCT
20461 CAACAGAATC CAGCCATGCT ATACCCTGCT CTGAGACTTC CAGCCTCCAG AACTGTGATA
20521 AAATTTTGTT GTTTAAACCA CACAATCTAT GGTATTTTTT TATGGCAGCC CAAGCCAACA
20581 AAGACAGCAT CATTGCTGTC ACTTACAGAC AAGAAACTA AGACTAGGAG AGAGAAAAGT
20641 TAACTTGTC CAAGGTCACA AAAGCCAGAA ACAAGTGAGG TGAGAAGTTG ACCTTGTTCT
20701 CCTCAATCCA AGGCCAGGAC TCCTCCACTC CACATGTAGA TAGCCACCTC ACAGTCAACA
20761 GCCAAATGTC CACACCCAG AGTCAGCAT AGACCAAGAT GTCTTACCAG GAGACAAATG
20821 CCTCATCTTG AATAAATATG ATCTAACAACT TTACCATGT AAAACATGA ATCTCATGAG
20881 AAACAAAAAT GCAAAGTATG TAGAAAACTA TGTTTACCAC TTAAGTACA GTGATAAAAA
20941 GCTTAATGAT ATCCTTATAG TCTTGGAGGG GTTTGTATAT GTGGTGAAC AGGTGCTCAC
21001 GCACTGCTGA TAGACTGTAA ATTGGTCCTA GAGAGAAAAA TAAATAAAT GGAAGGAGAT
21061 ATGCTGTATG TTTACTTTTT TTATGGAAC ATATGATATA CCTGGAAAT CGATTGACCA
21121 TGCATCTATT TCTTCAATGG GTATGCACAG TTGAGCTGTT CCCATGCACC AGGCACTGTA
21181 ATGGGACAAC TGCACATGAC AGTCAAAAT CTCAGTCTCA TGAAGTCGAC ATGCTCATGG
21241 AGAGGTGCTA CCCACTAAAC TAATATTTGT ATATCAATTA TGGATACATT GGGCCACATT
21301 TACAGAAATT CACTTACAGT GGGTTACCAG AAGGGATTTT TTTTCTTGAT TGGCAAGAAG
21361 GCTAGGCTGT TTTGTTGGGG GCTGGCAGGA GCTGTCTAGG CTGCCCAAGT ATGCAGGTCT
21421 CTTCTATCAT CCTGTGTTAA CCATCTTCCA TGTATCTTTC AACCTCATGG TCATCTGCAG
21481 CATGTCTAGG GGTCAATCT ATGTTCCATG CAGGAAAAAA GGGTAAAGGG AAAGGGAAGT
21541 AGGCATGTAC CATTTTAATG CACACCTTGG TTTTCAGAAA ATTTAAGAAG AAAGACTTTC
21601 TGCTTTTCTC TGAATATTCT GTATCTGGA TTACAACGCA ACAGAAACGT CACCTTAAAT
21661 TCTAATGTTT TTCTCTCCTT GCTTTCAAAA ACTGACTCAT TAACCTCCAC GTGGCTTGGA
21721 AAAATTATTT CAGTCATCCA GTAATGAGCT GTTCATAGAA ATGTTTGGGA CATCAAGTCT
21781 GTGTTGTTAG CATTATACAT GTTAAGCATT GAATAAAAAA CAACATGATG TGGGTAAATT
21841 TCTTTACTTA CATATAAGTA CTTATATACT TATAGCTGAA AAGAGAGGTT GAAATGTCAG
21901 GTGGAACAGA AATAAGATTA CCTAGATGTT TCTCCTATGG GTGATTTTCA GCTATGCTGA
21961 TCTTTCTTCT GGGTCAGGTA CTCCCAGAAC TTCTTAATTA AATGGTGGCC CTGATCTTAG
22021 TTCTCTCTC CTCTTAGACA TTTTCCAGGA CTACAGAAGA TGTGCAGTTT ATAAATGAGT
22081 AGCAGAAACC TACTGAACAA ATTATTCAGG CTCATCTGAA CAGAGAGGAC ACCTTCTCTG
22141 CTATACTCTC TCAGTGATTT CCTGCTTGG GGGTCAATTA TTGTCTTGGA CATTGATTTA
22201 AGCACATAAT AATTGTTGTC ATTGCTTATG TTTGGATTTT ATCTCCCAA ATAGATGGTA
22261 AATTCTTTAG TTTAGAGACC AAGTAATACT TAAAAAATA TTTTGTGTGT GTGTGTGTGT
22321 TTTTCTGTG TCTCTCAGCC CTGTAATAGC ATCGTACTTA CACTTGTTAG ATTTTLAGAG
22381 ACAACTTTTA CAAAACATGG AATTATCTAC ATACCCTTTC TACAAAACAG ACAAATTAAT
22441 TACTCAGTAG TTGAACCAA AAAAGCAGTT CAAATAAAAT ACTTGAAAT GAAGAAATCA
22501 TTTGAACAGA GTTAAAGTTA ATCGTAAAT AATGTCTGTA AAAATTATTG CCAATCAAAAT
22561 ATAAAGTTCA AAAATAGTGC TTGAAAAGG AAGAATCATA TGAAAAGGGA CTACTCATTT
22621 TAAAAATGTT AGATATCAGG AAAAGCCAAG AAGTGAGTAT GGTAAGAGTG CTGTCAAGTG

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22681 AAACCCTGCT AATCTCACTG AACATGTAAA AATCTGTAGA TGCCTTTTATT TTATTCACCTC
22741 ACACACATAT GTAGAAAAGAG AAATATATGG TAAACATTAA AAAAACCCAA TTAGAATGTA
22801 AAATTAATAC TTTAAAAAAT GGGCTGTATA CTTTCTTAT CACCGGAGAT AAGAATTTAT
22861 TATTTTAAAA ATAAAGTTAT TTTCTCTGTG ACTGTTTCCA TGACTTTGCT ACTTAGAAGT
22921 TAGAGATGCC AAAGTTTATC TAAGAAAATG TTTATGGAAA TATTATTTCA ATAATGAATG
22981 TTTAGAAGAC TGAATTTCTT GACTGGGCGC AGTGGCTCAT GCCTGTAATC CCAGCACTTT
23041 GAGAGGCTGA AGAAGGAGGA TCGCTTGAGT CCGGGAGTTC AAGAGCATCC TGGGCAACAC
23101 AGCGAGACCC TGCAGCAAAG TAAAAAGAAA AAAGAATTGA AAAAGGAAGA CTGAATTTCC
23161 TTTGGGCAAG TCATGTGACA TTCCTGTGCC TCAGTTTCTT CATCTATATA GTTAATTCCT
23221 ACATTTTGG GGAAGGAGGA GAAAACTTA GGATAGTGAC TGGCACAGAA GAAGCACTAT
23281 ATACTATATA TATGTGGATA TCATTTGTTT TTATGGTACC ATTTTAGCTA TCTAATGCAA
23341 AATATGAATC TTTTTTTTCT GGGTCTTAAA TTATGGAATG TAAGAATTTT CTAAATTCTC
23401 TAATTCTGTG TTAGTTTTAA AGCAATGGAG TAACGTATCT GTCAACTTGT AAATATAAGG
23461 ATCAACCTGA TCCACAATTT GACCCTTAGC CACTAATATT TAATAGTACA ACACTCAGAA
23521 ATTATCAAAG GTCAGAGAAG CCAACAAAT GTAAAAACAT ACAGGTGCTC AGAAAGATGC
23581 ACCTGTAATC TCTCTAAGGA GAAATATTTT CCAACTGAG TGACACGGTG CTTTAGTGAG
23641 TTGTGGAATC AATCTCATGA TTTCCAACCT AGTGTCTTTT TAAAAATGAA CTAGTCCACA
23701 GTAGAATATA CTAAAGTGCT GGTGCTTAAG ATAGTATTGT TTTCTGGAAA AAAAAAATAA
23761 ATTTTTTTTT TTTGAGACAG GGTCTCGCTC TTGCCCAGGC TGAAGTGCAG TGGCACAATC
23821 ATGCTCACTG CAGCCTTGAC CTCCTGGGCC CAAGTGATTC TCCCACCTCA GCCTTTTGAG
23881 TAACTGGGAC CACAGGTACG TGCCACCACA CCCGGGTAAT TTTTAAATTG TAGAGACAGG
23941 GTCTTGCTAT GTGCTTAGGC TGGCCTTGTG AACTCCTGGG CTCTAGTGAT CCACTAGCCT
24001 CAGCCTCCCA AATTATGGG ATTATAGGCA TGAGCCACCC TACCTGGCCT GTTCCCTGAA
24061 TTTTTTTTTT TTTAGGTGT TTGTGCATAT GTGTGTGTGT ATGGGTATAA CAGAGAGACA
24121 GAGAGAAAGA AACTTTTCTA TCTCACTTTG CAATCAGAAG TTTGAAGTCT TATCTTTTGG
24181 CTTTGTGTTT AGAAATATTT CAAATGTAGA CTCTCTCCTT TACCACACTG TCCCCTTAGG
24241 CAAGGTCTTT GCCATTCTTC TGAGACTATT GCAACAGACT CCCAATCTCT GACTGTGGGC
24301 CCTTCTCAA AATGATTGTT TATGCAATAA ATCTAAACCC AAGACAATA CAACAATACA
24361 ACAAATTCTC TGCTTAAAAA CTTCCAATGT CTGCCGGGCG CGGCGGCTCA CGCATGTATT
24421 CCCAGCACTT TGGAGGCAGA GCGGGGCAGA TCACTTGAGG TGGGAGTTC GAGACTAGCC
24481 TGGCCAACAT GATGAAACCC CATCTCTACT AAAAATACAA AAAATTAGCC AGGCATGGTG
24541 GTGGGCGCCT ATAATCCCAG CTAATTGGGA GGCTGAGGCA GGAGAATTGC CTGAACCTGG
24601 GAGGTGGAGG TTGCACTGAG CCAAGATCAC ACCATTGCAC TCCAGCCTGG GCAACAAGAG
24661 CAAAACCTCG TCTCAAACCA AACCAAAACA AAACCTCTAA TATCTACCAA ATGTTTCACA
24721 CAAGTATTTG GGGATCTTCA CAAATGGCCC TTATGGAGTT TTCCTTTGCT GAGACCCTAT
24781 GCTCTGGCCA CACTAACTC ATTACAGATC CCAGAAAGGC CTCAGCCTTT GTGAGCAAGC
24841 TCTTATCTCC AGGCCTCTCA CAAAGACCTG TTCCAGTAGA AGCTCAGGGG AGCACACTGG
24901 ACATTATTCC AACAACCCTT TCCCCACAGC TATGCAGCCA AATCTGCCAG CTCAGTTAAT
24961 TAATTAAGCA ATTACAGAGT GAGGGTCTGC CCAGGCTGGA GTGCAGTAGC TGCGACCTCA
25021 AGCTCCTGGG CTCTAAGTGA TCCTCTTCAG TCTACCCAGA AGCTGGGACT GCAGGCATGT
25081 GCCACCACAC CCAGCTAATT TTTTTTTTTT TCAGTAGGGA CCAGGCCAAC CTAGTCTTGA
25141 ACTCCTGGCC TCCAGCCTTC CGAAGTGCTG TAATTACAGG CATGAATCAC TCGCCCCAGC
25201 CAACCCGCCC AGTCTTGTTA GACATGGGTT CTGTAGTTTC TAGTAGGTTT TTGAGTCTAG
25261 GGTTCCTACC TCATGTTTTA TAGTTAATTT AGGGGAGGGA CTGTGCTGTG TTATCTGGGG
25321 ATGTAGGGGT GGGCAGGGGG ATAGAGGGGA CTTCAATTAA TGAAACCAGA AGCAAAACTC
25381 AGTTGAGGAC ACCGGTCATG AGAGTGGCCT GATTATGGCC AATCTTACAT AATGTGTGAG
25441 ATCTTGATAT TACCCCATCC TTGAGAGTCC TCTATAAAGC TACAGGGACT TGGGAGCACC
25501 TTTAATTACA GACAACCCAT GTTCTGTGG ATTATGATT ATTAGATTGC ACATGCCTAA
25561 ATAAAGACAT CCTCTGCAGT CTTTGGACAA TTCTATAAGC ATCTTCTGAC TCCGCAATTA
25621 GACAGCTAAG AGATCTGTGT TACTTCCCTC ACATATATAA ATAATTTTAA ATAAAAATCA
25681 TGGCGTGAAT AATTTCTTTC CTCTACCGAT TTGAAGCTAT CCATTTGGAA GACCACTCTG
25741 AAGAGATGAA ATAAGTCTTC TGCCAAAGAT TACTTATTAA TTTACAAGGA AAAGGGGAAG
25801 TTTTGTTCCT CTCCGTGAAT TTGATTGAAA ATCGAGGGCT TTCTCGAATA GTTTTGGCAT
25861 CCAGGGTCAT TTTTCATTAA AAAGAGAAAA GTCATGTCAA ATATGAATTT CCGCAGATTA

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25921 TTCAGCACTA GACCCTGGGA GATTCTGTAA AGAGGGGTTT TGTATACTC AACTTTTCCG
25981 GGTAAAACAA ACACAAATAC TCCTCCTCCA AGGGGCGGGG GCGGTGCCTA GGTGATGCAC
26041 CAATCACAGC GCGCCCTACC CTATATAAGG CCCCAGGGCC GCGCGGGTGT TTCATGCTTT
26101 TCGCTGGTTA TTACATCTTG CGTTTCTCTG TTGTTATGTC TGAACCCGTG CCTGCAGCTT
26161 CTGCCAGTGC TGGTGTAGCC GCTATGGAGA AACTTCCAAC CAAGAAGCGA GGGAGGAAGC
26221 CGGCTGGCTT GATAAGTGCA AGTCGCAAAG TGCCGAACCT CTCTGTGTCC AAGTTGATCA
26281 CCGAGGCCCT TTCAGTGTCA CAGGAACGAG TAGGTATGTC TTTGGTTGCG CTCAAGAAGG
26341 CATTGGCCGC TGCTGGCTAC GACGTAGAGA AGAATAACAG CCGCATCAAA CTGTCCCTCA
26401 AGAGCTTAGT GAACAAGGGA ATCCTGGTGC AAACCAGGGG TACTGGTGCT TCCGGTTTCT
26461 TTAAGCTTAG TAAGAAGGTG ATTCCTAAAT CTACCAGAAG CAAGGCTAAA AAGTCAGTTT
26521 CTGCCAAGAC CAAGAAGCTG GTTTTATCCA GGGACTCCAA GTCACCAAAG ACTGCTAAAA
26581 CCAATAAGAG AGCCAAGAAG CCGAGAGCGA CAACTCCTAA AACTGTTAGG AGCGGGAGAA
26641 AGGCTAAAGG AGCCAAGGGT AAGCAACAGC AGAAGAGCCC AGTGAAGGCA AGGGCTTCGA
26701 AGTCAAAATT GACCCAACAT CATGAAGTTA ATGTTAGAAA GGCCACATCT AAGAAGTAAA
26761 GAGCTTTCCG GGAGGCCAAT TTGGAAGAA CCAAAGGCT CTTTTAAGAG CCACCCACAT
26821 TATTTTAAGA TGGCGTAACA CTGGAACAA GTTTCTGTGA CAGTTATCTA TAGGTTTAAG
26881 TTGTGATGCA GCTGAGTTGA AAAGGCTTGA GATTGGAGAA TTAATTCAGG CCAGGCTTCA
26941 AGACCATCCT GGGCAACATA GCCAGACTAC CATCTATACC AGGGGTCTCT ATTTCCCCGG
27001 CCACCGACCG GTAACCGGTC CCTGTCCATG GCACGTTATG AATTGAGCCG CACAGCTGAG
27061 GGGTGAGCGA ACATTAACCA ACTGAGCTCC ACCGCTCTGTC AGGTTAGCTG CAGCATTAGA
27121 TAGATTCTCA TAAGCTCAAA CTGTATTGTG AATGGCACAT GCAAGGGATC TAGGTTTCAG
27181 GCTCCTTGTG ACAATCTAAT GCCTGATGAT CTGAGGTTGG AGCAGTTTGA GTCCGGAAT
27241 CATTGCTCCC AGCCCTGCA CCCCCTGGTC CGTGGTATAA TTGTCTTACA CAAAACGGTC
27301 TCTTGTGTCA AAAAGGTTGG AGACTACTGG TTTTACAAAA AAGTAAATTA GTCAAGCATG
27361 GTTGGCACGC TCCCTTAGTC CCTGCACCCA GCGGTTTAAG GATACAGTGA GCTATGATGG
27421 TGCTACCTCA CTCCAGCCTG GGTGACAGCG AGTCAGACGT TGTCTCAAAA CTTAAAAAAA
27481 AAAAAAGTTA AAACAGAAAA AGGGCTTCTT GTCAGAGACT GCCGTATATC TAGAGGTCCA
27541 GGAACATAAA AGTCTGATGT CCAATCCTGA AAAGCTCGAT GGTGCACTAG AGGAGGCTTT
27601 TACATGTAAG AGCATCTAAG TTCTGAAAT GCCAGTGTC GGGAGGGGAA GTGGAGAGCA
27661 ATTTGGCATC CAAACATAAC TTGCTGATAC TTTTTTTTTT TTTAACACAA GTACTACATT
27721 CTAGTCTTTC TGTGGTGTCA TTGTAACAT TGTTCCTTAA TATGCTATCC ACTGACTTCA
27781 AGGGATCAAT AAATAGGAAT CAAGGTGTCC CAGAATATGG ATTAGGGGAG TTTTTTTGTT
27841 GTTGTGTTG TTGTTGTTTT TCATCTATTC ATTATCCTGT AGCTGAAATT TAGAATTTTC
27901 TTCCATTGTG TGTGACTGAT AGAAATAACA AATTTGTAGG TTATAGTTGT TGCAAGAATC
27961 TGGAAATCGT GCTTGCTTAT TTCCGAAGTA CTATTAGGTA TATCAACAAA AACACACATA
28021 TTACGGTCAA GTGGTTTGAT AATTATTTTA ATATTATTGG TCTAATACAA TTGTAACCTT
28081 ATGAATTACT TTAAGTATCT TATTTATGAA AAGAATCTGT AAGTTTCATC AGACTACCAG
28141 AGCATACCGA AGACTGAAAA ATTTTAAGAA TCCAAACCTT AATGGAAATG TTGGAGGCTG
28201 CCCAATTAGG TTCTGAATTC CACCTTCCTG AATCACAAC TTGTTTAAAC TCTCAGTCTG
28261 AGGTAAACTA CGTTTCTCTT TAAACAGACA TAGTTTAAAT TTCTTTGAT TTTTGATTGA
28321 GTATTCTTAC TGATCATCAT AAATAACCAA TGCTAATGTT AGTCTACTTT GGACCATGGT
28381 ATTTTCGAGAA ACTTTGAACA AAGTCCCCTG CAAAACATG CATTGCATTA TTTCACATAC
28441 ATTTATGTTT TCCAGACGGT TCAATAGTAC CTCACCTTTC TGAACCTATT TGTATAGTTT
28501 GGCATCTTTT TAAAAATTGT GTCCTATAAT GAAAGGTTGT AAACATTATG TTTTAAATTT
28561 GTATAGATAA AATCAACCAC AGACCTTTCC TTGCTTGGAT GTAATTGCCA TTGTTTCCCA
28621 ATGAGTTCGG AATTACTAGG ATTGTGCAAA AATATGCCTC ACTTGCCTGA CATAGCAGAG
28681 AGCCATTTTG CCTAAATGCT GTGCCCAGCA ATGGACTGTC ACCAGATTCT CATCACATAC
28741 AGTGAGGATG AACAAC TAGC CTCTCCAGC AGCTGGCCCG TCTCTCAATA ATATGGGACT
28801 CCCTCAAGAT GGCTTCTGTC ACCTTTGCTC CTCTAGCCTT GTATGTATAC AAGGCTAGCA
28861 TGCCTGGCAT ACATAAGGTT AAAAACAAAA TCAATAAGTT ATGGTTCTTC CTCCAGTCTC
28921 GGGGATTATT AGACCACTTT TTTGTTTTGT TTTGTTTTGG ATGGAGCCTC GCTCTGTCAC
28981 CCAGGCTAGA GTGCAGTGGC ACAATCTCGG TTCAGTGCAA CCTCTGCCTC CTGGGTTCAA
29041 GCAGTCTCTT GGCTCAGCCT CCCACGTAGC TGGGATTACA GGTGCCCGCC ACCACGCCCG
29101 GCTAATTTTT GTATTTTATG TAGACGGGGT TTCACCATCT TGGCCAGGCT GGTCTTGAAC

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29161 GCCAGACCTC GTGATCCACC CACCTTGGCC TACCAAACCTG CTGGGAATAC AGGCGTGAGC
29221 CACCGCGCCC GGACTTAGAC CACTTGTGTT TGGCCAATAG GACAACAGCC ATAGAACCCT
29281 CCGCAAATGA GAGCTTGTC CTAAAGATGC TTTATTACA TAGCTGTGTG CCGCATGAGC
29341 CAAAAGGTGA TAACCTTGT TCAACACGCG CCTCCAGCCC TTCGGTTAAG TCCAAAGTAC
29401 CATTCTTAGA ATGCTCTAAA ATACATAATT TTTTTTTTTT TTTTTTTTTT TTTTTTTTGAG
29461 GAGTCTCTCT CTGTCTCCCA GGCTGGAGGG GAGTGGCGCG ATCTCGGCTC ACTGCAATCT
29521 CTGCTTCCGG GCTAGCTGGG CCTACAGGTG CAGACCACCA CGCCCGGCTA AGTTTTGTAT
29581 TTTTTTTGGT AGAGGGGGTT TCACCATTGTT GGCCAGGCTG GTCTCGGATT CTGTGATCTCA
29641 AGTGATACAC TAGCTTTGGC CTCCCAAAGT GCTGGGATTA CAGTCGTGAG CCACTGCGCC
29701 CAGCAAAATG CTTTTTGTGG AGCCAATCAC TTTATTAGCG CTTACCTCTC TATGCCACT
29761 TTATGCTTTG AAATTTTGTC ACAGTGTGGC CGGTCATGGC AAACACAATT CATTCTTATG
29821 CAGGATGTCA CGGTTATTTT TGTCATCCAA ACTCATTCTC GCAACGCATT TCAGCTCTTT
29881 AAACGACTTT GTGAGCGGCC CTGAAAAGGG CCTTTGGGTT TTTTGTGTTT TGTTTTTTGA
29941 AGTTCTCAGG AGACCGCGTA TTCTTAGATT CAGCCGCCGA AGCCATACAG AGTGCGCCCC
30001 TGACGTTTTA GGGCATATAC TACATCCATG GCTGTGACAG TTTTGGCCTT GCGGTGCTCC
30061 GTATAGGTGA CGGCGTCTCG AATAACGTTT TCTAAGAAAA CCTTAAGCAC ACCTCGAGTC
30121 TCCTCATAGA TAAGACCGGA AATGCGCTTG ACGCCACCGC GCCGAGCCAA ACGGCGAATA
30181 GCCGGTTTTG TAATGCCCTG GATGTTATCC CGGAGCACCT TACGATGGCG CTTAGCACCA
30241 CCCTTCCCCA AGCCTTTTCC GCCTTTGCCG CGACCAGACA TGATTCTTAT CGCAGTGGAA
30301 GGTATGAACT GAAACAGTTC CTAAATACA AACTTGGCGG ACCTGATTGA AAACAACATG
30361 AGTTGGCGCG GTTTTTTTTT TTTTCAAAT TTGGTCACCA AGTGGGTGGA GCAAGAAAAA
30421 CTGTTTCATT ATGGTTCATT GTTTGTATG GCCAGTGACA GCTTGCTCTT TGTGGGAGTG
30481 GAAGGGTGTG TGCAAGTTGA ATGCGCTGTA TTCCTGTCAG CTTAATGACG CTAAGCATAG
30541 CCCCATTCCA CATTTCTTTT TATTTCCACT TGCTAACTAA TAAATTACGG AATAGTTAT
30601 TGGGGAACAT ACAAATAATG TTTAAAGGAG GTCAGATTTA TAGGTCAAGG GATTACCCT
30661 CCCAATCATT TTAATATTTT TATTTAAACC AGGCATTTTG ATGGCCTTCT CTGTGCTGGA
30721 CAAGGTATAA GTTTGGCTAT GAAGTTTCAC TCCTAAAGAC CCTATGTTTT GGGAAAGCAA
30781 AAAGGTAGCC AAATAATTGC AAATTAACAC CTCATAAGTG CAAACTTCTT CCTCGTCACT
30841 TTCCCTATCT CGATTCAAAT ATTTGTTGAA TGACTCATT TTCTGCAAAA GTCTGAGAGA
30901 GACAGGGAAT ATAACTTAA GTCTGGATAA TATGTTTTCC CGGGACGCTC TTCCTGGTCT
30961 GCTGTGCCCTG TTTGCTGTGC CTGAAATTC AAACACTCTT CCCTTCCCTC CGTTTTTAAT
31021 CCCCTTTCAA CTTGCTACAG CTTTAGGAA AAGAACATTC GTTTGTACA GTTGGGGATT
31081 AATTGAAGTG TAGGGCTAAT ACTTGATTAA GGTCAATTACA AAATCTACAG GGTCTTCTC
31141 TGGGAGGTTT TTGTGATAAG ATTATTGGTG TTAATAAAG GCTAATCCCC TTGAAAAATA
31201 AATAGAATAG CAGAATTGGG TCTGAATGTG GTTTGAAGAA AGGGACTTCT CAATTCAAAA
31261 TTTTATTCTT AGCTTCCTGC GGGAGCTTTC CAGAATGCCC ATAAGATCCA CTTTTGTTTA
31321 AAAACAAAAA ACAACCCAC CCACCCTCT CTGGTTAATA AATGAATTC TATTGGGAAT
31381 ATTTAGAATG GGGCTGTGGC CTGTGAGAGA CATTATATAG TAACCTCAGA CTTGCTCACA
31441 TGAAGAGAAG AAATCCAGGA ATGGAGAAAA AAGACCCAGG AAAGGCCAGA ATGCTCTACA
31501 TGTCATATTG TTTGTATCAC TTCTGAAATA ATTGATTACA TTCTTCTGCC CCAAATTGAG
31561 TTCTTAGGTT CTTCCACTCA CTGTCCACAT GCCACAACAC AGACCTTATA ACTAGAGACT
31621 TAGCTAGGAA GAAATGTCAA ACATTACAGA GAAAAAATGC AGAGTCTGAG ATCATAAGTA
31681 AAACCTGAA ATCTCAACAT GCCTTTTAAT TCATGAAAAA AAAAAATATA GCAGCATATG
31741 CAATATGACA ATTCTCTGAA AACATACATC ATGTGAACTA CCCTGGAACA CATCTCGCCA
31801 AGTGCCATCT TCATTTTAAC CAGAGGTCTA GGATGCCTTT CCTTTATTTT GCCTATTATA
31861 TCATTATATA AACCCCATTT TTATTTTGAT ATTTTATTTA CTTTCTATTT CCTGCTCCTA
31921 ATATCTCCTT TCTAACTTT TCTCAATGAC AGTGACTCAA AAACAATGAA TGTCAGAACA
31981 AATATTTAAA GGATCTGTAC ATGTAGATAT ATATATTTAA AATGGATTCT TCCACTCTGC
32041 GAAGAATTCA GGCATACTCA ATCTTATGGT TAGGGAGAGA TTAGGCTCAC TCGCCTAATC
32101 TGTATGGCTT CTCGTTGCTT TTCCATTTCA CCTTCTCTC ACCCATCAGA TCAAACCTAT
32161 TCATTGAACA AGAGACCTAA GCCCTTCAGA TTAACACTCT GCAAACAAGT TGTGGTTGAG
32221 AGGATACATG AAGCATTCAA ACAAATAAAT CTATGATATT AATCAGAGGT TAATCTATGA
32281 TATTAATCAG AGGTAAATGC AGTGGCTCAC GGCTGTAATC CCAGCACTTC AGGAGGCTGA
32341 GTTGGGAGAA TCGCTTGAGC TCAGGAGTTC AAGACCATT TGGGCAACAT AGCAAGTCTT

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32401 CATCTCTACT TAAAAAATAA TAACCAGAGG TGTTATGAAA ATATAAATTG TCCAGAACTA
32461 CCCTCCACAA ACTAACTCTC TCAGAATATT CGATATGAGG AATGAAATAT GGTGTGTGTG
32521 TGTGTGTGTG TGTGTGTATG TGTGTGTGTG TGTGTGTGTA TGCACCTATA TATGGCACCT
32581 ATATATTCAA CAAACAATTC TGATAATTGG CCAGGGTTGA GAATGACTAG CAGCCCAGCA
32641 TACACTATCA GTTTTAAGTA TATAATTGCG CTTTAGTAAA ATGTAAAGAA ATCCCAGAGT
32701 AGAAATACTT TTAAGCTATA TTACAGGTGA GAAATGCGAT AAGTATAGTC TCACCCAAC
32761 TAGACTATGG GGGCTTTATA ATGTCACAAC AGTTGTTTCC AGGCATTTGG GGACATCACC
32821 ACTGGTCTTG GGCAAGAAAC TCCTCTAGCC AATGGCTGAT TTATCTCACT CCCATCTAAG
32881 GCTTCACTGC ATTTCTCTTT TTCAGCAACC TAACTTATTT AAAAATATCC ATTTTCTGAT
32941 TCATTTTTTT CTGAATTAAA CTGTCAGTAC CATTGGCACA CCTTTGGTTC CGTAGCATA
33001 CTGTGTCTCT GCTGTGTTTT TTTTTTACCT CCACTCCTTA CTTTTCTAGA AAAAAATCTC
33061 TGCTTTTTCT TTTCAGTTTA AATTATTTCA CAAAAGTTT TCTTGACTTG CACTTCCTAG
33121 GCTTGCTGTC CTTGTGTGGG CACGCTCCCA TAAACACTAT TAATACACTT CGATTTGTTA
33181 AAAATAAAGA TATCTGGACA GAAAATTTCT TTTCTTTTTT TAAGATTTTA AAATTTTAA
33241 TGTTTATTTT TTTCCTAGAC TGGAGTACAG TGGCACCATG ATGGCTCATG GTAGCCTACA
33301 CTTCCCCGGG CTCAAGTGAT CCTCCCACCT CAGCCTCCCA AGTAGCTGGG ACTACAGGTG
33361 TGCACAACCA CACCTGACTA ATTTTGTTTA TTTGTTTGT TTTGTTTTTG AGATGGAGTT
33421 TCGCTCTTGT TGCCAGGCT GGAGTGAAT GGCGGGATCT CGGCTCACC CAACCTCTAC
33481 CTCCCAGGTT CAAGCAATTC TCCTGCCTCA GCCTCCCGAG TAGCTGGGAT TACAGGCATG
33541 CATCACCACG CCCAGCTAAT TTTGTATTTT TAGTAGAGAC GGGGTTTCTC CATGTTGAGG
33601 CTGGTCTGGA ACTCCTGACC TCAGGTGATC TGCCCGCCTC GGCCTCCCAA AGTGCTGGGA
33661 TTACAGGCGT GAGCCACCAC GCTCGGCCAC TAATTTTGTA TATTTGTAG AGATGGGCTT
33721 TCCCTGTGTT GTCCAGGCTG GTCTTGAATT CCTGGGCTTA AGTGATCTGC CCACCTTGTC
33781 CTCCCAAAAT GCTAGGATTA CTGGCTGAG CCACCAGGTC TGGCTGGAAA GATAATTTCT
33841 AACATTATCC TCTCTTAAAC ATTTGTTTCA AAAATTTTAC AAACATGAGA GTAATTAAT
33901 TTGATTTTCA AAATCCCTT GAATACTTTC TTAATAGCAC ACAGAAAGCA CAAAGTATTT
33961 TACATTTGTT TTAATGATGA AATTGTGAAC CCAAACCTAC ACAAAGAAAA ACCCGTAACA
34021 TTATACCCAT ACTTAAACA GATGCCCTCA TATACATAGT AAAACTCTTG GGGGCAGTAG
34081 TGAAGTTGGT TATTTACTGT TTTATGAAAG TGCCATTCAG CCGGGTGCAG TGGCTCATGA
34141 CTGTAATCCC AGCACTTTGG GAGGTCGAGG CAGGCTGATC ACGAGGTCAG GAGTTCAAGA
34201 CCAGCCTGAC CAAAATGATG AAACCTGTG TCTACTAAAA ATACAAACAT TAGCTGGGCG
34261 TGGTGGTGTG TGCTGTAGT CCCAGCTACT CAGGAGGCTG GGGCAGGAGA ATCGCTTGAA
34321 CCTGGGAGGC GGAGATTGCA ATCGCACCAC CGCACTCCAG CCTGGGAGAC
34381 AGGGCGAGCT CCGTCTCGAA AAAAAAAGTGC CGTCATAGTG ACTCAGTTTT
34441 AAGGAATAAA TCAAGGATAT TTAACCTAAT AGACTACAGT TAGCTAACGT GACTTGCACT
34501 GAAAGTTATA CGAATATTGG TACTTATTC CCTGCCCCTG AAGTATGAAT TAAAGACTCC
34561 AAAATTCCTT TTAGAATCTT CAGAGTAAAA GCTAGAATTT GATTTTTTTA AATAATAAAA
34621 AAATACTTTG TATCTAAATC TGGTGATATA AATAACTTGG TGGATGATGC TTCAAGGCTA
34681 TCCATCCCCA AATTTCTCCC TGAATGATAA AGAGAATAAA TGAATATGTC AATTCAAAAG
34741 TTAGAAATTT GGCCGGGCAC GGTGGCTCAC TCCTGATAAT CCTTTCGGAC GCTGAGGTGG
34801 GTGGATCGCA TGAGTCCGG AGTTCAAGAC CAACCTGGGC AACATAGCCA GAACCCGTTT
34861 CAATAAATAA TAGAAAAAAA TGAGCCAGGC GTGGTGGTCC CAGCTACTCA GTAGGCTGAG
34921 GTGGGAGGAT CACTTGAGCT CAGGAGGTCG AGACTGCAGT GAGCCGTGAT CGCAGTACTG
34981 CACACCAGCC TTGGTGTGAG ACTGAGACCC TGTCTCAACA ACAACAAAAC AAGTTAGAAA
35041 TTTGGCTGGG CGCGGTAGCT CACGCTGTA ATCCCAGCAC TTTGGGAGGC CAAAAGGGC
35101 GGATCATTTG AGGTCAAGGAG TTCGAGACCA GCCTGGCCAA CATGGTGAAA CTCCATCTCT
35161 ACTAAAAATA CAAAAAAAT TAGCCGTGCA TGGTGGCATG CGCCTGTAGT CTCAGCCACT
35221 TGGGAGGCTG AGGCAGGAAA ATTGCTTGAA CCCAGGAGGC AGAGGTTGCA GTGAGCCGAG
35281 ATCATGCCAC TGCATTCCAG CCTGGGTGAT AGAGTGAGAC TCCATCTCGA GAAAAAATAA
35341 AAAATCTGT ATGAACTGAA CAAATATCC TTAATTTTA AAATACATCT GAAAGATATT
35401 TCAAAATATT TAGGAAAAAA ATTAGGGGA TCAGGCAAAAT TCTGAGATT CTCTTTCCCT
35461 GCAGCAACAA TTAGGAGTGC TGCTGTTCTT AAAAAATGG TAACTGTTGC CACACCGTAT
35521 GTTTCCTTGG CTCAGACATA AGGTTGTGTA GTTGTATTTC CAGAAATAGCT AGAATAAAAA
35581 TCCAGCACAT CATTTCTTTC AGCAAGTTAA CTAACCTCTC TGTGCCTTGG TTTTATAACA

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35641 GCAACATAAG CATAACAGAA TAGCAGCAAT AGCTCCTACC TACCTCATAA GATTCTTTGG
35701 AGGAATTAAA TTAAGATTCA GAACACAGCC TAATATCTAG TAAGTAATAA TAATTGGCTA
35761 AAAAAATTTT CTTAAGATTA TATATATTCA TGGGGTACAA GTACAATTTT GCTACATTAA
35821 TATATTGCAT TGTGGTGAAA TCAGGGCCTT CAATCCATCC CGGAAAAAAA AAGTTTTTGA
35881 AAAGATTTCT GCCATGGAAA ACTTTTAATG TACAAATTCA TCCATCCAAG AAATAGAAAA
35941 TATATAAGTA TCAACTCCAA ATCCACCATA TCTATCTCTT CTACACCTTA AACAATTACT
36001 CAGAAATAGA ATGCTTGAGA TACCAGAATG CATGCATATC AAGTAATAAA TGCATGCAGG
36061 ATGTCAACGC ATCCTAGGCT TTCAAATAAA ATTGTCATAC AAAATACTTT AATATTGTAG
36121 TAACATTCTA CATGTTAGAG TGTAGAAGTT AATCGCTGAT GCAAAAAAGG AAAAGAACAC
36181 ATTATACCCA AAGCCTACAG AGAGAATCAC AATTACAAAT ATCAGCCTGC ATGTGAAAAAT
36241 CTTTAATTTG AAAGTCAGAA ATATTTAAAT GATAGTCATT GTTAAATCAG ATTGTGGTTT
36301 GAAAAAAGT TAGTTTAAAA CTGAGTTTAT GAAAAATTTG GGGATTTTGT AGACAGTGTT
36361 TTGTTTTTAA ATGTGTGTGA GTTTGTGAAG AATGTTTTAT AAAATACTGA CAGTATTATA
36421 AGATGACATT ATTATAATAC AACATAAGAA TTTTGGCCTG TACCTCTCAG CAGTCTCAA
36481 TCACCTGCTG TACTTGACTC AATGATTATC AGAGTGGTTT GTTTTCCTTC TGTGTGTTT
36541 CCAGTTCAGG CAGCTCAGCA ATGGCCTGTG ATTCCAGCAA TCCAAATAGC TGGTAAGTAG
36601 TTTCTTGTTT GTTTTCTCAA ATTTTCAGGG GCTTTTCTCT ACAAGTGATT TCCAGTGCAC
36661 GCCCTCCAC CCATTCTTTA TTCCTTTACC TTCAGGAAAA CCCTCAGCGC TGCATCTCTG
36721 GTCACCGGAC CACCGTGGTA CATTTACCTA TGGCCACCAG GTGTCACCCT TCTCTTACT
36781 ACCATGGTTT GTGAATGGTT TTGCCAGAGG TGAATAAGAA TTTAAAATGC AGGTCTTTGA
36841 TTTTTCAAAT GTAGTTGACC TTAAGAATTT ATGAATAAAG CCAGAAAAAT TAAGCTTAAA
36901 AAACACCGAA AGAAAATGAG GACTTAAAT TTCTATTAAA AAAATTAACA GGCCACAGTT
36961 GCTGATGTTT AGTAAATGTG TTAGTGAAT GTGTTACTGT GAAGACTGGG GTGTTTCTTG
37021 AAATCTCAGC CCAGGTGAAA TAAAACCAAT ATAAAACAAA TGCTTACCTA ATAAATTAAT
37081 TGTAACATAT TCCTTATGAG GTAGAAGAGT AAGTGAAGCC TTATAGCAGT CTGCTTTTCA
37141 TATAGTAAGA TATTAAGAGA GAAATAATTT GTCATATGCT TTCAGAATGG TTTGTCTGTA
37201 AAATAACCAA TGTCTTACAA CTTAGACGAC AATGTCCCTA GAGTGAAGAA ACACGATTAA
37261 TTCGGCTACC ACAGTTGAAT GAAAATATTC CGTAAGACAA AATGTAAAGA AATTAGAAGC
37321 AAAATAAATG TCTCCAAAAT GACAAAGCGA TTAAGTATAT ACACAAGATG AACAAGAAGT
37381 TCAATAAAAT CATGCAGTAT ACAATACAAT ATACATTTAT TAAAGTATAT GCATTTTTAA
37441 TGCAACAATA ATACTAACAG GTAATAGACA AGTTGTTAAT AGTTTTTCAC TGGCTAATTA
37501 AATAACAGCT TTAATTGTAT TCATTTTATA GCTTTTCTAC AATGAGCGTA AATCACATTT
37561 ACTTTTTTCT ACATAACTTT TCTAACCA CA AAAAAGAAA ATGGTTTAAA AGAAGAGATG
37621 AGATATCTTT GCTAAAATTT AATGCCTAAA GAAGAAACTT CTGAGCTGTA TATGGTATCC
37681 TGAAGCACCT GCCCTTCAAG ACAGAATGCT TGTACCACAT TTATGCAGCC AAGTGCATGT
37741 AGTAACATAA AGTAAACACA TGCCATCTGG ATATATATAT TAAGACTCTT TTGACGGCTG
37801 GGCAGGGTGG CTCACACCTG TAATCTCAGC ACTTTGGGAG GCCGAGGCAG GCGGATCAGG
37861 AGGTCAGGAG AGTTCGAGAC CAGCCTGGCC AACATGGTGA AACCTGTCTT CTAATAAAAA
37921 TACAAAAATT AGCCGGGCAT GGTGGTGAC GCCTGTAATC CCAGCTACTT GGGAGGCTGA
37981 GACAGGAGAA TCGCTTGAAC CTGGGAGGCA GAGGTTACAG TGAGCCGAGA TCATGCCATT
38041 GCACTCCAGC CTGGGCAATA GAGTCTCAA AAAAAAAGAA AGACTCTTTT GAACATGGTG
38101 AACTGATTTT CCAGAACTTA GCAATTCCTG AATGTCCTGG TTAGATTTTT TTTTTAATGT
38161 GCACCGGAAC CCCAGTGGCT CCATGGAAGG ACCTGGGCAT CCTTAAGCC ACTTGGTGCC
38221 TTCCATTATA CCATCTCAA ATGAGAGAGC TTACTCCACT TCATTGAGGG AAATACCACC
38281 AGAGTTCTGA CTCCAGAGGC ACTGGCCTAG GGAGGACACC GTGTGTGAAG CCCAGCAGGG
38341 CCACTAGCTG TCCCCACCAA TTACAGTCCT TGCCTAGGGT CCAAAGAAAT GAATGCCAAA
38401 GAGAGCAACA GAGGAGCAAG GGAGTCACAT TCCAGGACCT TCCTTCAGGG ACTTTTAAAG
38461 GAAACATGAC AGCTGAGGAT CAGTTGGTTG TTTTCTGCTG TTCCCTTCA TGTGATTCAA
38521 GCTCACTCAG AAGAAACACA ATGAGACAAG AGAAGAGCCA TCTCCTTCTT TCTCTATTTA
38581 TTCTAGGCAT CTAACTACT GAATGTAGTG GTGTCTGAGA TGTATCAAAC GGTGAGATTG
38641 ACTGAGTTTG AAACCTGTTT CTATCACTGA CAAACTATGA GATACTCTAT ACTTCACTTT
38701 CTTTTTTTTT TCATTTTTTT ATTTTATTTT TTATTTTTTT GAGATGGAGT CTCACTCTGT
38761 CACCTAGGCT GGAGTGCAGT GGCGCAAAC CGGCTCACTG CAAGCTCTGC CTCTGGGTT
38821 CATGCCATTG TCCTGCCTCA GCCTCCGAG TAGCTGGGAC TACAGGCGTC TGCCACCACG

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38881 CCCAGCTAAT TTTTGTATT TTTATTAGAG ATGGGGTTTC ACCATGTTAG CCAGGATGGT
38941 CTCGATCTCC TGACCTCGTG ATCCACCCGC TTTGGCCTCC CAAAGTGCTG GGATTACAGG
39001 CGTGAGCCAC CGTGCCCGGC CTACTTCACT TTCTTCATTT AAAAAAGAAA TGGGGATAAT
39061 AGTACCTATC TCATAGAATT ATTGTAAGAA GTGCATGCAG TAATGCATGT AAGTAGGTGC
39121 TCAGAAGAGT CGGACACGAA GTAAGTGCTT TTATCATCCT TATCATAATT TTCATTATCA
39181 GAACAAGGAG AGACCAGGTA GAAAATTATT GTGATTCTTC AGGTCTGGAA TACTAGAGTA
39241 GCATCCCAAA TGAAGGCACC ATTAACTTT GCAAATCTGT ATGACACCTT CATGCCAATT
39301 AGAAAAACA CCTCTTCACA ACCCCTTTCA AGATATTTGC CTCCTACCTG CTAAAAACAC
39361 CCATCATACT ACCCACAGAT AGCCATGATG CTTTTTCTGG GACAGGTGCC TCTTCCATTC
39421 GTGCAGTGTA CAGCCTTCAT AGCTGTGCAA CTCACATCAC AATCAGATGG AAGAATCCCC
39481 AAGGCTTGGT GACAGATGAG TTAGTGGGTA ACACAGAGAG AGGATTCAAA GGAAAAGTTG
39541 AACGGGTCCA GAAAATGCAT AGATACATGT GTAAAAATCT GGTAAGGTTA TGACTAGCCA
39601 CGTCCCAGGG TTCAAAGCTT TTCTCAGATG TTTAAATGAA TCATGTAAGT CCCCCAAATT
39661 TAAGGAGTCC TCTTCCAAA ATAGGAAATG AAATGACATA GGTGTATGTC TCTGAGGTGA
39721 CGGAGGAAAT GAAGGAAGCC TCTAGATGCA GCTTGAGGTT CATGAGAGAC AGTTCAGGG
39781 GAGAGGTCAC AGCTAGGGAT CACCGGCATG CAGGAECTCA GAAACCTAAA TGGGGAAATC
39841 TTTTGTAGGA AATGAACAGA GAAGGCTAAA ATCAAGGAGT TCGTCAGGCA ATTTCTATGT
39901 TTAGGTTCAA CTCTCTCCTG AAACATGAAG AGCTCATAAA TGCACTCCCT CTTTGAGTCT
39961 CTAGTTTTGT CTCCTTCCCA CAGTGAGTCT GCAGGCTGCG TGTCACTCAC GTTCAGCTAA
40021 GACGTAGTGC CCCATGGCTC CTCCTGTGGA GACAAGAGAC CCAGGAAAGA GGCATCACAA
40081 ACCTAGGCAC CATCTTGCTT CTCTCTCTT CTTATTTTC CTCATTCACC CATCTCAATT
40141 TAGACCTGGG CACTATTGGA TTTCAAGAAC CATTATCTCT CATCTGGAAA TGCTTATTGG
40201 CTTTCTAACT GGTCTCCTCA CCTCTCATCT AACTTCTTAA CAACACATTC ACCATAAAG
40261 GGAGATCGTG GTCCTCCTT CTTAGGATCC TTCAATGACA CCCCAGTGAT CATAACCCAA
40321 TATCCCAAAA GACCCTTGGG CTCTGTATGA GCTGGCTTCT TTCTGATTCT CTTTTCCCTA
40381 CACCACAGAT GTTCAGGGGG TAGAAATGCA TAATTGGTGA GTGATAGCTA CGCAAECTCA
40441 GGGTTAAGGT ACAGTAATTA TTTCTAATCT CCCAGTATGC CTTATACTCT CCTACTTGGC
40501 ATGGTTGCTC CGTCTGTGTA GACCTCCCAT CATCTTCAAC CTCACCTAAT GGAATCCAGC
40561 TTCTCCTTCA AGATCCAGAA GGCTATCTTG ATCCCCAGCT GAATGTGATC ATTCTTTCCT
40621 TTGACACCCT AAGCATTGTC TTCCTGCCTG CTTTAGGACC TCATGGGGTC TTCTTTAACT
40681 ACATTTACTT GCTATCAATT TCATTCCCTA CCAGATTGG GTTCTGAGAA TAGCCACAGT
40741 GACTTCTCAA CCTCAAAGCC CTTGACTTAC CTTAAACAGC TCTTGCAAAA TAGTAGTGC
40801 TCTGAAGATG TTTGTTGAAT TAGAGACTTT CATTCTGGGG AGAACCATA TTTTCTGTCT
40861 CCCAGGGAGC TGCTGGTGTC CCCAAAGAAT ATAAATGAGA AAAATGCTTC CCATGGATGC
40921 CAGATCCCCT CTGCCCTCT TCCCCTGTG CCCTGGGGCA GAGGTACTAA GAGACTTCCC
40981 CCTGTTCCT ACTCACTGA ACCCTGCCTC TTCCTTAATA TTATGAACAA AATTCCAATG
41041 AACAGATGA CGACAAAAC AGCAATTCCA CTGATGACTC CAATGACTAG GGTGCCAGAC
41101 GGTGAGGGCT CTAAACAGA AAAAGCAAGT TAAAGCCTTT GATTGCCACC CTCAGCCCAC
41161 CCCCTAACAA AGAGCAGATC CTCATCTCAC TGCCATAATT ACCTCCTCAG GCACTCCTCT
41221 CAACCCCAA TAGATTTTCT CAGCTCCTGG CTCTCATCAG TCACATACCC CAGATCACAA
41281 TGAGGGGCTG ATCCAGGCCT GGTGCTCCA CCTGGCACGT ATATCTCTGC TCTTCCCCAG
41341 GGGGTACAGC CAAGGTTATC CAGCCTGGT AGGTCCCATC CCCATTGGGC AATACGTCCT
41401 TAGGTTGCAA CTCCTTGGCA TCCATTGGCT GCTTATCCTT CAGCCACTTC ATGGTGATGT
41461 TCTGGGGGTA GTAGTTCAAG GCCCAGACCC GTAGAGTGGT CACTGAAGAG GTCACATGAT
41521 GTGTACCTT CACCAAAGGA GGCCTTGAC AGGAAAGAGG AAGGATGAGG AGAGGGGATC
41581 TGTTTACCCT TGCCAGGAAG ACTGGAACCT TCACCTCCTT CTATAGGTTG GAGGAAGGAA
41641 ATACCCTTTT CAGAAAAAA CAAGCTACAG GAGAGACACC ATTTTGTGTC CTAAGATTGG
41701 ACTCTAACAC AGTGTCACTT GGAGAGCAGT CAGATCAGCT TGTTCTCCTC ACATGTAAAT
41761 ATACATATCT GTTACCCATG TTTCTTGTTC TGATAGATAA AATTGCCCTT TATGTGCATT
41821 GAAAATGATT GAATACAGAT GGTGAGTTTC ACCTGGGTCA ACCTAGGAGG CATTGTTATA
41881 AGAAGCGGAC TTGTAAGATA GGTAGCTTCA GTGATTATTG CTATGTTCTA TGAAAGAAAC
41941 TTTTAACCTA AAGGATTCTT CTACTCTGAT AAGTGGCCTC ACTTGATATT TTGTCCTGGT
42001 ATTCATATGA TAGCTGAGAT CTCTGAATTC TCTTTTTTTT TTTTTTTTTT TTTTAAAGAT
42061 GGAGTCTCAC TCTGCTGCCT AGGCTGGAGT GCAGTGGCGC GATCTTGGCT CAGTGCAACT

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42121 TCCGCTTCCC AGGTTCAAGC GATGCTCCTG CCTCAGCCTT CCAATTAGCT GGGACTACAG
42181 GTGCGCATGA CTGTGACCAG CTAATTTTTG TATTTTTTTA GAGACGGGTT TCACCATGTT
42241 GGTCAGGCTG GTCTCAAACCT CCTGACCTTG TGACCACCCG CCTCGGCCCTC CCAAAGTGCT
42301 GGGATTACAG GGGTGAGCCA CCGTGCCCGG CCTTGACATT TCTGAATTTT TAACAGGTAT
42361 AAATATACAA AAGATTATTG GTTAAATAAA AAGCAAGGGC CATAGACACT TCCCTTTGAG
42421 CCATATGCAT GGAGAAAAGA AATTAAACCC ATGACTTGTG GCTGTCTCAT ACATCTCAAT
42481 TATAAGGTAG AGACTCTAGG ATTGAGAAAG TCCCTTCCCA GAATTTGGAG AGGCACACAG
42541 CCTCAGCCAC CTCTGAAACT CCAACCAGGG ATTCCGTGCC CTGCAACCTC CTCCACTCTG
42601 CCACTAGAGT ATAGGGGCAG AAGTGTGTTT CCACCATACC TTGTTGGTCC AAAACACCTC
42661 TCCCCAGCTC CAGCAACTGC TGCAGCTGTG CAGGGCAGTC CCTCTCCAGG TAGGCCCTGT
42721 TCTGCCTGGC CCGAATCTTG TGCCTTTCCC ACTCCAGCTT GGTGGGCCAG GCCCTGGGTT
42781 CTGCTGCTCT CCAATCCAGT GTGTCAGGGC AGAATTCAAG GTGGTCTGTC CCATCATACC
42841 CGTACTTCCA GTAGCCCTCG GTACTGTTGT CTTCTTGCAT TTCACAGCCC AGGATGACCT
42901 GCAGGGTGTG GGA CTCTGGA AAAATCCCCA GCCTTGTTAA CTGCAACCAA AGGAATAGGT
42961 CCCTATTTCC ACCATCCCCA AGGACCAAAT GATCTCAGGA AGCAAATTCC TTCCCTCTTC
43021 CCTGCTCCCA CAAGACCTCA GACTTCCAGC TGTTCCTTC AAGATGCATG AAAAGATGAA
43081 AAGCTCTGAC AACCTCAGGA AGGTGAGGCC CCCTCTCCAC ATACCTTGC TGTGGTTGTG
43141 ATTTTCCATA ATAGTCCAGA AGTCAACAGT GAACATGTGA TCCCACCTT TCAGACTCTG
43201 ACTCAGCTGC AGCCACATCT GGCTTGAAAT TCTACTGGAA ACCCATGGAG TTCGGGGCTC
43261 CACACGGCGA CTCTCATGAT CATAGAACAC GAACAGCTGG TCATCCACGT AGCCCAAAGC
43321 TTCAAACAAG GAAAGACCAA GGTCCTGCTC TGAGGCACCC ATGAAGAGGT AGTGCAGAGA
43381 GTGTGAACCT GGAGACAGAG CAACAGGCCT TAACCATGTG TAGTAGGAGG GGAGCAGGAT
43441 GTTGAGGCTC CACACACCTG CATCAACTCA TACCATCAGC TGTGTCTGGT CCTCATTTTG
43501 TGAAGGGTGA GTTGAGTCC TGTCTTTCTT CCATATGACA GTCCTGGGTG CTCTTTCTT
43561 GTGTGCTTTT CTCTGCCACA CGTGGCTGCC ACCCCCTCAC TGCCCCCAGA TCCTATTCCA
43621 ATACTCATGA TTAGACAGAC TCCACTAAAG CTGGTGGATT CTAGAAAATG TTAAGGTGTG
43681 TCTAGCCATG GTAGTTGAAC TCAGGAGTTG GTGCTCAGGG CAAATTAGAC CCAAATCCTG
43741 AGGAATAATT CCTTCAGTTT TTTTTTTTTT TTTTTTTTTT TTTTTTGAGA CAGAGTCTCA
43801 CTCTATCACC CAGGCTGGAG TGCAGTGGCA CAATCTCAGC TCACTGCAAC CTGCACCTCC
43861 TGGGTTCAAG GGATTCTCCT ACCTAAGCCT CCTGAAAACC TGGGACTATA GCGGTGCGCC
43921 ACCACACCAG GCTAATTTTT GTATTTTTAG TAGACATGGG GTTTCACCAT GTTGGCCAAG
43981 CTTGTCTCAA ACTCCTGACC TCAAATGATC TACCTGCCTC AGCCACCAA GTGCTGGGAT
44041 TACAGAAGTG AGCCACCGTG CCCAGCCTTG GTCCTGAATT CTTACACTGA ACTGCCTATG
44101 TGGCCTCACC ACTTGGAAGC CTGACTGTAA TCTCAAACCT AACATGTCCA AATGCAGATC
44161 CTTGATTTAC CCCAAACTGC TCTTCTCTT GCCTTCACCA TCTCAGAAAT GGCATTGCCA
44221 ATTACCCAC TGCTCAGGCC AATAAAATTA AAATAAAGAA CAAAGTCAAC TTTAACTCTT
44281 CTCTTTTCA GGGGGTCAGG GGAGACAGGG TCTTGCTCTG TCACCTAGGC TGAAGTACAG
44341 TGGCACAGTC ATGGCTCACT GCAGCCTCAA CTTCTGGGC TCAAGCAATA CCCTCCACCT
44401 CAGCCTCCCG AGTAGCTAGG ATCAGAGGTG CATGCCACCA CACCCAGCTA ATTTTGTAT
44461 TTTTGTAGA GAAGGGGTTT TGCTGTGTTG CCCAGGCTGG TCTTGAACCT CTGAGCTCAG
44521 GAATCTGCTC TCCTTGGCCT CCTCCTTGGC ATGAGCTACT ACACCCAGCC AATTCTTCTC
44581 TTTCTCTCAC ACAACATAGA ATCCTTCAGC AACTTCCTTC AGAATATATT CAGGAGACAA
44641 TGGTTTGTCA CTCCCTTTTC TGTTCCTCAG CAGCCACTC CACTACCTCT TGCCTGGACT
44701 GTGTAACAGC TTCCTGGCTG GGCTCCCTGC TTTTACTGTT GCTCCCTTCA TTCTGCTTTC
44761 CACATAGCAG CCAGAGCAAT CTTTTAAAAG CCTGTGACAG ATCACTGTTA CTCCTTGGCT
44821 AGAATTCACA CCACAGCCTA CAGGCGCCTG CACAACCTG TTTGTGGCTC CTCTTCTGAG
44881 CCCATTACCT ACTTCTTGGC CTCTACTCCC CAGCACTACT TGTTTATTTT TTTCAACCCG
44941 AGCTTCTTAA CCAGGAGTTT GTCTACTAGG TGACATGTGG CAAAGTTTAG AGACATTTT
45001 GGTGTGCAAG ACTGGGGGAG TGCTCCTAGC ACCTAGTGAG TAGGGAGGAC AGGATACTGC
45061 TAGACATCCT ACATGCAGAT GGTAGTCCCC CTTCCCACCC CCACGCCGCC CCCCCCCCCC
45121 ACACACACAC ACATGAGTAG TGCTGAGAAA ACCCGCTTTT TAATCCAAC TGCCAGGCCC
45181 ACTCAGTTTG CCTGGGAAAT ACTGCTCCCA GTCAATATCA TTCTTATTTT CTTCATGTCT
45241 CTGCTCAAGT GTCAGCCCCA GAGTGACTTG CCCTGACTTC TCTGCTTCTC ACAACACCCA
45301 TGATTTCTCTG ATGTTGTATA TCTTTCTGCT CATTTGCTTA TTGTCATCTC TCCCACTAGA

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45361 ATGCAAAATA TCAAAGGGTA AAGACTTGTT TCCCTGCTCT CTCCCTTGGG GCTTGAACAG
45421 TGCAACACAT GGCTGGGACT CATTTACACT TGTAACAAT GAATATTTCT GCTCAACATG
45481 AAATTTTATT ATTCAACCTC TAATGCAGTG TGATGTTTAA GAATCATAGC TATGAAGTGG
45541 AGACATGAGC TCTGCCACCA AAGCCCAGTG TACCATTGAA TAAATTTGCC AGGAAGCAGG
45601 CCGTGCCATG CCTCATTCTT GTCATGTGTA AAATGTGGAT ACACGTAGTA CCAAAACTCA
45661 AAGTGCTGTG CTGAGGCCGG CGTGTGACCC ACAGAACACT GTGCTACACT ACAGGGCAAA
45721 ATCACTGTCA ACTAAGATTA GAAGCAGCTG TAGTACTTGA AATAACATCA GAAAACCAGA
45781 TTATTTATGT TCTTTGTAACT CTGAAAAGAG TTATATAATC TGAATTCAG TTAACCTCTA
45841 GTAAATATAA CGTATTATTA GCTCCTACCT CCCTATGCCT AGTGAAAATC AAATAAGATC
45901 AGATATGAAT GTAACCTAGA AGTGAGTGCA TTGCTTACAT GTTCATTATC AGTACTTTGT
45961 AGAGAGGCCT CTTAATTACA CAGCACATTG CAAATCAATA AAGCCTAGCC GAAAAGAGAA
46021 TTGTTCAAGT CAAACGTTCA AAATAACAT ATACTTAATT TTCCAGGCAA AAGAACAATT
46081 GCCAAGAGTG GGGAAAAGCC CGAGGTAGGC CTCTCTCAGG AGCCTCCAC CCTAGAGACC
46141 TCCACCCAG GTCTCACCAA AAGTGGGTGG AATGGTGAAG AATTAGATC CCCAACGCCA
46201 CTCTTTTCGG CCCCCACCGC CCAACGCATT CGTTCTGAGG TGGAAACCCG GTGCGGATCC
46261 TGCTGTGGGT TTGCTCAGCC TTCTCGGCAA GCACTCAGGG AAGAACTTCC TGTTTGGAGA
46321 TGAAGTGGGA AAAAAGTGA CAGCTGACAT TGGAAATAA CCCGAGTTCC AGGTTCAAGG
46381 AGCCCCAGGC TTAGCTCAGC TCAAGTGAGG AACTACGAGA TTTATTTAAA AGCATTCTAG
46441 TTGGGGGAAG GGAGTGGGCG GTTCCAAAAG TCACTCCGCA GAGCCGGGAC AGCCGGGGGA
46501 GGGGCGAGGT CCTGGGGCGA GGGACCCCTA TCTGCAGTTC AGTGGTAGGC ACTCCCTCAC
46561 GGGGTCTGGA CGCAGAAAGT AGGGAGAGGG GCTTGCAGGAT AGGGTTGAGC AGGTCTCTCA
46621 AAGTTAGCAA ACTCCCAAGC GCAAAGAAAA AGCTAGTTTC GATTTTTCCTA CCCCCGCCGC
46681 GCCCCTAGTT CGCCCCGAGC CCTCGGACTC ACGCAGCAAG CGCCCCTGCA GGACCGCGGT
46741 CTGCAAAAGC ATCAGGAGGA GAAGCGCCGG CCTGGCTCGC GGGCCCATTT CCCAGCTCT
46801 GGCCGACGT CCCCCGTAAA TCTCCGCTTC TTTTGGGGGG CGGGGAAACG GGGATGGCTC
46861 CAGAAGTCAC CCTACAGCTA TTGCCTAGGC TCAGGAGATG CCCAGTAAAA CTCTCTGGTG
46921 AAAAGCAACA GGTCTTTTCA AACTTTAGTT CTCTCTCTCC TACAGCAGAA GGTACCTGCT
46981 TGTGAAACAC TAGGTGATCC AGTGTCCTCC TTGGTTTTTA AATCCTGAAG GGGTGTGTGT
47041 GATTGGGGAA AGTAGCTTCG CAATGTTCTG ATCTGAACTT TAGATATTTA AATATTTATG
47101 ATTTTCAAAA TTCAATCATA CATTAAAAA TTTTATCTCA ACCTTAGACC AACTTATGTC
47161 TTATTTGACT TAGAAATATA AAGCTTTTTC ATTTTGTTTT TTGATTCAAA TTAATTAAGT
47221 CATAACATTA ACCAATTAGA TCCTACTGAA ACACCTTCCA CAGCCTTCAT AATTGAATTA
47281 TCTGACAAGT GTTTCACAAA CTTTACAGTA TTGGGATTAT CTGGAGAATG ATTAACATA
47341 TTGAGGCCTG CTCCTAACCC CAGACACACT GATTTAATGG GTAATTGTGA GGTAGTTAGA
47401 CATTAGCAGT TGGGAGGGGA TGACAGAAGA GAGCGGAAAG GCTGTCACTA AGACAGCCAC
47461 TGGCCACCT AAATTCAGGC CCAAGACTAC CCTAATGCCA CCCTAAGGGA TGGAGTTTAT
47521 GATAAAGTCT GTGGCCAAAA TATCCTGGAG AAAGAGAAAG GAGGGTACAG GTGGAAATTC
47581 CCTAAGGTGG CACATGCCCA ACAACACAAA AGCCTGTCTT CAAGTTTACC CCAAGTTTAT
47641 CATGCCATCA TTATAATAGA ATTTACATAC AGTTTTGCCC CCCCATCCCT GGGAGGCTTT
47701 TCTTAACAAA TTATAGGTAA GACCATGCAC AGTTTAATTT TAGATTGTAT AGCTATACAC
47761 TTCAATCAAA TAACATCATC CTGTCACTCA GATACAGCCC AAACCTCAAC TCCTCCCCAC
47821 AAACCCCAT AAGACACCTT GAGCTCTGTA AAGAAGTGCT GAGTTCACTT CGCAGAAATA
47881 AGCCCGCTGT CCTCAGAGT GTATTATTGT GCTTCAATAA ACTTTGCTTT AAGCTTGCAT
47941 TTTGGTGTGA GTTTGTAGTT CTTTGCTCAC TATCACAAGA ACTGAGATTG CTGGTTCAGA
48001 GCTCCGGCTA TAATAATCTC CTCGGTTAAA GGATCCATCC CAATGCATAA TTCCCAGTAA
48061 CAGTATGGGA TGCCACCTGG GCAATGGGAT TTTAAAAGCT TTCCTTCTCC CTCAACGAAG
48121 TTTGGGAATT ATTGCCTTAG ACATTTCAAA CAATATTAAT AAATTTAATA CACCTGATTT
48181 GCTCCAAACC TTTACATATC TAGCAAATC AACAGGCATT ATTTTGTAA GCATGTATGC
48241 AAATTTTGGC AATTCAAGAA AATCAAACAG GATATCAGGG CCTCGACTGT AGGCAAACAG
48301 ATACAATAAC ATTGGAACA TGTAAGATAT TGATGATGGG CACATTGGGG CTGATAGTAC
48361 TATTCCTTTT TTTCAATTTT TGGTAAGATA TAATTAGCAT ACCATATAAT TCATCTATGT
48421 AAAATGCAAA AATTGGCCCG GCTCAGTGGC TCACGCTTGT AATCCCAGCA CTTTGGGCGG
48481 CCGAGGAAGG CAGATCACCT GAGATCAGGG GTTCGAGACC AGCCTGGCCA ACATGGTGAA
48541 ACCCCGCTCT TACTAAAAAT ACAAAAATTA GCCGGGCGTG ATAGCAGGCA ACTGTAATCC

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48601 CAGCTACATT AGAGGCTGAG GCAGGAGAAT CGCTTGAACC CGGGAGGCGT AGGTTGCAGT
48661 GAGCTAAGAT CGTGCCATCA CACTCCAGCA TGGGAGACAA GAGCAAGACT TCATCTCAAA
48721 AAAAAAAT TAGCTGGGTG TGGTGGCATG CACCTGTAAT TCCAGCTACT CGGGAAGCTG
48781 AGACAGGAGA ATCGCTTGAA CCTGGGAGGC GGAGGTTGTG GTGAGCCGAG ATCATGCCAT
48841 TGCCTCCAG CCTGGGCAAC AAGAGCGAAA CTCCGTCTCA AAAATAAAAT AAATAAAATA
48901 AAATGCAAAA ATTAATGGAT TTTAGTATAT TTACAGAGAT GTGCAACCAT TACCAAAAT
48961 TTACATTTCT ATCTCCCCAA AAAGAAACCA TGTTCCCTTA ATTCAGTACC CTTAATTCAT
49021 CGCCTCCAG ATTCTCCAT TCTCCTCCTC CTCCCTCCC AGCCCTAGAC AATCTTTAAT
49081 CTACTTTCTT TCTATTGGA ACATTAGTA TACATAGAGG CATATAATAT ATTGCTTTGC
49141 CGTGACTGGC TTCTTTCATT TAGCATAATG TTTTATGTA TGTTTTTCAT GGACCAATAA
49201 TATCTATTAT AAGGACATAC CACAACATAT TTTATTATT CATTATCAG CCGATGGACA
49261 TTGGTTTGT TCTACTTTAT GGCTATTGGG AATAGTGCTG TTATAACAT TTATGTACAA
49321 GTTTTTTGT AGACTTATGT TTTGATTCT TTTGGTTATA TATCTAGAAG TGGGTTGCT
49381 GGGTCATATG GTAACACTGT TTAACCTTT GAGGAATTGC CACATTCTTT TCCAAAGTAA
49441 GCATTTTATC CTCCTATCAG CAGTGTATGA GAGTCTGAT TTCTCTCCAT CTTTGCCTGG
49501 GTTTTTGAAT CAGGGCCCCA GATAGAACAA AAATGTGGTT ATTCAGTTGT TCCACCATCA
49561 CTTGTTGAGA AGACTCTTTT TTCATTGAAG TGTTTGGCA CCCTTATCAA AAATCAATCT
49621 ACCATAAATG TGAGAGTTTA TTTCTGGAGT CTCAATTTTA TCCCATTATG CTATAATCTA
49681 TAATCCTATC TTTTTTTTT TTTGACAGAG CCTCACTCTA TTGCCAGGT TGGAGTGCAG
49741 TGGCCCAATC CCGGCCACTG GCTCCTCCTC CCAGGTTCAA GCAATCTCTC TGCCTCAGCC
49801 TCCCAAGCAG CTGGGATTAC AGGTACCTGC CACCATGCCT GGTTAATTTT TGTATTTTAA
49861 GTAGAGACGG GGTTCACCA TGTGGTCAG GCTGGTCTGG AACTCCTGAC CTCAGGTGAT
49921 CTGCCCACCT CAGCCTCCA AAGTGTCTGG ATTACAGGCA TGAGCCACCA CACCCAGACT
49981 ATAATCCTAT CTTTATGTCA GGACTACACT GTCTTGATTA CTATAGCTTT TTAGTAAAT
50041 GAATTCAAGA AGTTTCTCAA CTTCAAATTT GATCTTTTTT TGGAAGACTA TATTAGCTAT
50101 TCTCAGTCTG CTGAATTTCC CTAGGAATTT TAGGATCTAT TATCAATGTC TATTTCTATT
50161 TTGTATATGT TTTAATATTT TCATAAGAAA CTTTTTTCAT TTAACCTTTT TTTTTTAAAG
50221 AAAATAGTGA AAATCAGAAC ACTGGGGGTC AGGCGCATT AACAGGCAGA AGAAGAATAA
50281 AAATCTGTCA TATAAACAAA AAAGAAATGA CCAATCACAT TGTGGAAGCC ATGGAGTGGT
50341 TATAGGTGCC AAAGGCTGCA GAGAAATGGT GTCAGATATA CCTGAAAATT GTCCATTGTA
50401 TTTGGCCATT AAGAGACTTA GAAGACTTAA GCCATAGATT GCTCAGTGAG ACCCCGAGGG
50461 CAAATGGTCT GAAGGTGAAT AGATCAATTC ACCTTTAAGA GAGCAGGTAG GAAGCTATAA
50521 ATCCAAGATT AAAAAGTTGA CTGAACCTTT AAGGAAGAAA CTCTAATCTT GAGCCACCCT
50581 ATCCTGGCTC CACCTTCTGC TGCAAGCAAA CAGAAATGCT GAAATTCAAC ACTCACAAAG
50641 GCTGGTAAGC TGGAAATGAC AAAAATTACT CCTGGGAAAG TCAGATTTAG AATTAGGCCA
50701 TATTTGTTGG GGTTCAGATT TTCATGTACA CTTGGGAAAG GGTTTAGCTT ATAGGCACAT
50761 GCATGAAGGG AACTGGTATA GGGCTGTGTT CATAAGGTCA AGAGTTGAAG GCCAGGCATG
50821 GAGGCTCTTG CCTGTAATCC CAGCACTTTG GGAGGCCGAG GCAGGAGGAT GGCTTGAGCC
50881 CAGGAATTCA AGACCAGCCT GGGAAACATA GGGAGATGCT GTCTTCACAA AACAATTAAA
50941 AAATAAAAT AGTCAGGTGT GGTGGCACAC ACTTGTGGTC CCAGCCACTC AGGAGGTTGG
51001 GAAGATCACT TAAGCCTGGG ACATTGAGGC TGTAGTCAGC CATGATAGTG CTAATGCACA
51061 CCAGTCTAGG TGACAGAATG AGACCCTGTC TCCAAAAAAA GAGCTGTATC CACATCCCAG
51121 GAAAGTGGTT GAAGATCTAC TTTTCTCTGT AAACCTAATA AAGAATAGAG TGACAAATGT
51181 GTGTTGTGGA AAGAAATGGG GTGAGAGCTA CGTAGATGCA AAACAATACA TCCCCACATA
51241 CCACTTGTTA ATCATCCTTT TCCACCCACT TATGGGATGA ATTGCATCTC CCAAAAGAT
51301 ACTCTGTCTT AACCCTCAGT AGCTGTGAAC CTGACCTTAT CTGGAATACG GTGAGTTCAC
51361 TGGTTAAGAA GAGATTATAG TGGAATAGGG TGAGTCTCTC AACCAATGAC TGGGGTCTCT
51421 ACAGACACAG AGGGATGATG GCCAGGTAGA GATGGAGGCA GAGATTGGAG TTATGCTGCC
51481 ACAAACCAAA CACAGGAAGC TGCTAGAAGT GGAAACAGGC AAGAAAGAAAT CCTTCCCCAG
51541 AGGCTACAGA GGGATCTTGG CCCTGATAAT ACCTTGATCT CAACTGGCCT ACGTCACTGT
51601 GAGAGAATAA ATTTCTTTTG TTCTAAGCCA CCCAGTTGAT AGTACTTTGT TACGGAAGCC
51661 CTAAGGAATC TGATATACAT TTCTTTTACT GTCATAGAAG TTTTGAATCT TTTAAGTAGG
51721 TCTGTACCCT TCCTCCAGT GTCAACACAT GGAATTCCTC TCCTTGTGCC TTGAAAGTG
51781 AAAGGTGTTT GAACTGGTAA TGAAAGAAAT CTCAGCATGA GGCCAGATGC TGTACCTCAC

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51841 ACCTGTAATC TCAGCACTTC GGGAGGATGA GGC GGCGCAGA TCACTTGAGG TCAGGAGTTC
51901 TAGACTACTC TGGCCACAT GGTGAAACCC CATCTCTACT AAAAACAAAA AATGTTATCC
51961 TAGCCGGGCA TGGTGCCGTGT AGTCCCAGCT ACTCAGGAGG CTGAGGCAGG AGAATTGCTT
52021 GAACCCGGGA GGTGGAGGTT GCAGTGAAGT GAGATCACGC CACTGCACTC TAGCCTTGCT
52081 GAGAGAGCAA GACTTGGTCT TAAAAAAGAG AAAAGAAAAA TGAAATTTCA GCATTATAGA
52141 ATAAAAATGT TTCCCTTCC CCCCAACTT TAAAAAAGCA GAAGTCTGCA TCATAAAATG
52201 GTCTTTGCCA ATGTTATTTT TATTATAACA AAGGAATCTT GCAAGGCTAC CAGATCTCAG
52261 CAATTGTCAC TATGTTCTGT AAAAATCACT TCCTAAAATG TCTGAATTGA CTGCTTGTCT
52321 CATTTATTTG TTTCTCGTGT CATACTGCAA TGGATATCTG TCTTGTTAGT ATAAATATTT
52381 GTGCATTTTG TTGTTGTAA AACAGCTTTT TTGGCCTGTC TTCTTCCACC TATGAGGTAA
52441 TATAAACTC ATGTTTAAACA CTTATTTTGT TAGCAGGACA AGCTACAGAC AAAACCCCTC
52501 AGACACTGAG TTAAAGAAGG AAGGGCTTTA TTCAGCTGGG AGCTTTGGCA AGACTCACAT
52561 CTCAAAAAC CGAGCTCCCT GAGTGAGCAA TTCCTGTCCC TTTTAAGGGC TTGCAACTCT
52621 AAGGGGGTCT GTGTGAGAGG GTCATGATCG ACTGAGCAAG TGGGGGTATG TGACTGGCAG
52681 CTGCATGCAC CAGTAATCAG AACAGAACAG GGATTTTCAC AGTGTTTTTC CACACAATGT
52741 CTGGAATCTA TAGATAACAT AACCGGTTAG GTCGGGGGTC AATCTTTAAC CAGACCCAGG
52801 GTGCAACACC AGGCTGTCTG CCTGTGGATT TCATTTCTGC CTTTTAGCTT TTACTTTTTTC
52861 TTTCTTTGGA GGCAGAAATT GGGCATAAGA CAATATGAGG GGTGGTCGCC TCACTTATTC
52921 ACCCCCTTTG AGAATCTCAC TCATTAGTGG GAGTTCTCAC TTTTATTCTC ACTACCTATG
52981 TCTTCTTGAA AGACAGATTG ATAATGATT C ATATAGTACA CTTGTGCTGA AGCATTTTGG
53041 TGAGCTAAGG TAGTGATGAA GCTTTTATC ATTTGGAGAA GTACAGGTAG CAAACAAGGA
53101 AGCAGTAAGC AGGTTTCTAT TAATATTATA ACTCCTATTA TAAGAGTTTT AAATCTTCTT
53161 AGCACTCGGA ACCATTTTTC AAACATGGCC CCAGAAACAA ATCCATACCA CACCTACATG
53221 GGCACATGTG CCACCTTTGT CATATTTCTA ACTATGTCTT CAACTACTTG CCCTTAATCA
53281 TCTATGTGTA GACAGCAATT AGTAAGGTTA AATTTCTTAC AGACCCCTCC TTCAGTTGCT
53341 AGCAAGTAGT CGAGAGCCAA TCCATTTTGA TAGATAGCAT TTTGCATCTG AGTTTCTTGC
53401 CAGGCCACAG TAGTCAGGGC TCTGCTGGTC TTATTAGTAA TTATTTCTAA GACAGCTTGT
53461 AACCGTATGA TTCAGTTGAG CATGTAAATG GGGGTCCCAT ATCCCCACAA GCCGTCTTGT
53521 GCCCAAGTAG CAGGCCCAT AATTTGTATG ATTCTCTCAG GGGGCCATTC ATTATTTTTTC
53581 CAATTTTCTA TAGCTATGCT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTGCGG
53641 GAAGCATATA CAGGGAAGCC CAGGAGTTTG CCTGTCTTTA TGGGCAGTAG GAAGAAAGAT
53701 GGTTTAGTAG TGTCAATAAC ACAACTACCT GCCCACTGGT CAGGTAATTT GGCATAAGCT
53761 GTATGCCAC ATATCCAGTA TAATCCAGTG GGGGCTGTCC AGTCCCGGTG GGAATCTGGG
53821 TGGGTCCACA CAGTTTGCAA CTTTGGGAAT TTACTAAATA GATTTTCTT AGTGTGGTTT
53881 GAACTCCACT AGGTGGCTGT TTTTATAGTA CTATTATACA GTTTTGGCCC AAGGCAGCTG
53941 AGTCTTCCA CAGGAAGGGT GAAGTCCTTC CCCACTTTTG CTATACAGTA TTGTCTAATG
54001 ATTGAGGCTT TTAGGACCCA GAAGTTATCA GGGTGAGTCT TTTGAGCTGG GAATTTATCA
54061 GGAAGTGGGT CTGTAGGTAC TAATCTCGT GCTTCCCATG GCCATTGATC TCCCATTACA
54121 GTTCTCCAC ATACATACAT AACATGAAGT GACATTGAGA GACTGGGCTA CATGCTCAGC
54181 TAATTGCAAA AACAAATTTT TTGTTTTTCC TGGAAATTTCT AGTACTGGCA CATTCAGTTC
54241 ATCATAAGAA GGTTTGAAAT ACTGGCTCAG GGGAGCATTT ATAACTTCT CCTCAAACCA
54301 CCATATTTAC TCAAGGATCC AGTCCAGCCC CAACTATTTT TAAGGTTACA CGATCCCCTT
54361 TTTTCCAGTG AGAATCAAGG GGGTTGGTTA TTACTAGTTC TAAGGGGTTA CACTGACCAC
54421 TGGTACAGGA AGGGCCACTT TTCCCTTTCT GAAGGTGGAC AGGATTCTTT TTATTTTTTA
54481 ACCAAGTTGC CTAAATGACA CAAGACCAGT ATCTACATTT ATTTCCACGC AGTCTTAATT
54541 CATGACAAGC GTACTTATTT TCTGCCATAT AGCCTCTTTC CTAATGAACA GAACCACATC
54601 CTATTTCTAA CTTATTACTA TTAATGACAG CACAGGCATC AAATTTCAAG GTGACTTGTT
54661 TGGGCATTCC TTTTCTTCT GTTTTGGCTA ACACCTTACT CGTATCGTTT ATGAACCCCC
54721 ACCAGTCTC AGTCTCAAT CTTATTTCAA AAAGTGTGGT CGTGGGAGGC TCAGATGGGT
54781 CATAACACAC ATCAGGTTGG TCATTCTTG GGCTACCTAC CTTGTATAGA ATAGCATTAT
54841 ACAAACAAGT TATTTTLAGA GTCTTTGTAC ACTTATAATA ACCATAAAAT AATAAGACTG
54901 TAGCAACTTT TTGTCCTACC TCAGTGACTT GATGTATACA CTGGGAACAG CCCTCAGTCT
54961 GAGGAAGGTT AGTTGAAGTC TTTACTGTGC AAGTCCAAAT TTTAAGGAAA ATGAGTCCCT
55021 TGATGAGTTT TCTCATGTTT CGGCCATGCA TGGACCAGTC AGCTTCCGGG TGTGACTGGA

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55081 GCAGGGCTTG TTGTCTTCTT CAGTCACCTT GCAGGCGTTG GCGAAGCTGC CACGTACAGC
 55141 TCACAGTCTA CTGATGTTCA AGGATGGTCT TGGAAAGTTG GCCCACTAGA ATTAAGTGAG
 55201 TCCAATACCT CTAATCAGTC ACTTTCAACT GGGCTTTCTG ATACCAGGAG CAAGGTGGCA
 55261 GGTTTTAGGG TGTTGCAAAT TTCAATGGTT ATGCAGGGAT TTTCACATAG CAAACTTTGG
 55321 TACTTGGTTA ATCTAGCATT TGTTAGCCAA TGATGTATTT ATTAAAGTCA CCACAGCATG
 55381 GAGGGCCTTT AAGTTTAGGT TTTGTCCAAG AGTTAGCTTA TCTGCCTCTT GTGCTAGCAG
 55441 GGCTGTTGCT GCCAAGGCTC TTAAGCATGG AGGCCAACCC TTAGAACTC CATCTAGTTG
 55501 TTTGGAGGCC CAGCCTCGGC CAGGGCCCCA CAGTCTGGGT CAAAACCTCA ACCGCCATTT
 55561 TTTCTCTTTC TGACACATAG AGTGTAAGG GTTTTGTCTG GTCAGGTAGC CCCAGGGCTG
 55621 GGGCCGACAT GAGTTTTTCT TTTAACTCAT GAAAACTCA TTGCTGTTGG TTGTAATAGA
 55681 TGTAATTTAT CCAATCTACA TTTTATTAA CTGTCACCCA CCAAATATT GACTCAAATC
 55741 CTGCAGCTAT TTGATTTTGG GATTTAAAT GATCTGCTAT TCCCTGTGGG ACTCCAATTG
 55801 CATCTAAATA GATGTGAGAG TTGAAAGACA CATAAGGGTC TTCTCTTGCT TTACGATGTC
 55861 TTATTTTCTC TCCCTCTGGT TGATGAAATG CTAGGGTGAA AGGGATAGCC AATTGGACTA
 55921 AAGTACAAGT GCCGCTCCAG TTATTTGGCA GAGTGCCCAG TAAAGGTCCA CCACAATACC
 55981 ACCACACATC CGCTTGGGGA TGAACAAAGG CTGACTGATT GAGAAGCTCC TGAAAATTCT
 56041 TAAGCTCACT GCATCCCTTC AGGTCTCCAA GGAATGCTAA GTTTCCTCCC TGTCATGAGA
 56101 GACAAGAAGT GAACTTAGTT TTGGGAGATG GAAGCTGGAT GGCCCTCAGG GGTGACCTG
 56161 CAGGGTGCTG GACTTTGGGA TATAGCAGAG AGAGCTTGGC ACGACTTATT ACTCCAGGCT
 56221 GTAGAATCCT GGAACACAGT TACCATGCAG CCCATGCCTG GTCACACAGG GGACCACCTT
 56281 AGTGGAAAGG GGATAATCTG GCCCTCTGGC CTGCCATGTG CACAAGCATA ACAATTGGTT
 56341 TTGTTTAAATG TGTGGACAGA ATATTTGATC CATTCCAAC TCCCTGTTGC ATCTTGGTAT
 56401 CCTGCTTAAT TATCAAAGTT TGTTTAAAGT CTTTAACTTC TATGACCTC TAGTAAATG
 56461 AATGTATGAT TTTAGGAAAT TACAAAAACC GGTGGGGGCA GTCCATCCTT GCTCTTTAGT
 56521 GGTCCACACA ACATTCGACC AACTATGGCA TAAAAGCTCT ACATCGGGGG GCAAGACTCC
 56581 TCGTTGACAC TGGGGTCTTT ATTGAAATCT CTCTGGAATA AATGGTCTCA GTTTACTAAG
 56641 GCTCAGTCTG AGGAGAGTCA GGAGGGACAG AGGTACTTTT CTGAAGTACA GAGATGTCTT
 56701 CGACTTGGCA AGTCCCCACA GGGTATAACA AGGCAAGCAT TAAATCAAT AGTTTGAGGC
 56761 AAAATTGACT TGGTTATGTT AATAACTAGA TGGTCAGAAA TAGAGTGAGG GAAGAAGAAA
 56821 GAGTAAATAGA ATAGATGAAG GAGTTAAAT TTTCTTAGCT TTAGTTTGGT AGGGTTTTCC
 56881 CCTGGGACTA TGGCCCATGA CTCTGGAGGG GGTGGCACTT TCTTGACTCG GGTGTGATGA
 56941 GTCCATCCCT TTTTCACCGT ATGAACAACA GTCTCGGTGG TTAGCAGCAC AAGGTAGGGT
 57001 CCTTCCTAGG CTGGCTCAAG TTTTCCTTCT TTCCACCCTT TGATGAGAAC ATGATCTTCA
 57061 GGCTGGTGCT GGTTTACAGA AAATTCTAGG GGTGGTACAT GTGCTAAAAG ACTTTTAGTT
 57121 TTGAGGGAAA GGAAAGTGGA AGATAAACCA AGTATATAAC TTTTAAAGAG TTGACCTTTT
 57181 GTTTTAAATG TGGGGACATC AGCAGTGGAC TTTATAGTCC TTGGTGCCCT CTTACTGAGA
 57241 AATTTCCCTT AGCACCTATT TTTATTAGTT TTTAGACCAA AGAAAGTCAA ATGCCATTTT
 57301 ATATTTGACA ACGCTTCTTG TATGTTTATA CCAGATAAGC TAGATTTTAC CTTTATATTG
 57361 GTGTGTTATT AATGTTAAAC TTAGTTTATA TAAACTCTG TAGACATATT TATTTGATT
 57421 TTAATGTCTG ACCATAAGGT AAGATTTTAA TAGACTTTTC TTTAACCTTT TATAATTTT
 57481 GTTAAAGAAC AGGTAGTGC TTTAAGAAAA ACCCGTTGTG TTTTATTTT AATGTTTCACT
 57541 TCACAGAAAA ACTGTATGAT ACCCCTTAAC TTTAGCCAAT ATGTTTAGAC ACAGAATTTT
 57601 CTTTACAATT AAGGTTTCAA AACTTGCTTA AACCTTCAA ACAATTTTGT TAACCTTTTA
 57661 ATGTAGGTAA AAATCCACAT TCTTATGCAT CCTCATAATC CTTTACCAA AGGTATATT
 57721 TACTTTCCTT ACATACCTTG CACATAAACT GTTTATTCAA TAGTTTACA TTTAGAAAGGA
 57781 GGCCTAATTA CTTTTAAAT ATACAACATT TCTTACATAA ATTTATTTT CTAACACACA
 57841 TTTTTCAT GACTTTCACA GACAATCTT CGACATGCCT CAACCTTCTG ACTTATTGCA
 57901 AACATCCCTT TCTTTAAACA ACTAGTTAAT TTATCTCAGG ACAAGGATTT TCCATACAA
 57961 ATTCTTTTTT ATATAAATTC TGCCCTCTCT TTATTTCTT TTTTTTTTT CCGAGGATGA
 58021 TAACCATTCT TTTCCAAAGC GAACCTCTT TATGTCTGTG GACTAGACTG TCTAAGGCCA
 58081 CAAGATTAGA AGTTACTATA ATACATGTTA CACTGTTAAC TTTTAGCAAA CTTTACTTTT
 58141 GTTGAAGAAC TTGTAAAGTT GGGATTTCOA TTATCCTTTG CTATTAATAA GACCTTATT
 58201 AGTCCAAAT AACTTAGAAT TGGTATAGAT GGCTTTTTT TTTTTTAAAT TACCTGGGAG
 58261 GAACCATCTA TCCTCTGTG CTGAAGGGAG TTCCTCTAG GTCTGGTCAG AGCTTTGTAT

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58321 GGTAATTAAG ATTTAGATCC CCTGTTAGGA AACCTGCCGG GTTAAGAGAA TTTTCAGTGG
58381 TTAATGTAA ATCATCTTCT TTTTCTTTT TTCCTTAGGA TACTTCTGAA CCGGTGAGGT
58441 GTGCTCAAA TGAGGTTTCC TGTAAGAATT ATTTTTTTAC TTTCTTCTGT TAGCAAAGCA
58501 GTTGCCGCTA CAGATTGAAT GCATTTGGGC CATCCGCGGG TTAAGTGGGT AAGGATTTTT
58561 GATAGGAAGG CCTTAATGCT TTTGGAATAT GCCCTGACAA CAAAGTGCCA GTTCCTTCCC
58621 GGTGTTGAGC CACTGCGTTG ATCCTCCACG AGGCGCTGCC ACGTGCTGCT CTGGTGAGGC
58681 GTTCCACCGG GGCAATTGCC TACCTGGGAG CGCTCTCCAG ATCTGTGTCTG CTCAAAGTGG
58741 CTGGAGTTCC CCGTAGGGAT GCTCCACAGG GCAGGCCTAA GTCGCCTAAG GGGCTGCCTT
58801 GACCGTCCGT TAATCACCTC TGTCTCCAAA AACCAGCTCC CTGAGTGAGC AATTCTGTGC
58861 CCTTTTAAGG GCTTACAACCT CTAAGGGGGT CTGCATGAGA GGGTCGTGAT TGATTGAGCA
58921 AGCAGCGGGT ACGTGACTGG GGCTGCATGC ATCAGTAATC AGAACAGAAC AGAACAGCAC
58981 AGGGATTTTC ACAATGCTTT TCCATACAAAT GTCTGGAATC TATAGATAAC ATAACCTGTT
59041 AGGTCAAAGG TCGATCTTTA ACCAGACCCA GGGTGCGGTG CCGGGCTGTT TGCCTGTGGA
59101 TTTCAATTTCT CCCTTTTAAT TTTTACTTTT TCTTCTTTG GAGGCAGAAA TTGGGCATAA
59161 GACAAATATGA GGGGTGGTCT CCTCCCTTAA TTTAAACAAA ATTTTCAAAG TCCTACCCCA
59221 AGTAAATTGG CAAATATTAA TAAAGTTATG GCATAGAAAA TAAAAATGAT TGTAAGAGGC
59281 GTAAAGATAT TTCTGTGGGG AAAACATTTG TTCATTAGTT ATCAGTTAAA ATTCTGTGAA
59341 AAATAACCAC TAGAGACCTT AAAGTACCCA GGGGCTAATA ATAAGAAGGG AGGAACACCC
59401 TCTCACTCCC CACCGTTACC TGCCACAGAG GGAAGAGGAA GAGGTGACT CCAGGAGAGC
59461 TGTGGTCTCC CCTCCCCATA TGTCCACATA TACCTGACCT CCCCTCCCCA AAATATATAC
59521 CCAATATCTC TCCCATATAT ACATATTTAT CTGACCTCTC CACATATGTA TACCTAAACT
59581 TTCTCTATAT ATCCACATAT ACCTAACCTT CTCACACACA TATAGCTGAC CTCCAGTGGA
59641 GGAAAATGGG GAAGAGAGAA GAGTTATCA AAGGATAAAT CTAGGTGATA CTCAGAAATG
59701 TGAAAAACAA AAACCACACA CAGAAAAAAA AAACACACAC AAAAAAGAAA TTGATAAATT
59761 TGTTTGTGTC AAAATTAAGA ATTCCGGTTC AATGAAGGAT CCCATGGATA AAGTTAAGAC
59821 ACTGCTGTAA GGATGGTAGA GAATTAATG TCTGAATCAG ACGAAAGGAT GAGTAATTAG
59881 AATGCACAAG GCCAAGAAGA ACAAACAGA AACTCCACAT AAAAAATGTA TGAGGCCGGG
59941 CGCGGTGGCT CATGCCAGTA ATCCAGCGC TTTGGGAGGC CAGGGCGGGC CGATCAGGAG
60001 TTTGAGACCA GGCTGGCCAA CATTTGAAA CCCCATCTCT AAAAAAATA CAAAAATTA
60061 GCGGGGCGTG GTGGTGGGTG CCTATAATCC CAGCTACTTG GGAGGCTGAG GCAGGAGAA
60121 CACTTAAACT CAGGAGGCAG AGGTTGCAGT GAGCTGAGAT CACACCATTG CACTCCAGCC
60181 TGGGTGACAG TGTGAGACTC TGCTCAAAA AAAAAAATA TTATATATAT ATATATATAT
60241 ATATATATAT ATATATATAT ATATGAAATA AATGAACAAG AAATTTAGAT ACAGGAAAT
60301 CCAAAGCACT TGGTAATGAA AGAAGGTAA AGTGATGTGT CCTTTTGCAT TTAAGAGAGA
60361 GCATTAACAA ATTAGAGAGC TGAATAATGC TCAGTATTGG TGTGGATATG GAGACTCAGG
60421 AATCCTCATA CACTGCTGAT GGGAGTGCC ACTCCCTGGG AATATTTTCC AAATATCATC
60481 TCAACATAT CCCATAAAGG TGACAGGAAA GTGTGGGCTG ACTGATATCC TTCAGTGAGA
60541 GAGGTGGAGG TAAATGAAG TCACTGCACA ATATAGAGTT GGAAGCAATG GATTAGATGT
60601 CCACATAGTT ACGTGAAGA ATCCGTAAGA TACACACACA CACACACACA CACACACACC
60661 TTTGTGTATA TTGTTCTTGG CAGGTAGGCA TGGAGGTTTA GAGGCTTTCT ACATCACACC
60721 TACTGCACAC AGTAAATGGC CAGGCTGAGC ACTGACTTCC ATGAAGGGAG ATTGAAGGTA
60781 AGAGATTGAA GATTGTTCCC TGCTGTTGGA CCTTGCAACT GAATATGCAG AAAAAAGTAC
60841 ACCCGCCAC CCCGCTTCCC ATCTTTCCTA CCTGATTAGA ATAGCTTTTT CAGAAAACGT
60901 TGGCCAGGGG TTGTGGCTCA CACCTGTAAT CCCAGCACTT TGGGAGGCTG AGGCGGGCAG
60961 ATCATCTGAG GTCAGAAAGT CCAGACCAGC CTGGCCAACA TGGCGAAACC CCATCTCTAC
61021 TAAAAATATA AAAAATTAGC AGGGCATGGT GGCACACACC TGTATCCCA GCTACTCGGG
61081 AGCCTGAGGC AGGAGACTCA CTTGAAGCAC AGTGATGGAG GTTGAAGTTA GCTGAGATCT
61141 TGCCACTGCA CTCCAGCCTG GGCAACAGAG TGACACTTTG TCTCAACAAC AACAACAAAA
61201 CCCACAAAA CTTTAAATCT ACCTATGGCC AAATGCCTGC TAAATGAGC ACCCAAGAG
61261 CAGTGTTTCA GAAAGTCAGA TGAATACCTT AAAATTAGAT GCAATGTTGG CTGGTCACAG
61321 TGGCTCAGGC CCTGTAATCC CAATCCTTCT TGGGAGGCCG AGGCGACAGA TCGCTTAAGC
61381 TCAGGAGATC GAGACCAGTC TGGACAACAT GGTGAGACCG TGTCTCTACA AAAACGTACA
61441 AAAATGAGCT GGGAGTGGTG GCGCGCACCT GTAGTCCAG CTACTCAGGA AGCTGAGGTG
61501 GGAGGATCTC TTGAACCCAG AAGGCGGAGA CTGCAGTGAG CAGAGATCAT GCCACTACAC

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61561 CCCAGCCTGG ATGATAGAGC CAGACCCCCA TCTCCAGAAA AAAAAAATAA AGAGAGAGAG
61621 AGATGCAATA TTTAGGGTTC AACAAGACTG AATTTCTGAC TCCTTTCCCT ACCTCTCCAG
61681 CATGTTAGAT TCTGGGTCTT TCATCCTAAC CCCCTGTTCA TGCCATAGCC ACCCTGTGGT
61741 ACCAACTTTG GAAGCCTGGA TCTTCATCCC CTCATGATAA TGAGTGTCCC ATCAGGTCTC
61801 CATGCTCAGC TTGGCAAGAG TATCTGTCTT CTCCTCATGG GACGGTCACA TTCACCCAGC
61861 ACTGACAGGT TCCATTCCCA CTAGGGTGGC ACCCTATATG GTCTGAGTCC AGGCCTTCCT
61921 GGTCCCTCAG TAATCTCAGC ATGGTAGCAC AATCGAAAAG GGCTAGGCAC GGCAGCACCA
61981 TTTCCCACCA AGAGGTCTGA TGGCTCATCA CATAGACTGA AGGAGATTCT GAAGAGCAGA
62041 GGTGGAATGA AGAATGAATC GTGGGCTCTG CTCTTCCTAG GCCTGTCTTC CTCTCTCCCG
62101 AGATGTTAGC TAACTCATGA GAGCCAGAAA CCAACTGCAG GCTGGCCTCA GGCACCTAGG
62161 TAGTGCTTCA GCCTCAGCAG TCCACATTCT AGGAACCCTC ATAATATGGG TTGAAGTATG
62221 CATTTCCACA AAAATAAAGT TGTGTAAGTC CTAACCACCA GTACTGAAAT GGGAAAAGTT
62281 CCCTTGTCCT GCTCGCATGG CATGTGATAG GAGTGTGGCT AATTTCTTCA GTGCCTGGCT
62341 GCTCAAACCT CTAGGGGAAC ATTAAGACGG GCAGGTTGTG GGTCTCCAAC CCCATGACCC
62401 CACCACAGTG TCTAGGGTTG CATTGTTTACA GCTCCTGAAG CCACAGTGGG TGTGTGTTAC
62461 AGGGTGCTCT TTTAGTTTGG CATTGTTATAG GCAGCTGGTG TTAACCAACT CAATTAGACC
62521 GTCTACCTTG TCCCAAGGAC AGAAGAAGGC TTTCTGTATC CCAGGTTCTT GCCTTGGTGT
62581 ACCGGAATAA ATCAGACCAC ACCTGGGCTT AGAGAAAGAG TGCAAGGTTT TATTAAGTGG
62641 AGGTAGCTCT CAGCAGTTGG GCAAAGCCAA AAGTGGATGG AGTGGGAAAG TTTTCCCTTG
62701 GAGTCAGCCA CTCAGTGGCC CAGGCTCTCC TCCAACCACC CCAGTCAAAT TCCGCCTCAT
62761 TTTGCCAGGC AAACGTTTGT TGTGTGCTCT TCTGCCAGTG TGCTCCCTG GACGTCCAGC
62821 TATTGCTGTC TTGTGGCAGG CCAGGGGAGG TCTTGGGAAA TGCAACATT GGGCAGGAAA
62881 ACAAAAATGC CTGTCTCAC CGTGGTCCCT GGGCACAGGC CTGGGGGTGG AGCCCTAGCC
62941 GGGGACCACG CCCTTCCCTT CCCCCTTCC ATATCATTTA AAGGGACCAT GCCCTTCCCT
63001 TCCCAGCACT TTCCCTTCC TGTATCAGGA CCTGTGAATG TGGCCTTATT TGGAAATAGG
63061 GTCTTTGCAC TTCATCAGTT AAGATAAGAG TGGGCTCTAA CCCAACATAA AGGGTGTCTT
63121 TATAAAAAGG AGAAATGTCA TACACAGAGA CTGACACCTA TAGAGAGAAA ATGTGGTGAG
63181 TAGACACAGG GAGAAATCACC ATTCAAGTCA AGCAATGAGT CTGGGGATAC CAGAAGCTGG
63241 GAGAGAAACC TGGAACAGAT TATCCCTCAT TGCCTTCAGA AGGAATCAAA CCTGATGATA
63301 CTTTGATTTT AGACTTCCAG CTTCAGGAC TGTGTGACGA TAAATATCTG TTGTTAAGCC
63361 AACGAGTTTG AGGTACTTTG TTA CTGTCAGC CCCAGAAAAC TAATACAGTA GGTACTATGG
63421 ACTGAATTGA CTCCCCGTCG CAAAATTCAT ATGTTGAAAC CCTAACCCCT AGTGTGATGG
63481 TACTTGGAGC TGGGGCGTTT GGGAGTTCAT TATATTAGA CAACTCATC AGGATGTGTC
63541 TCTCATGATG AAATTCATGC CTTTATTAAA AGAGACAACA GGCCAGGTGC AGTGCTCAT
63601 GCCTGTAATC CCAGCACTTT GGGAGGCTGA GGTGGATGGA TCACCTGAGG TTGGGAGTTT
63661 GAGACCAGCC TGGCCAACAT GGTAAAACCC CATGTCTACT AAAAAATACAA AATTGGCCA
63721 GGTGTGGTGG TGCACGCTTG TACTCCCAGC TACCTGGGAG GCTGAGGCAG GAGAAATCCCT
63781 TGAAACCAGG AGGTGGAAGT TGCACTGAGA TCACACCACT GTACTCTAGC CTGGGTGATA
63841 GAGACTCCAT CTCAAAAAAA AAAAAAATAA AGACAATAGA GCCAGGTGCT GCAGCTGATG
63901 CCTGTAATTC CAACACTATG AGAGGCTGAA GCAGGAGGCT CGCTTTAGCC CAGGAGTTCA
63961 AGACCAGCTT GGACAAAATA GTGAGACCCC CAACTTCTAA AAATTTAAAA AATGAACTGG
64021 GTGTGGTGGT ACACATCTGA GGCTCCAGCT ACTCTGGAGG CTGAGGTGGG AGGATTGCTT
64081 GAGCCCAGGA GGAGGCTGCA GTGAGCCATT GCTGTCCAGC CTGGGCTACA CGAGAACCTG
64141 TCTCGGGAAA AGGAGAAAAC AGTGAGACCT CTTTTTCTCT CTTCTTCTC TCCACTGCCT
64201 AAGCCCTACA AGCACAAAAA GGACACCACA TGAGCACATA GTGAGAATGC TGCTGCCACC
64261 AACAAAGTCAG GAAGAGAGCG TTCACCTAGA AACTGAATTG GCCAGCACCT GGATCTTGGA
64321 CTTCTGAGCT TCCAGAACTG TGAGAAAGTT ATTTTTTTTT TAGCGACTAA GTCTATAGTA
64381 TTTTATTACA GCAGCTCAAG GTAACATAA TAGTAGAAGG GATGAATTAT GGAGATCACA
64441 AGTCCACGCC TCCAGAAAAA GACTTCCCTA AAAATTAGTC TGAGCAAAAT TCGAATGATG
64501 AATTATTTTT AAGAACTTTT AAGGGATCTG ACAAGTTTGC AAGAGCTAGA GAATGCTTTA
64561 CAACGTGATA ATAGAATGCT CTGTGATGAC AGAAATCTTT CCACACTGTT CAAAACATAGC
64621 TACTGGCCAC TTGTGACTAT TGTGCACTTG AAATGTGACT GGTGTCTGAG GAGCAGAATG
64681 TTTAATTTTA CTTAATTTTA ATTCATTACA ATAGCTACAT GTAGCTAGGG GCTACTGGAT
64741 TGAACAGCAC AGCTCGAGTC TTTTAGAGGG AGACAGGACT CACCAAGATG GATGCTGGTG

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64801 GCCAAGCAGC AATGGCAGGT AGTACACACA CAAGAGGCAG ATGATACAAC ACATCCTTCC
64861 CAAACCTGGA GATAAGCTCA CCCACAATC CCGCCGCTGA AATAGAGTTG ATGTTACCAA
64921 TGTGCATTTT TATGTCCTTT TCCATACAGA AAGATCATTC AGCAAGTACT ATGGTACTTA
64981 AAAACAACA TTCAATTCAT TATTATGACA AAATTAAAT AATAGCTCTT CCTTAACTT
65041 TTAAATTCOA TTTACAATGC TTACTATTGG CATTTATTAA TCTACCAATT TTTTCCCAT
65101 GAACCCATAG AACAAATAAT CTACCAAATT TTTAACATT ATTTTGGCA AGGCTTTTGC
65161 AATTTGACGA ACTTTAAGAA GAAAACCTTAT AAATTGCAAT TTTTAAATCT GACATACTGG
65221 ACTTTTAAAG TATCCAATTG ACTAATGAAC AAAACTGCTC CAAATTTTTT AATTCTTAAA
65281 AATCTTAAGA CAATACTTAA TATGGCAAAT CTTAACTTCT TAAACTTTGT AAGAATGCTA
65341 ATCAACTTAG ATTGGTATAA AGTTGAGTTA AAAATCACAG GATACATCAT CTCAGCTATA
65401 AGTTTTTCATG AGTTGAGTTT TTACAATCAC TTGAAATGCT TAGAATAGGA AATACGTATA
65461 AATTATTTAA CATAAAATAT TGTTACAAA CCTCTGGAGT GTCAGTTTCT CTGGCCAGAC
65521 TTTATGCTGC AGCACCTTTG CCTGAGTTCT TGTCTGTCAT CCAGGAAGAA TTAGGTACAG
65581 AGGCAAGAGT CAAGAAGATT AGTTTTCCAA TAGTTCAGCT CACCTAGTTA ACTCCTGTTC
65641 ACAATCTTCA AAGTTATCAG AAACCTGCAA TTGAGGGTTA TAATCCATT TTTGCAGAGT
65701 TTCAAAACAA GACAAACATTT GTCTATGAAT GTTAAATGT CCTAGGGTAG TCACAGTCAA
65761 AAACACAATT GACAAAGAAA TTTAGTCACC TCTGTGATTT ACAATAGCCT AACACAATAA
65821 CTCTAATTAT AACTGATGAC ACAAACCTCAG ATATCAGAAC TCTAGAAATC CCCTATAATT
65881 TTGGAACACA CATTCACAGT TTTCACTGAA ATATGACCTG AAGATCAAAT ATCACCTTAT
65941 TTCAACAATC CTATATAACT AAACGTGTCA AATGATCCTG TTTACCTCTC CTTTGGATAC
66001 TCCAGGGGCC CTCTGTAGCA TCCAAAAGTT AGGGGTTAGC AAAGACAATT TTGAAGCTGT
66061 AAAGGCTCAA AACACTTAAT GAACCTCTAG TCATATCTGT TCTCTACTCA CTAAATGCTA
66121 GTAGCACCTC TCAGTTGTGG CTAAGCTGGG AGGATCTCTT GAGCCTAGAA GTTTGGGGAC
66181 GCAGTGAGCT ATGATTATGC CACTGCATC CAGCCTGGGC AACAAATCAA AATCCTGTCT
66241 CAAAAACAAA AACAAAAAAC AAATTGCCTA TGCTGTGGTT ATCTCACAAT TAATAAAAAG
66301 GAAAAAATAA GTATGCAGTC TTTGTAGGTC CTGGGGTTT GTTGGAACTC AGAAAAAAT
66361 ACCCCAAAAT AAAGACCGCA GAAGCCAAAG TTTTCTCTG ATCTTCTCCT GCCCTCCTGT
66421 CTCTGAGTCC CATCTCCTCC GGAGTCTAGC CATAGAAATG AGAATTCCTC TTCCTCAAGT
66481 TAGGTCATAG AAATCAAAAC ACCTTTTCCC CAGAGCCCAG CCATAAAACC TAAAAATATT
66541 ACTCTAATT TCCCTCTGTT TTTCTGTGTA AAAACTGGCC ATAAAGAAAT TATCTGAACT
66601 ACCTTATTTG ATCATAGATC ACCAGACCGC ATTCCAGAGA GGATCCAGAA GGAAGGAATG
66661 CTGCACAGAG AGGCGAAGAA GAATCTAGC AGACAGGCCT TGCTGGGTTT CCCTACTCTG
66721 TTTATTAGCA ATCCTATTTT TACACGGCG CCCATACTTT GTTGAATCTA AAAAATAAAA
66781 ATGGACAATT TCCCCTGTAC ATGTTAATAC ACATTAATAA ATTGGATATA AATTGGATAA
66841 TTTATTAATA TACACATTAA TAAATTGGAT GCAGCCGGGT GCAATGGCTC ACGCCTGTAA
66901 TCCCAGCACT TTGGGAGCTG AGGCGGGCAG ACCACGAGGT CAAGACCACC CTAGCCGAAA
66961 TGGTGAAACC CCGTCTCTAT TAAAAATACA AAAGTTAGCT GGGCGTGGTG GCACATGCCT
67021 GTAGTCCCAG CTAAGCTCCG GGCTGAGGCA GGAGAATTGC TTGAACCTCG GAGGCGGAGG
67081 TTGCAGTGAG CCGAGATTGC GCCACTGCAC TCCAGCCTGG TGACAGAGTG AGACTCCGTC
67141 TAAAAATAAT AATAATAATA ATAATAATAA TAATAATAAT AATAAATTGG ATGCATTTTA
67201 TCCTATTAAT CTTCCTCTTG TCGGTGGTTT TCAGCGACTC TTCAGAGGCC AAAGAGTAAG
67261 TTTTCCCTTA GCCCCTACAG GTTCTTATGT TTAATTTGTT ACTCTCATTT AAGACATAAT
67321 TAAAGTGGCT TCTCCATGAA GATTATTTCT GCATCCATTA TTTGGTAAGA TTGGCCGTTT
67381 TCTCCTTTGA TCTCTACTTC AACTGACCC ACATAAAACA TCACTGCCTG TTTTCTTGT
67441 GTTGTGTTT GGAGACGGAG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG TGGTGTGATC
67501 TCCGCTCACT GCAAGCTCCG CCTCCCGGAT TCACGCCATT CTCCTGCCTC AGCCTCCTGA
67561 GCAGCTGGGA CTACAGGCAC CCACCACCA GCGCGGCTAA TTTTGTATT TTTAGTAGAT
67621 ACGGGGTTTC ACTTTGTAA CCAGGATGGT CTCGATCTCC TGACCTCGTG ATCGGCCCCG
67681 CTCAGCCTCC CAAAGTGCTG GGATTACAG AGTGAGCCAC TGCGCCCCGG CCCGTTTTT
67741 TTTTGGTTT TTGCATGTCT TCTCCCTTT ACTGTAACT ATTTCCACTA CCAAGCTAGT
67801 TATCATTTCT ACTGCTTAAT AATTGTTTT GGGAAAGTGAA TGCATCAACC CACATGAATT
67861 TCTTGTCTAT TTGACAATTT ATTCTCTTTA GGAATAGTAT TAACTCCTAA GGTCTGGGA
67921 GCCAGTCTCT GTACTTGGCT GCTCCAGGGT CCTACTTCAG TTTCCAGCT TCTCAGTACT
67981 GTCAGTGTCA ATTGTGGGTA ATAATTATTT TTGTCCACCA AAAGACTCTG TATGTGAATG

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68041 AGTTTTGAAA TCTGCTGAGT AATACAGTGT CAACCCAGTT AATGATTTGC CGGGCGGCTT
68101 GATCAGGGGC TGTCCAAC TA CCGGCATTTT GATTTGGAGC GTCATCTAGT GTCTGAAAGC
68161 ACAAACAACA TCCTACATTG TAAATGCCTT TGGCTACAGA GATTGAAACC AAAGCAAACC
68221 TATGTTTTGA ATTGTTATTC TTCAGCAGTT CTGCTAGCTT TGAAAAATCT AAAAGTTAAA
68281 AAAAAGCTTT ATATTTTCATT TTCTGCCTAA ACTCTTTAAA ATTGCTAGTT GACAATTAGA
68341 TATTTTCAAT TTAATGAAAT TTTTTTTTAG TTCACAGATT AATACACAAT GGGGGAGGGT
68401 TCTTATCTG TTGGACTTTT ACATAACCTC CACTTTAGTG CAGTCTGCTT TATGGGGTCT
68461 TGTTTGAGGT GTGTGTGTGT TTAAGGGAAT GTGGTTTACA ATCAAAATAT TGGGTGCTC
68521 TTAGGCACAT TGTAAGTCA CACACCTGTA TTCTTATTGA TACATAATGA TTAATAACAT
68581 TATTATTACA GCCTGATCAC CATCATTATT GATATATCTA AATAATGAAT TTTATAATTT
68641 TGCTTCCTGT CAGGCAAGAG CCAATTTTCAG TGCTACCATG TTTGTATAGC AGTATTTATG
68701 TCTGTCATCC TCAGTCATTT TACTTCACTT GTTCTTAGCC AAACGGCCGA GAAGCGATGG
68761 TCATTTTACT TCAAAAATGA AAAGAATTAA TATTTTACG TTTCCCTTAA AGACCCTATG
68821 TTTAACCTCC ACTCCTGGGT AAAATGGTCT AGTCCCTCCT TTTTCATATCA TCTCTGATAT
68881 CTTTTGCACA GCCACTATTA CCTACCGTTT TCTAGATCCC TATTCTTCAA ACACCACCAT
68941 GAAGGTAGAG CCTGTCTGAA TTATTTTCTT GTCCCCGAA CTCAGTACAT TGTTAGGCTT
69001 CTTGAAGATG TTGATCAGTT GTTTGTGGAG TGAATGAATC AGCTAGCATG ATTTTCTAG
69061 ACCACTGAGA CAAGTGTCTA AGACACTTGT TCCTTCCCAT GTTCTTGCCT GCCTGTGCAA
69121 TCCATGCAGT CTCATGGCTT CCCAGTGCCT CAGAATTATC CCCTGTCAA CAGGCATTAT
69181 AATTTCTGTC CACTGAAAAG GACAAAAAAC TAAGTGTATA GCTAGAAGTT AAAAATTACC
69241 GGCCAGGTAC TGTGGCTCAC TCCTGTATT CCAACATTTT GGGAGGCTGA GCGGGGCGA
69301 TCACCTGAGG TCAGGAATTC GATACCAGGC TGGCTAACAT GCGACCCCG TCTCTATCAA
69361 AAATGTA AAA GTTAGCCAGG TGTGGTGGCT CGCACCTGTG GCCCCAGCTA CTCAGGAGGC
69421 TGAGGCAGGA GGATCGTTG AGCCCTGGAG GTTGAGGCTG CAGAAAAATA GGAATATACT
69481 CTCTTCAAG AGTTCGTGGT TTTGACTGCC ACCTAGCGTA CATCAGAAAA ACCCGATGAC
69541 ATAGGAAATG CCTGTGACAG AGGGGTAAGG TGAGAGAGGT TGATGAAGAA TGTATTGAAG
69601 GAGTGAAAAC GCTTCCATCC CTCTACTTAC TAAATATATT AGTTAAGTAG TTGGGGCATA
69661 TTTTAATTCA TGCATTTTGT AGATAGAAAA ACAAAAGTTT TATTCTGTTT GATTTAGTTG
69721 ATACTTTAAT ATGTGTGTGT TTAGGATGCA TGATTATATA TCAGTCTGCA GCACTTCTTG
69781 GAGAAGTCTG AATTCCTATT CTCCATTTC TATTGGCAA CGTGAGAATG ATTACAATGG
69841 TGGTTGTCTC ATAGAATGCA GGGAGTCAGA ATGAAAATAG TCCATATAAT GCCTGGTGCA
69901 GAGGAAGGGT TCAGTTAACT GTCTGTATTA ATATTACTGA TAACAGTCAT GACAAACAAA
69961 AGCTTAACAA CAACACCACC AACAACAGTT GCAGAATTGA GCCACCAAT TGCACACAAG
70021 ATTGTAGGTA GGATGTTTTA GAAAAGTTAT TATTTAATAT ATGTATATAT TTTTGTACTT
70081 AAAATATGTC AGAGGTTGTT CTAAGAACTA TTTAAATGTT AACTCCTTAA TCCTCATAAT
70141 GACCCATGAA ACAGGTAGGC TTATTATTGT CTCTTTACAT GTGAGAACAC TGAGACACGA
70201 AAAGGTTTAT TAACTACCCC AAAGTCACAC AGCTGGTAAA ACGGCAAAAT TGAATTTGAA
70261 CTCAGACATT CCAGGTTCCA AGACAGTCTA ATTATTCTTT TGAATAATAT ACTAAGCTGC
70321 CTCTGTATTT TTCCTTGATT ACTTTGTAAA AGTATGAGGA AAATATAAGT GCTTCAAGTA
70381 ACCATGAAAA ATATAACAA TCTATGTATC AACTGAAGCA TAATTACAAA TCCTTTGATA
70441 AGCAAACATA ATAAAAATTT GATATCAATC AAAACTTTCA TGTAAATGTA GCAGGTTGAG
70501 ATGAATTCTA TAGTAAAAAA GTGCAGAGTG CTGGAATACC ATGCTCCTAA TATATTGGCT
70561 AGGCACACCT GCCTGCTATC AAAGGTATGC ACACACCTTG GATACAGAAA GTTGGGACTG
70621 GGTAGTTATG TGAGTGTCT CATGAATCTT TCCCCTTGG GAAAGAATTG TCCATCATAA
70681 GCTTGGATGA TGGACAAGGA GTGAGCTCCC AGAACAGTGA TGTGGGGATA CATCCTCACA
70741 TCACAGTGAG AATGAGTGTT CTAGACTGTT TACACACCTA CCACTCCTAA ATGCACACAT
70801 ATAATTGCTT GCACACACAC ACATACACAC TCATCTCTTC TCTGGTGGTC CAGCTCTATC
70861 TCTTATCATT AGGCTTCTTG GGGCTAGTAC CTAGGGCCTG TATCCTTTCA GAGGCAGCTA
70921 AGGGAAGCAC ACATAATTAG AAAGAATGAA CCAGCTTGTT GGATTGGGTC TCTTCGCATC
70981 CAGCCCTCCA AGTTAAGGAG AGTACCATCT TTCTTAGGGT CACCAAAGGA AAAAAA
71041 AAAGAAAGAA ACAGAAGGAT ATCATACAGC AAGGATCTAA TGCAAATATG CCTCAAATGA
71101 GAGGCTACTG TGTGCTGATC CCAATCCCAG GAACTGTATG CACATTATCT AATTTAATCC
71161 TCACTGTATT TCTGGGAGTA TTATTCCCAT TTTACAGAGA AGGAACTTGG CAGGGTAACC
71221 AAGCTCATGA ATGAGAAAAC TGGGATTAAA TATAAAGCTT CCTTGCTCCA GAACTGCTGT

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71281 CTTTCTGCTC TTCCACACTA CCAGCTCAGC TGTGCTCTCT ACATGCAGGC AGTTTTACAA
71341 GTTTCAGATT AGCCTGGGAC TTCCAGGGTT TTGAATGGGT TAGGGAATGG GGAACTTTTG
71401 GGTTTACTTT CCATTTTTTC TTCATACATA TGTAATATAT AACATAAATC TATGGTATAT
71461 ATGATAAATA TATGGCTACA TATGAACAT ATAATCACAT ATATGCATTA TAAATAAATA
71521 TTAATTTTAT AATATTTTAA AGGTTATCAA ATAAATATTA ATATAAATAA TTAATAAATT
71581 AATACTCAGC TTTGTTTTCC AAAGTGATAA ATGCCTATAT TTAGCAAAAT ATTTTTTGGA
71641 GGCCTGATAG TTTTtaggag TGTAAGAAG TCCTGATATC TAAATGTTA AGAACCACATA
71701 TTTTAGGCTG TTGTCTTCTG TCTTATTTTC CCAGCTAGAC TGGTAAATAC TTGAAGGCAA
71761 ACGTTTAGCC AGCACATTAA CATTTTATGT TTTTATTCTT TTGTGCTCTC AGTGGCTGTG
71821 TCTTTTCTAT CGATTTCTCA CACTGTATGA TGGTTATATT TGTCTGTATC TGTCCCACCA
71881 GGTATAAGTT CTTGAGAGGA CACACTGCTA GGCTGATCTT AGTTTTTATT ATTTCTCCTG
71941 GTGTCCTGTG CTTAACAAGT GCTCATTAAG TGTGTAAAAA CACAGCACAG TAAAAAACTA
72001 GACATTAAAA AATAATGTCA ACCAATCTAT TGAAATTTGC ATTTCCATGT TTCTTCCAAT
72061 ATAGTCATTG TGTCAAGTTA TGTACTTATT CTGATGAAGA CTATTGCCTA ATATACGTTT
72121 GCATCTTGTG CTTTATAACT GCCTTCATAT AGACACAGAT TGAGAAGGTG TAAAAATGTG
72181 CATATCCTCA CAATTGACAA ATTCTTATCC TTTGAGGGTA GGTTTGACTT TCTGAAATGC
72241 TTTGACATCA TTTGAAAGAA GCTTGAAGAA TAAGATAGCT GTTAATGACC CAGTTTCTCA
72301 TGTCATTAT ACAATTATAA TGGCAATTTT AAAATGTTAG GTAAATATAT TTTGCAATAT
72361 ATTGTTCTT TTGTAATACT CTCTATGTAT TTATTATAT TTTTAAATTT TATATTTATG
72421 TATTTATTTT TCTGGACAGA GTCTTGTCTT GTTGCCAGG TTAGAGTGAA GTGTTGTGAT
72481 CATAGCTCTC TGCAACTTCA AACTGCTTGG CAAAAGTGAT CCTCCTGCCT CAGCCTCATG
72541 AGTAGAGTAG CGGGAACCTAC AGGCGCATGC CACTGCACCC AGCTAATCAC TATTTATTAT
72601 GCTCCTACTG TGTGCTTTAG TATATTTTCT GTTGTTTTCT GCAACCCATT TTGAGGGCGT
72661 GTTAGGGAAT ACAGATGCAG TAACTTTCGT CTCAGCCCTT GAGGTGAGGA AATATTATTAGC
72721 CTCAGGTTTA ATCTAATTGT TGGCCATTG CCTTCAAAGA TTGAAATATG AGCAAACTG
72781 TGGCTCTGGG TTATATGTTA AAAAAAGTT TATGGGGCTG AAGCCAGGCA ACAGACAAGA
72841 GCCCTACAA TCTTATTTAG GCTGAAAATA TCCTGGAGTC CCTGTATTGT TGGTCTCAAG
72901 CAGATAGCAA CACTAACCT TACTCTTGA GGCAGGCACT GCCAGTGGG TGGCTGTTAT
72961 TATTAGCTTC ATTAATTGGT GAGTCAGGAA AAAACAGCTT TAAATCATTC AAAGTCTCTG
73021 CCTATACAGG ATTTAGTAAT ATTAGGTTAG CTACATCCAA AAGATGACAG AACCTACTC
73081 TAAGGCTGGG CTGGTGGTT CACACCTATA ATCTCAAAC TTTGGGAGGC TGAGGCAGGA
73141 GGATCACTTG GTGCCAAGAG TTTGAGACCA GCCTGAGCAA CATAGTGAGA CCCCTGTCTC
73201 TATCAAAAAC AAAGAACTCT AATTGGCATA GTAGAAGGAA AAAGTGAAAG AAAAACCCAGC
73261 TGTCACCCTC ATTCCTTACA CCTGTCTTAA CAACTCCTCT CACTATCCTT TGAATATATC
73321 TTGGCTGTTT GAGTCTCTCT CTAGCCCAT TACTGCTGTT TGGACTTGAC ATTTTGTCTC
73381 GCATTTTTAA CTTTTCTACC AGGGTTTCCA GACCTGAAG AGTGTGGCAT GAAACAAAAC
73441 TAGTCAACCT ATAATATTTA TGATGTGTGT GTAAATAAAA GAATACACAA TATATTGCAT
73501 TACAATATTT TAAGTGCTC CTCAATTTGT TTGTGGCTTT CTTGAGGACA TCAGTTTGG
73561 GTGGGACGAC CACATCCTTA ATCTGAACCT TCCCTTGAG GTCAATCTCCT TTTTGTGAA
73621 ATAGAGTCTC GCTCTGTAC CCAGGCTGGA GTGCAGTGGC GCAATCTCAG CTCACTGCAA
73681 CGTCCGCCTC CTGGGTCAA GTGATTCTCC TGCTCAGC TTCCAAGTAG CTGGGATTAC
73741 AGATGCACGC CACCATGCCG AGCTAATTTT TGTATTTTGA GAAGAGACGG AATTTCAACA
73801 TGTGGTCTAG GCTGGTCTTA AACTCCTGAC CTCATGATCT GCCCACCTCA GCCTCTTAAA
73861 GTGCTGGGAT TACAGGCGTG AGCCACCCCG CCCGGCCAGA GGTCAATCTA ATAGACTTTT
73921 TTTTGTGTTG TGCTCACAGG CTGTGTTCAAT CTTATTTCAA AATTTGAGAA ATACAGTTTC
73981 CATGGAACAC CAACCAGATA TCAGGTGCT ATGGAGTTGA TAGTCAAAAG CTTTGTATCT
74041 TCCAGTTTTT CAGAAATGGCT TCTAAAGGTT CTGATTGAGA GCTCTTAGGC GAAATTGAAC
74101 AACCAAGTGT CAAAGTACAA CATTCAGGAA GTTAAAAACA TGACTGACAT ATATGTACTA
74161 TATATAGTGA GCTTGTGAT GTGTCAATGA ATGATTAAAT TCATTAATGA AGGAGGAAGC
74221 AGAATCACAA TTAGGTCAAA GGAAGATACG GGGAATAAAA ATATGTATTT GGTACAGGAA
74281 AGGATGTATA CTGGAAGAGG AAGGGAAAAT CAGATATAAA GTTGTTTAAT GACTTATTAG
74341 GCAATACAAT AATAACTTTT AGGGTCATTT TTTCTATATT AAGAATTCAT TTCCATCTCT
74401 ATGACAAAAT CCTTATTAAT TTATTAACT TCTACAAGTG AATGTTTACT TTTAGATAGT
74461 CTGGACCCAA TAAATGTAA ACATTAAGTC AGAGTTACTT TCACGTAGGA CAGTGTGTCT

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74521 CAATAAGGTA CCACTAGCTA CACGTGATCA TTGACCATTG GACTATAGC TAGACTGATT
74581 TAAAATGTTC TAAAAGTGTA AAATACACAC CAGGTTCTGA AGATTATATCA TTTAAAAAAG
74641 AATGTCAACT GTCTTTTTTT TTAGCTTATT TATTATATGT TGAAGTGATA ATAGTTTAGA
74701 TATATTAAGT TAAATAAAAT ATCTTAAAT TAATTTTACT TGTTCCTTTT CATTCCTTCA
74761 ATGTGACCAC TAGAAATCTG GAAAGTATTT ATGTGATTCA CATTCATTTT TACTGTCTAG
74821 TATTGCCTTA CATCATCAGG TACCCCATAA GTAGGCTTTT TAGATAATTC TCTAATATAG
74881 CTTGGAAGGA TATGGAGAAA TATTTTTCG TTGCTTTTAA GTTTTGCATA ACTTTTTCAA
74941 CACACTTTAT AAAGGATCTA GAAAAGGGT GGTACATGT TTCTCTGTCT TCTGGCCTCC
75001 ACCATGTTGC CAGGAGGTTG GGGACAAGAT TCTGGGTGGC TGGATGTCCT AATGGCTTGA
75061 GGTCTGGACT TGAGATTTGC ATATAAAGAG ATGTGATTAG ATTGAGTCGA CTAGAAAAAT
75121 CATATTAGAG AACTGAATCA CAGCGATTAA ATTTACATGT CGATTATATA ACCAGGACAC
75181 CAATTTATAG TGAAAGAAGG TCCAGTTACC TGGTAATCAA GACGTTTCAT AGCTATTTTC
75241 ATGATGGATA TACTTAGCTG AGTTTAAAT GAGAAGGGGG TTCATTGCAC ATAGAATAAG
75301 ATCTAAGTGA AATGTTTATT TTATTTTTT TTTTGTGACA TGGAGTCTTG CTCTGTTGCC
75361 CAGGCTGGAG TGCAATGAGG CAATCTCGGC TTCTGGAGTG CAATGAGGCA ATCTCGGCTT
75421 CTGGAGTGCA ACGAGGCAAT CTCGGCTCAC TGCAACCTCC ACCTCCCGGG TTCAAATGAT
75481 TCTCCTGCCT CAGTTTCCTG AGTAGCTGGG ATTAGAGTTG CCTGCCACCA CGCCAGGCTA
75541 ATTTTTGTAT TTTTTTTAGT AGAGATGGGG TTTCACCATG CTGGCCAGGC TGGTCTCGAA
75601 CTCCTGACCT CAGGCGATCT GCCCGCTCA GCCTCCCAA GTGCTAGGAT TACAGGCGTG
75661 AGCCACCAAG CCTGGCCTAA GTGACATGTT CTTATATTGT TCCTTTCTTT CTTTTTTTTT
75721 GCAGTGAGTC TCACCCTGTT GCACAGGCTG GAGTGCAGTG GCGTCATTTT GGCTCATTGC
75781 AACCTCTGCT TCCCGGGTTC AAGCGATTCC CTGCTCAG CCTCCTGAGT GCCACCAACC
75841 CCAGCTAATT TTTGTACTTT TAGTAGAGAT GGTGTTTAC CATGTCGGCT AGGCTGATCT
75901 CAAACTCCTG GCCTCAGGTG ATCCGCCCCC GAGTCTCCCA AAGTGCTAGG ATTACAGGCG
75961 TGGGCCACGG GGCCAGCCT TATATTATT CTTTACTAC AATATATTAG TATGATGCAG
76021 GTGCTTCAAT TGTTTATACA CTTTCCATAA TTTTGTATAA TTCTTATACC CTGTCACTCT
76081 GAGGAATAGC CGGTCTAAGT GTTTTCCAC CACTGCTAAT TCATCCATCA CTAATCTCAT
76141 TAGACTGTTA ATCCCAGAG GACATAAGCA CACAAGCAGA CAATGTTTAC AAATGTTGGA
76201 CAAATGTTAT TTAATAAAAC AATGGGGTCA CCCTTAGTCT AAAAGATGTT TCACTTTTCA
76261 TTTGTCAATG AACTCTTATT TGTAGGTTCC CTTTGTACTT TCCACAATC TAAGGCTGTT
76321 CTCTTTAACA CATATTTTCA TGAAACATA TATTTGAGCA GAAATTGTTG GGGAGTTGTA
76381 ATATTACCTT TGTCCCTAAA TATGAATCTA TAATTATATC AAATATATGG GCAGACAATT
76441 TACTTTGCCT TTAATCTCAA GAAAAAATA GCAATTACTT GGGGTCGGAG AGTAAAAATA
76501 GAAGTAGTGA ACCTTAAAGT AGCAAACCTT AGAACAGAAT AGTTTCAGAG GGGATGAGAA
76561 GAGGTGATTT TTCAGCTCAT CAACAACAGA TCTTATAATA AATTACATGT TCTGGTACTT
76621 TTCTTGTCTT TCTGTGTTAA ATTTTGCTAT TTAATAAAT AAATTTCAA TACATTGTTT
76681 ATCTTAAAG TCAAGAGTGT GTTTTATTAA AGTCAGTTGC TTTATTTGCA ACTCAAAGA
76741 TATATTTGAG TTCCCAACTG GAGATTGTCC TATATGGTAA CTTGCGTAAG GTATGGTTAC
76801 TGAAAGTAAC CTACAATTTT CATGGGCTGA AATTCATTTC TATATTGCAG CGTACAAAAA
76861 TAAATAAATA AAAAATGCTT GTTTTCTTTG AAAACATATT ATCTCAGTGC CTCTAACTGC
76921 CAAATCTATT GGCTTTTTTG CAGGCTTAAG GGCTCTCCCT TGTTCCCTTA TGATCTCTAT
76981 CTTGAGGGCC AGACCTCCTG CCTTACACAA CTCAGAGGGG GACCTCAGAG CTCTTTAAAA
77041 AGAGCCCAAT TTCTCGCCTG TAGAGAAGTG AAAAGGATGC CCCACCCCA TCTATGAAAA
77101 GAGGGATTG ATAGTTTCAA TGTCTTCAA TCAAAGATT AAGTCTGTAG CCCCCACCA
77161 CCCCAGGACC TAGCAAGGCT CATGAACCCC CTCCCATCCC GCCCTAATTG CTTTGGACTG
77221 GCCGTGGAAT CCTTGTCCCA GTCCACAGTT CCTGTGCGAC TGCACGAAGA ATTCACAGAG
77281 GACCTGTGTT ACTTCCCTTG TGAAGAAAC GAATTATCAT GAAAATTTAG GTGGAAACCA
77341 TTTGCTTTT TTCTTCAAAA ATAAGGGAAG CATGTGCCCA ACCACCCCTG GGAAAAAGAA
77401 CCTTCAGGGG CAAAGGAGCG AACAGGTAAT TTATAAGAAA AACAGAAAGT GGTCTCTGAC
77461 TGCCCCAGAC TTCCTTCGGA GTTGGGGGAA TTGGGGACGC CTGGACGCGT TGTTTTTTGT
77521 TTTGTGAAA AAATAAATGA AGAGCATGAA GCCCGAGGCT TCTGAGATCC TTTCTGACC
77581 AAACCAAGT GATTTGGTGC GGGGAATTT AATATTTTTC CCCTTTGTG AGGTGGAACA
77641 AACACAACCT GGGAGCAGCG CAGCGGCTCA GAGCCTGCCA GCCAGGCGGG CGACCAGAGC
77701 ACCAATCAGA GCGCGCCTGC GCTCTATATA TACAGCGGCC CTGCCAGGC GCTGCTTCAT

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77761 CGGCGCTTTG CCACTTGTAC CCGAGTTTTT GATTCTCAAC ATGTCCGAGA CTGCTCCTGC
77821 CGCTCCCGCT GCCGCGCCTC CTGCGGAGAA GGCCCCGTGA AAGAAGAGG CGGCCAAAAA
77881 GGCTGGGGGT ACGCCTCGTA AGGCGTCTGG TCCCCCGGTG TCAGAGCTCA TCACCAAGGC
77941 TGTGCCCCGC TCTAAAGAGC GTAGCGGAGT TTCTCTGGCT GCTCTGAAAA AAGCGTTGGC
78001 TGCCGCCGGC TATGATGTGG AGAAAAACAA CAGCCGTATC AAACCTGGTC TCAAGAGCCT
78061 GGTGAGCAAG GGCACCTCTG TGCAACGAA AGGCACCGGT GCTTCTGGCT CCTTTAAACT
78121 CAACAAGAAG GCAGCCTCCG GGAAGCCAA GCCCAAGGTT AAAAAGGCGG GCGGAACCAA
78181 ACCTAAGAAG CCAGTTGGGG CAGCCAAGAA GCCCAAGAAG GCGGCTGGCG GCGCAACTCC
78241 GAAGAAGAGC GCTAAGAAAA CACCGAAGAA AGCGAAGAAG CCGGCCCGCG CCACTGTAAC
78301 CAAGAAAGTG GCTAAGAGCC CAAAGAGGC CAAGGTTGCG AAGCCCAAGA AAGCTGCCAA
78361 AAGTGCTGCT AAGGCTGTGA AGCCCAAGGC CGCTAAGCCC AAGGTTGTCA AGCCTAAGAA
78421 GGCGGCGCCC AAGAAGAAAT AGGCGAACGC CTACTTCTAA AACCCAAAAG GCTCTTTTCA
78481 GAGCCACCAC TGATCTCAAT AAAAGAGCTG GATAATTCTT TACTATCTG CCTTTTCTTG
78541 TTCTGCCCTG TTACTTAAGG TTAGTCGTAT GGGAGTTACT GAGGTATCAG ACGAATTGGG
78601 TGACGGGGTT GGAGAGTGGC CGTGGTGAGG TTACAGCATT TAAACCTTTA TTGCGGCTTC
78661 TAGGTCCCTG ACCGGAGGCT TTTCTCGCTG GCGGATGGTT TTGGGATGGC AGTCCCGCCC
78721 CAGGCCTGTG AACGGCAGAA AAGACCGCAA AACAAGAGCC AGTTTCTTAG TCTAAAGGGA
78781 TGTCCGATT GGAATAAAAA ATTTTCAAAA GTCCCGCCCT GCTCCCGGGT TGGTCCGTTT
78841 TTCTAGTACA TGACTTTCAT TCTGTATTTA ATTGGATGGT GGAAGACGTT GCTTATTCTG
78901 TGTTTTTTGC TTTACTGTGA CTTAAAGTT TTGCCTCTTT TCTCTTTATA TTAATGTCTG
78961 GGATTTCCGA CGCTTTCCAT GTTGTGGTA GTCAGTTGA TGTCTCCTGG AGGTAGTGGC
79021 AACATCCAGC CCTGGGAGGA GAGTGCCTGC AGGTACCTTT GTCCTACATT CCTCTGCTGT
79081 TAATTTCTCA TTCCTGTGGC AACGAAGGAA TGCATTAAAA AAACAGCCAC AACACGGCA
79141 ATAGCCCTTC CTCCACCCAA GGCAATCGTG GACCTAGGGA GTTTTTGTG CCACATAACA
79201 TGTAGCCTTC CGCTAACTG ACAGGTTTGA GCGTATCGAT TTTGAGCGTA TCGAAAGCAC
79261 AACTTTTAGC CAGCCATTTT GTCCTCGCAT GACTACGGTT GCTTATCCTG TTTAGACAGA
79321 CAGCAACATT TAAAAATCGA AGTTCCTTTA AACGTATTTT GTTTGGCAGT CCAAATGTTT
79381 CTATGCAGAA AACAGTATTT GTACTATTAA CTATGAAGAG TGTATGGATA AATGGGAGAC
79441 ATTTCTAATA AAGGCCTTCG TTAATGGTTC CCTCTGTTTG ACATCCATGG TGCTTCTGAA
79501 TACAGAAAGC CTAGCGTCTT ATATTCGCTT CTTTTAAAAAT CTGGTGGGCA CATTTTGGTG
79561 AGACCTAAAT TATGGGACT GGGGCTTCTG GAGATAAGCT GCTCAATTAT TCTACCATCT
79621 CCACAATGAT TAATATAGTG AGTTGATTTG TTAGTGATAG TGACCACGGA TTCATCCCAA
79681 GAAAGAGAAA GGGGAGGGAG GCAAGCAGAG AGACAGGAAG ACAGAGGCAG GGAAGAAGGA
79741 GAAAACATTC TCCCATGGTT TAAGTAATTT TGTGTGTTA ATTTTACATT ACAACACGGT
79801 TTAACATGGT GAACCTCTA TTTTGGTGTA AGGTTTAAAC TATGGACATA TTTTCCCAA
79861 GACCATTAT GAACTTTCAT TTCTGCTTCC CCCTTCTTCC TCCCGTGCCA CCCTCCACGC
79921 TCCTATCAAT TTTGCTGTT TTGTATAGG CTAATACGCT ATAATTTTAT GGACAGTTGG
79981 ACTGTCTTAG GTTCTCAGG TTTCTATTTT GTTCTTTTAG TCATTTCCAC AATTCTTAAG
80041 GTAGAATTGT ATTGTTTTAA ACATTGTGTT GTGTGCTATC CTCAATGCTG AGATGATTAT
80101 GTGACAAATG GCAAGTGTTT AACTAATACC TAAATCTGTA GTATCTTATC AAGCCTAATG
80161 CTACTTCACA ATGCCTACTC CATTACGCTC ACTTTATCTC ATTACTGGCA TTCTGTCTATC
80221 TCACATCATC ACAAGTAAAA CGGTAAGCTA TTTTGAGAGA GATCACAGTC ATATAATTTA
80281 TATTTATATT TATTTATTTA TTTATGAGAC GGAGTTTCCC TCTGTACCC AGGCTGGAGT
80341 GCTGTGGCAG GTTCTCGGCT CACTGCAACC TCCGCCTCAC GGGTTCAAGC GATTCTCCTG
80401 CCTCCGCCTC CCGAGTAGCT GAGATTACAG GGGCTGCGCA CCATGCCCCG CTAATTTTGT
80461 TATTTTATAGT AGAGACGGGG TTTCACTAAG TTGGCCAGGC TGGTCTCGAA CTCCTGACCT
80521 CAGGTTATCC GCCCACCTCA TCCTGCCAAA GTGCTTAGAT TACAGGCGTG AACCACCGTT
80581 CACAGACTCA AATCATTTTT ATTACAGTAT ATTGTTATAA TTGTTGTTTT ATTATCAGTT
80641 ATTGCTAATC TCTTACAGTG CCTGATTTAT AAATTAATTT CATCATTTGC ATGTGTATAT
80701 AGAAAAAAAC AGTGATATA CGGTTAGTA CTATCTGTGG TTTCAGGCAT CCACTGGGGG
80761 TGCAGTTTAT TAAACATGCA TTTACATTAG TCTCCCTTTT GGGAGACTAA TTAACCTGAGA
80821 TGTGTAAACG TGACTTTAAT AGCAGATAGA GCTAATTTTC TCTCATTACT CTTCTTTTTC
80881 AGAATTTTCC TGGTTATTCC ATTTTATTAT TTTCCATATG TATATTAAGA TCTCTTCCAC
80941 CTCTCTCTGT TTCTCCATCT CAACATCAAA CAATTAAGAA AAAAAAAG GCTGGGCGCG

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81001 GTGGCTCAGC CCTATAATCC CAGCTCTTTG GGAGGCCTAG GCGGGTGGAT CACGAGGTCA
81061 GGAGTTCAAG ACCAGCCTCG CCAAGATGGT GAAATCCCGT CTCTACTAAA AGTATAAAAA
81121 TTAGCCAACC ATGGTGGCAG GCGCCTGTAA TCCCGGCTAC TCGGGAGGCT GAGGCAGAGA
81181 ATTGCTTGAA CCTGGGAGGC GGAGGTTGCA GTGAGGCGAG ACCTTGCACT CCAGCCTGGG
81241 TGACACAGCG AGACTCCGTC ATAAAAAAA AAAGCCGGAA GCAGTGGCTC ACGCCTGTAA
81301 TTCCAGCACT TTGGGAGGCT GAGTCAGGCA GATTACCTGA GGTCAAGAGT TCAGGACCAG
81361 CCTGGCCATG AAAATACAGC CTGGCCATGA AAACACACAA TAAATTAGCT GGGCGTGGTG
81421 TCACACACCT GTAATCCTAG CTACTCGGGA GGCTGAGACA GGAGAATCAC TTGAACCCAG
81481 GAGGCAGAGG TTGCAGTGAG TTAAGATGAC GCCACTGCAC TCCATCTGGG CGACAGAGCC
81541 AGACTCTCTC TCAAAAAACT AAATAAATAA AAATAAAGTT ATGGTACATT GAACTTCTGT
81601 GTTCCTTTCT CCCTTAGATA CTTTCATGGC TACCCATTTA ATTGATGTTT TTATCATCTC
81661 CAAGAGTTAG TCAGGAGAGG AATCAACCCA AGCAAAAATA GCTGATTTTC TAATTTTCCT
81721 TCAATGCCCT TTGGGGTCTT AATCCATTGT ATTTATGTAC TTTCAATTAA TCCTAACCTC
81781 GAATGTCTTC TGCAACATG TTTCCACAGA TGAAACTCGT CAAATGAAAC ACATTCCTTT
81841 AATTTATAGA GTTAAAAATT AGAAAAATTT TCAATTCTAT TTGGCCTTTA GATTCACTCT
81901 TGCATATGTT TTCTCAATTT TGTTCACTGT CTTTAGTTTT GTTTTATTCC ATCACAATTG
81961 TTCACATAGC TTAAGGCTT AGGCTAATG AACCATTCTT TTGGAAATTA AAATTGGCCA
82021 TTTTAAGATG AAAAAGATTC TTGCTCAAT TTTACTTAGT TTTTGAAACT GTCAATGAGG
82081 ACACATGTTT TTCTGTACTC TTAGATTAC TAAGTAGTGT CTTGCAAAAT TAAGTACAA
82141 AGGACAGATT AACATGCGAA AAAAAGAGCA TGCAATTTTA TTAGTATATT ACATGCACAG
82201 AGTTCCCAA GAAAAAATAA TTGAACCTT AAAAACGCGG TTAGACTCAC AGACTTATAC
82261 ACCATTCCAA CAAAGGAAAG GGAGTTTGCA CTTTCATGGG TGACGAATTT GGGAAATGTA
82321 CAAGGAAATA AATACATGGG CAATAAAAC CATGGAAGAT AAAATGAAAG ATAGAAATAA
82381 TTGTAGTAAG GTTTGTTTTT GCAGAGTCAT CTCAGTGCCA ACCTTCCATA TCTAGTGATA
82441 AGAATTGCTC TCTTTTCTCT GGTATAGCAG TTGGGGACAC TTTTACAAGG GAAATTTCTG
82501 TCACCTTCAC AAAGGGAAAT TTGGGTAAAG AGAAGACAGA GACCTCTTCC TACACCTGTT
82561 GATTTTCAAT TGCCCTCAGC TGAAAATAAC TTTTATGCCA AAGTAGAATA ATTTGGGGGT
82621 GACATCCTGA TATCTTCAA AACTTATATT TAATTTTACA TTAGTAATTA TATCATTTTT
82681 GATTTTTTAA TTAGTTTTAT AAAATAATTT TGAAAAACGG TAATAATATT CAAATAATTC
82741 CAGAAACACT GCTGATAAGC CAAAAACATC AATGAATATT GCATAAACAA CTGATAATTC
82801 AACCATGAAA ATTTATGACA TTGTTCTTGT GTGATAAAAC TATGAGTAAC ATAAAACTA
82861 GAGGCTACTT GTAATGCATT ATTCCAAACT TTCTGTTTTT TATTTATTTA TTTATTTATT
82921 TTGAGACATA GTCTCTCTCT GTCACCCAGG TTGGAGTGCA ATGGCGTGAT CTTGGTTCAC
82981 TGCAGCCTCC ACTTCCCCGG TTCAAGCAAT TCTCCTGCCT CAGCCTCCTG AGTAACTGGG
83041 ATTACAGGCA CCTGACACCA ACCCCGGCTA ATTTTTTTGT ATTTTTAGTA GAGACGGGGT
83101 TTCGCCATGT TTGCCAGGCT AGTCTCGAAC TCCTGACCTC AGTGATCCAC CTACCTCGGC
83161 CTCCCAAAGT GCTAGGATTA CAGGCGTGAG CCACCATGCC CGGCGCATT A TCCAAACTT
83221 TCATACACAG TGCTATCATG GCTACAAATT GAAGTATCAT ATTATACACT CCTAGGCAAA
83281 GCTCTGGATA TTTTGGCTAT ATAAGCCTGA GGGAAATGTA GTAAGGACAT TGTGGTTGAA
83341 ATTCATACCA GAGATGAACA GGCCAGTGTC AAGACAGAAT TACATCACTA AAGGATATCA
83401 GAAGAGAATA GGGATTTAGG GTACAGTGCC AACAACAGTT TTGGGAACCT GCATTTTTTG
83461 AGCACTTATT TACAATATGC CAAGCACTGT TGCTGATTAC TCTATATTTA TTTTCAAACA
83521 CATTCTTGTC ACAGCACTTT GAAGTAAGTG CCATTGTCAT TCCCATTCA GGGTGAAGGA
83581 CTAAAGCTTG GTGTCATTAA GGATGTAGCT AGTTAGCTGT GTGTGTGTGT GTGTGTGTGT
83641 GTGCATTTTT TTTTAAATTT AAAGTCAATA AATTTTTATT TGAAGAATTT CACATCAAGG
83701 TAAACTTTGT TCCTCTAAAG AGCTGGAGTC AAAATGTATC TTCAAAGAT TCATCTTCAA
83761 GTTAGCCCTT CTTAATAGAA CTGATGCTTA ATCCACAGTT GTCAGCCCAC AGTTCTTTTA
83821 TTTTGACTTT TTTTTTTTTT TTTTTTTGAG ACGGAGTCTC TCACTGTCAC CCAGGCTGCT
83881 GGGCAGTGGC GTGATCTCGG CTCGCTGCAA CCTCTGCCTC CCGGGTTCAA GTGATTCTCC
83941 TGCCTCAGCC TCCTTAGTAG CTGGGACCAC AGGCGCATGC CATCGTGCTC GGCTAATTTT
84001 TGTATTTTTA TTAGAGACAG GGTTCACCTA TGTTGGCCAG GCTGATCTCA AACTCTGAC
84061 CTCATGATCC GCCTGCCTTG GCCTCTCAAA GTGCTGGGAT TACAGGTGTG AGCCACTGCA
84121 CCCGGCCTTA TTTTGCCTTC TTTAATCTCC ATTTGAACAT ACACATACTG ATGAAAACTA
84181 CAACATTCTT CACCAAAAAA CTTTGGGATT TAATTTCTTC AACCACCTTA CTTTGGGGTC

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84241 ATTTTAAGAT TAGGTGTATC TGCCTGGTTC TCAATTTGAC ACCCTTTCTC TCTAAACATG
84301 AATGAGTTCC AATCATATTT ATTCTAAGC TATCAGACTC AAATATACTA CAGATCTGTG
84361 GAATATGCCA AAAGTTAAGG TGAAAAATTA AATTATTAGG TATTTCATAG TTTTGCTAGT
84421 TTTTGATCTG TGAGTGAATA TAACTATCCT CTATGTCCTG GCACTGTTCC TCAGAAACAT
84481 AGGGTCCACA TATGTAATTT TAAATTTTTT AATAGGCACA TTTTAAAAAG TGAAAAAGA
84541 AATCTATTTT AATGATTTGA ATCCAGTGTA ACCAAAAATT GTTTCACAA GGTATCTAAT
84601 ATTAAAAATAT TGAGTTTTTA CTTTGTATT TTTAGTTC TTTGAAATCT GGTGTGTATT
84661 TTACACTTAA AGCACATCAC AGTTTGGAGT AGCCACATTT CCAATGCTTA ATACTCACAT
84721 ATGGTTAGTG GCAACTATCT TGGACAGGAC AGCTTTTATA CTCTGGGAAG ACACAAGCAA
84781 ATACTTGCTC TGCAGCAGAA TCCAGATGTT TTCCAAGAAA ACACCTTTTTC TGACCTGTTC
84841 CTGAAACCCA GGTAGTGTCT CTAATACTTT ATATTTTATT GGTTTGTCTT ATTGTAACCA
84901 CCCAACGGGC TCTCCTTGTC CACTTCCTAG ACAGAGCTGA TTTATCAAGA CAGGGGAATT
84961 GCAATAAGGA GCCAGCGCTA CAGGAGACTA GAGTTTTATT ATTACTCAAA TCAGTCTCCT
85021 TGAGAATTTG GGGACCAAAG TTTTAAAGGA TAATTTGATT GTAGGGGACC AGTGAGTCGG
85081 GAGTCTGCTT TGGTTGGGTC AGAGATGAAA TTATAGGGAG CCTAAGCTGT CCTCTGTGTC
85141 TAAATCAGTT CCTGGGAGTG GTGGGGTGGG GGACTCAAGA CCAGATAATC CAGTTTATCT
85201 ATATGGGTGG TGCCAGCTAA TCCATTGTGT TCAGGGTCTG CAAAATAGCT CAAGCATGTA
85261 TCTTAGGTTT TAAAATAGTG ATTTTATCCC CAGGAGCAAT TTGAGGTTTA GAATCTTGTA
85321 GCTTCCAGCT GCATGACTCC TAAACCATAA TTTATAATCT TGTGGCTAAT TTGTTAGTCC
85381 TGCAAAAGCA GTCTGGTCCC CAGGCAGGAA AGGGGTTTGT TTCTGAAAGG GCTGTTATTG
85441 TTTTTGTTTA AAAGCAAAAG TATAAACTAA GCTCCTCCCA AAGTTAGTTA ATCCCAAAC
85501 CAGGAATGAA AAGGACAGCT TGGAGTTTAG ACGTTAGATG GAGTCGGTTA GGTAAGATCT
85561 CTTTCACTGT AATAATTTTC TCAGTTATGA TTTTGCAAA GGCAGTTTCA CTGTCCACTT
85621 CACCTCACAT CAGGCCTCTG ACTAGAGATG TCCAACAATA CTTAGGCCAG GACACCACCA
85681 TGTCTCCTTA TCCACCCTGA GGGAGTCCAA TTCTGAAAC AAAGGAAACT ATATATGATA
85741 GTATGAAACT ATATATGAGA AGGAAATTAT ATATGATAAT CAATTTTAGG GTTATCTTAT
85801 TGATTAGAAG ATATTAAAGT GTGACACTGC CTGGCAATGA TATCTGCTGG TAGTAAGAAT
85861 TTGGCGAATT TAGTGAAATT CCTGAGGCTG AACCTCCACT TCTGTAAAT GGAGACAGTG
85921 AGATAATTTG CCTTACAATG CTGAAGTAAG AATTTTACAC AATAATTCAG ACCAACCCT
85981 TCATGTGGTA CTTGGCCCCG GGAAGACTAT CAATGACAGT TAGTTTATAG TTTATACTAT
86041 TAATGAATCC TTTGTTTCAT TGTATTTCC TTCTACACGT TGGCCTCTCT AAAAGAAGGT
86101 AATATTCAT ACAAATAAAG TTAACACAGC TTGCAGAGTT GTCCAGGGA ACTCACTTAA
86161 CCACTGAAGT GTTCAAATTG CTTAAGTTTG ACTTTATATT CTCCTGACTA ACCTTTCTCC
86221 TTCTGGTATT TCTTCTGAGA ACAGACCAC CATCCAAAGC ATCATGCAA CAGTGGTCAT
86281 CCCAGACCAG TAATTCTCAA CTCACAGGGT GCTCCTGCAG AGATGTATT GAATAGAGTG
86341 GTAGGATGCT GAAGAAGGCC ACGTAAATTT TGGCCAGTGA TCTGGGGCAG ATTTATCCTG
86401 AAGCTAATGA AACACAAGTG TAAGGGCCTG TACTTCCAAG GTGCAGAGAG GGGCCCTACA
86461 AATGTGTTAG TTTGTCTCTC TCTCTCTCTC TGATTTTAAA ATTTGCAGTA TTAAGGTACT
86521 TTAATCACGG ATGGTTCAGG CTGCTATTTT CACTCAATCC TCCTTTTTAT TAAAATCACC
86581 ATTGTCTGAT TATGTTAGAA TCCTGATGAA AATATTTGGA ATTTGAGTAA GAGAAAGTTT
86641 AGTTGAAGAT GTATCTAGTA TGGGGATAAT AAGTTACGTG ATTTGCATAT GTGATCATGT
86701 GTACTTCATT CGTTGCCAGC CAATCTGACG TAAGAATGGC TTCAAGGAGG CCGGGCGCGG
86761 TGGCTCACGC CTGTAATCCT AGCACTTTGG GAGGCCGAGA CCGGCCGATC ACGAGGTCAG
86821 GAGATCGAGA CCATCTTGGC TAACACGGTG AAACCCCGTT TCTACTAAAA ATACAAAAAA
86881 TTAGCCGGGC GTGTTGGCGG GCGCCTGTAG TCCCAGCTAC TTGGGAGGCT GAGGCAGGAG
86941 AATGGCATGA ACCTGGGAGG CGGAGCTTGC AGTGAGCCGA GATTGCGCCA CTGCACTCCA
87001 ACCTGGGAGA CACAGCGAGA CTCCGTCTCA AAAAAAAAAA AAAAGAATG GCTTCAAGGA
87061 ATGTTCCCTAC TGCTCACTGG AATAACTCAC CTAAATTCCT GGCAAGATGC AGGTCTAGAT
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87181 TGGAGAGTAG AAACGTATAG AGCCAGAAGC TAGTCTGGAA AGAATCTTA CAAAGTTTAC
87241 AACTTACATG TGAAAGGAGC TTAACAGAGG ATTTTCCAAA TTTGAAAACA ATCCTAAAAA
87301 CTTACTTGAC ATTACCAATA ATGTGTTTTG AAAGTGAAT ACTTCTAAGT TATGAAGAAA
87361 ACATATTATC ATCAGCCACC CTGGAGGAAA GATTGAATTC TATTTCCATT ACCTATAGAC
87421 AACATTACAA AATAATTTTC ATCTGAAGAT GGAATCAGAG TATTCAGTCA AAACACAGG

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87481 AAAATATACT TGGTAGTGTC ATATTCAGAA GTTAATAAAA TATGCTATTT TCTGAATTTT
87541 GTGATGGCTG TTGTTTTGTC AGCTTTTATA AAATTGGAAT TTGATTTTAT TTTCCCATTA
87601 TAAATTTATA TTTACAGTCT GCAGTACTTT TGCATTTTAT ATTTTACATT ATAGTTTTTTA
87661 ATAGTTAACA AGTTGTAAAA GGTTTGATCC CCAGAAAACC TTGATCTACC CCATCAGTTA
87721 AGTATACTAA TATATTTAGA AAATGGATGA AATCAGCATT TGAATATTTT TAAATATTTA
87781 TTAAGAGAGG ACATGGGTAA AAGAGCTTTG CAGTTGCCAC CCTTCATTCT CAATTTCCCT
87841 GGATAAGGAT GACCGCATAA TCTTTGGATG GTCATACGCA AGTCTTGTGT ACTTGTTACA
87901 TAAATCTATT TAGTGGACTT TTGGCAGTGT GTACTGAGGC CAGTTTCTTC CACCTGAGCT
87961 CTGACTCCAC CTCCAGCAGC CCAAAACCAA TACTGAATTT TGGGGTCAGC TATTGTTTTT
88021 GTGGACTTAG GTAACCTACAC ACACATTGTC TTTATGATAG CTTTAATAAT ACTGCCATCA
88081 GAACTAAAAT TGTCACGTGG ATTAAGGA GTGACGGTGG TGTCCCGAGG AGCCTTTCAA
88141 TATGTAAGTA TTTACACATA TACATGCTAA AAAGACCCCT AGGAATTTTT TAACAAGGGC
88201 AAAACAGTAA CTCAGCTTGT TTTCTCGCAG TAAAACCGGT TGAAAAGGCC TGATAGACTT
88261 GTCTGCAGTT ACAAACCTTG TGTGTAGTTA TCACCTTTAT ATCTCCTGGA AACTAACATA
88321 GACAACCGAA TGGGTTACAA CTGTTTTTAA GTGAAATTGT GAGTGGCTCT GAAAAGAGCC
88381 TTTTCAATGA GGAAGAAACG GGCAGACTTA TGCCCTTTCC CCACGGATGC GACGTGCCAG
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88501 TTCGAAGAGT CCCACCAGGT AGGCCTCACA AGCCTCCTGC AGCGCCATCA CCGCAGAGCT
88561 CTGGAACGCG AGGTCGGTTT TGAAGTCCTG GCGGATTTCT CGCACCAGGC GCTGGAACGG
88621 CAGCTTCCGG ATCAGCAGCT CGGTGGACTT CTGGTAGCGA CGGATTTCCG GCAAGGCCAC
88681 GGTGCCCCGG CGGTAGCGAT GAGGTTTCTT CACGCCACCG GTGGCCGGAG CGCTCTTACG
88741 GGCTGCTTTA GTAGCAAGCT GCTTGCGCGG AGCTTTGCCG CCGGTAGACT TGCGAGCTGT
88801 TTGCTTCGTA CGAGCCATTT GCAATGAGAG CACACACAAA AGTGTAGTGA ACTGAGAGCA
88861 AGTGGCCTTT AAATATAGTG AGAAACATTC TGATTGGTCC TGTAAATTTT CAAAAGTCCC
88921 GCGCGATAAA ATCATTGGCT GAAGAGTGAC CAGACTGATT GGTTCAATAC TAGACAATCT
88981 TATTGGATGA GTTGCCCCAC CGCCCATCCT GTCCTTTTCG TTTTCAGTTAT CTGCAGCGAC
89041 AAATTGTCTA AAATTCTAGT TCATCCAGTC CCAAAGAACA GAGTGTATAA CAAGGTATCT
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89161 TTCCTGACAG TCTCGCAAGT TATCAATGCT GGTGAACACT CACTAAACCA CCAGAAACGT
89221 TCAGACTCAT GTCGGGAAAT AACGCTTATA TTCAGAGAAT GAGATTCCAT GCTATTTTGT
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89521 TCACTAGAGG CCAGGAGTTC AAGACAACCC TGGCTAAAAT GGTGAAACCC CGTCTCGCAT
89581 AAAAATACAA AAACCTAGCTG GCGCGGGTAG CAGACGCCTG TAATCCCAAG TACACAGGAG
89641 GCTGAGGCAT GAGAACCGCG TGAAGCGGCG GGGTGGAGGT TGCAGTAAGC CGATATCGCG
89701 CCGCTGCACT CCAGCCTGGG TGACAGAACT AGACTGTCTC AAAACAAACC AATCCAAACG
89761 AAAAGCAAAA AATACCCTAA CAGAAGCAAG TTATCATCCT TTCTTGTTA ACTATGGACG
89821 GCTCTGAAAA ATGCCGTTT AAGTGTAAGC TACGTTTTCT GATTTGAGTG TTTACTTGAC
89881 CTTGGCCTTA TCGTGGCTCT GTTATTTTGG CAACAGGACG GCCTGAATAT TGGACAGGAC
89941 GCCTCCCTGA GCAATAGTGA CGTTGCCAG CTGCTTGTG ACCTCCTCGT CGTTTCGGAT
90001 GGCCAGCTGC AGGTGGCGGG GGATGATGCT GCGGGTCTTG TCACGTATGG CGTGCCAC
90061 CAGTTCTAAG ATCTCGGCGG CCAGGTATTG TAAGTACACT GGCGCACCAG CTCCGACCAG
90121 CTCAAAATAA TTGCCCTTTC GAAAAAGATG ACGGACTCTG CCCTATTGGG AACTGCAAGC
90181 CCGGTAGCGA CGAACAAGTT TTTGCTTTAG CTCCATTTTC CACGTCCGCA AATAGCGACC
90241 TATGAAAGCA GCGGAAACT GTGAAAGACA AGCAAGCTGG AATGGCGCCT GAACAAATCC
90301 TTTTATACAA ACTGCAAGGC TGCAATAGGA AGCTATCCTA TTGGTCAATT ATGTTTGGTG
90361 CTTTATCCAA TAGAAAAAGA TAACATAAAT TCCATATTG CATAAACCCC ACCCCTCAGT
90421 GAAACCGTGT TTCTTTTGTC CAATCAGAAG TGAGGAATCT TAAACCGTCA TTTGAATCTC
90481 AGGACTATAA ATACATGGGC TCTGAAGTGT TCTCTGTACT ACTCTGTAGT GGAGAGTGTT
90541 AGTAGCTTTT CTATTCTGTT TAGGAATAGC AATGCCTGAA CCCTCTAAGT CTGCTCCAGC
90601 CCCTAAAAAG GGTTCCTAAGA AGGCTATCAC TAAGGCGCAG AAGAAGGATG GTAAGAAGCG
90661 TAAGCGCAGC CGCAAGGAGA GCTATTCTAT CTATGTGTAC AAGGTTCTGA AGCAGGTCCA

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90721 CCCCACACCC GGCATCTCAT CCAAGGCCAT GGGGATCATG AATTCCTTCG TCAACGACAT
90781 CTTGAGAGCG ATCGCGGGCG AGGCTTCTCG CCTGGCTCAC TACAATAAGC GCTCGACCAT
90841 CACCTCCAGG GAGATTGAGA CGGCTGTGCG CCTGCTGCTG CCTGGGGAGC TGGCTAAGCA
90901 TGCTGTGTCC GAGGGCACTA AGGCAGTTAC CAAGTACACT AGCTCTAAAT AAGTGCTTAT
90961 GTAAGCACTT CCAAACCCAA AGGCTCTTTT CAGAGCCACC TACTTTGTCA CAAGGAGAGC
91021 TATAACCACA ATTTCTTAAG GTGGTGCTGC TGCTATTCTG TTTCAGTTCT AGAGGATCAA
91081 CTGGAATGTT AGCGAAGACA AGTTTTAGAG CCAAGGTAA CTTGGACGGG GCCGTGCGCG
91141 GTGCCTCTTG CCTTTAATCC CGGCAATTG GGAGGCCGAG GCGGGCGGAT CACGAGGTCA
91201 GGAGATGGAG ACCATCCTGC TTAACACGAT GAAACCCCGT CTCTACTAAA AATACAAAT
91261 AATTAGCTGG GCGTGATGGT GGGCGCCTGT AGTCCCAGCT ACTCGGGAGG CTGAGGCAGG
91321 AGAATGGCGT GAACGCGGGA GGCGGAGCTT GCAGTGAGCC GAGATCGCGC CATGGCACTC
91381 CAGCCTGGGT GACAGAGCGA GACTCCGTCT CAAAAAATAA AAAAAAATAA AATTAAAAAA
91441 ATATGAAGTT TTGAAGCAGA AATTATTTTG TCGTATGTTT TTTCATAAAT TTTTGCCTG
91501 CCTGCCTTCT TCCTTTGTTA CAGAACTCCA AACTTACCC AAAGGTAGCT GTTGGGTCAG
91561 GGTTCCTGTA CTATAGTCCC TTCTGTGGT GCCAGAAATA TGTTACAGGA AAGAGGTCCC
91621 CATCCAGACC CCAAGAGAGG GTTCTTGGAT CCCGCGCAAG AAAGAGTTCA GGGTGAGTCC
91681 GCAGTGCAAA GTAAATGCAA GTTTACTAAG AAAGTAAAGT GGTGAAACGA CAACTACTCC
91741 ATAGACGGAG CAGGACATTC CCGAAAGTAA GAGGAGGAAG GCATCCACCC TAGGTACAAT
91801 ACTGTATAT ATGGGGAGAT GTGCTCTGCT ACAAGTTTGT GATAAAGGAT TAATTTTCTT
91861 AGTTACTATA TTTTGCAAGA ATCAACATTA TTATCTTTAA ACAAATTA GAATGCCTTT
91921 GTTCTCCAGA TATAGGGATA TCTGGACACT CCTAAGTCTG AGTCTGTTTA GTAAACATTA
91981 TTTATTTGTT CCCTTAACCG TAAACATCTA GAAGCTAGGA ATGACTGACT TTCTGGGAAT
92041 GCAGCCCAGA AAGTCTCAGC CTCATTTTCC TAGCCCTCAC TCAAATGGA GTTACTCTGG
92101 TTCAAGTAAC TCTGACACTT TTCTCTCTT TTTTCTTCT TTTTCTCTT CTTTATTTT
92161 TATTTTTTAT TTTTGAAATA AGAAATCAAG AATACTTGAT GTTTCATCTA AAACAATACC
92221 CATAATTGAT AAGCCAAAAC AAAACCTAG GTCTTCTAAC TCAAACCTAG GATGTTTTGC
92281 TGTCTCTGCT GATACTCGGC TGATCGTTAA TAGGTAATTA ACAAACAAGC CTTGCTATGT
92341 CCCCTCAGT TTATTACCAT TAGATCATAT GCCTACTGTC AATCATATTA ATCCACAAC
92401 ATGCATTTCA CAAAACCTGC CATAAAAT CACAGGTTTC CCGCTTCCCT CGAGTTTTCA
92461 TTTCCGAAGG GTCCCATGTA ATATAAACT TATATTAAAT ACATTTGTAT GCTTTTCTCT
92521 TGCTAATCTT TTTTTTTGTT TTTTGAGACT GAGCCTTGCT CTGTCAACCA GGCTGGAGTG
92581 CAATGGGCGG ATCTCGGCTC ACTGCAACCT CCGCTTCCCA GGTTCAAGCG ATTCTACTGC
92641 CTCGCCCTCC CGAGTAGCTG GGACCACAGA TACGTGCCAC CATGCCCCGC TAATTTTTGT
92701 ATTTTTAGTA GAGACAGGGT TTCACCGTGT TGGCCAGGAT GTTCTCAATC TCCTACCTC
92761 GTGATCCGCC CGCCTCGTCC TGCCAAAGTG CTCGGATTAC AGACGTGAGC CACTGCACCC
92821 GACCAATCTG TCTTTTGTA GAGGGGCCCTC AAGCATGAAC TTAGTGATGG GTGAGAAAAA
92881 CAGAATTTTC TTTTCCCTA CAATATAAAC ATTAATTGTA ATGTTATCAT TCAGGACATT
92941 TTGGTGACCA ATCTTACAGA AATTTATCT TGTGCAAGTC TATGCAACC AATATGTAAA
93001 TCTTCTATAA GTGAGATTGT ATTTCACTTT TCTAGTATCC TTTTAAATTA ATAAAAGAGA
93061 TTCTAATGAT TATTTTCATT ACTGCATTTT ATTGTAGGGA AGTAGATAAT TGCCCTTTAT
93121 TCACTGACCT TCGCTTTTTA AAAATTTAAA CCATGTTACC ATGAAAATGC TTTTCAGTAT
93181 TTCTCTACAC ACAAGATTGC TGTAAGGGCA AAAATAGAGA TAGGAATCAT GCATCCATTG
93241 ATATACATAT TTTGATTTTT AATACATGTT ACCAAGTTGC CTCCTGAAGG TCTGTTTACA
93301 CTCTACCAA CAGGGTGT TTCTCTGACT TCCACAAATG CTCTGAACA GTGGGTGTGT
93361 TAGTCTGTTT AAATGCCGA CATGAACAAT TAAATCTCAT TGTGTTTTT ATTTTTAAGA
93421 CAATTATTGT TTGAGACTGC ACATTTTGAT AATAACATTT CTCTATTAT GGTGTTGATTA
93481 CTCATGATTC TTGCCATTT TCTTTGGGA TGTGCTTGA TGTACATTAT TTTAAATAGA
93541 TAGCTCCATG TATTAAGAA TTATTAAGTT TGAGGGCTTA TGATATGTCA GTTACATTTT
93601 TAAGATTTTT TTTTTTTTTT TTTTGAGAC GGAGTTTTC ACTTGTTGCC CAGGCTGGAG
93661 TGCAATGGTG CGATCTCGGC TCACCGCAAC CTCGCTCC AGGGTCCAAG CAATTCTCCT
93721 GCCTCAGCCT CCCCAGTAAT TGGGACTACT GGCAAGCGCC ACCACGCTG GCTAATTTTG
93781 TATTTTTTATT AGAGATGAGG TTCTCCATG TTGGTCAGAC TGGTCTCGAA CTGCCGACCT
93841 CAGGTGATCC ACCCGCCTCG GCCTCCCAA GTGCTGGGAT TACAGGTATG AGCCACTGGG
93901 CCCGCCACA TTTCTAAATT CTTTATAAGT ATAAATTCAT TCAATCTTCA CCAAACCTCA

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93961 ATGAAGTGTG AGTACTATTA TTATCATTTG TTTACAGATC AAAACAAGTA ATACAGTCAC
94021 TTACTGAGTT CTATACACCT GGTAATTTTT TTGTTTCGTT GTTCTATCAA TTATTGGGGA
94081 AGGGGTGTTG AAATCTCTAC CTTTAAATCA TGTATGTGTC TATTTCTCCT TTCGGTCTTA
94141 TCAGGTTTTG CTACACATAT TTTGCAGTTC TGTATTGTTG TGCATATACA TTTAGAATTG
94201 CTTGTTTTTC GTATTGGATT GACCCTGTTA TCATTATGTA ATATCCCTGT CTGTTCCTAG
94261 TAATTTTCTT TGCTCTGAAA TATACTTATC TGATATATCA TCCAAAAGAC CACCAGGATG
94321 GCTAAAGAGT AGAAAGGAGA GATTTACTGG CAATACTAAT TTGCAAGCCA GGAAGAGATG
94381 GTCCCAAGAC CTGCCAAAAT TACTCTCTCT TTGGGGAGAA GGAGCAGGTT GGTTATTTTT
94441 ATGCCTCATA GGCTATATAT TACACAATAG AGTCATACAT ATTTAGCACG TTTGGGGGGA
94501 CAGCTATATA TATTATGAGG GGTGCCAAGT GCATTCACAA TGGATAAACA CGTGTAATAT
94561 ACCTCCCATG TTCACTTCGA GGTTAAATTT TGGTTAAAAT GAGGTAGAAT TTAGGTCTTT
94621 ACATCACAAG GTGAACTATA GGAACAAAGT TTACGTGCTG CCTCTAGCAG CTGGCTGAAA
94681 ATGGCTTAAG GTCTACAATT ACGTGTAAGA ATAGAATGTG TGTCAAGGCG GTCCTCTGTC
94741 CAAACAGAGT TGTAGTGGAC TGGACTGTAA ATCAGAGTTA GGAGGGCTTC TGATAGCTCC
94801 TATAGTTAAG GAATTTAGCA AGTGTGAGTT TTTGGTAGT CTTTGAATT TAGGAATTTG
94861 CCATGCCAGC CAAGCCATGA ATGCTCTACC AGTAGGTAAC TTTGTTTGCT TAATCTTAGA
94921 GTCTGTCTTA GTTGGTATAG GGGCATCTAT TTTGGTCTTT CAGATCCCAG ATATTATTAA
94981 TACAGATACT CTTGCAGTTT TGGGCTGATG TTTATATGGC TTATCTTTTT TGCAGCCTTT
95041 AATTTCAACC TGCGTTATGT TTATATTTGA AGTGAGATTC TTGCAGACAG TGTACAGTTG
95101 TTGTTTTTTT TTTTTTGAGA TGGAAATTTCA CTCTGTTGT CCAGGCTGGG GTGCAGTGGC
95161 ACAGTCTCAG CTCACTGCAA CCTCCGCTC CTGGGTTCAA GGGATTCTCC TGCCTCAGCC
95221 TCTTGAGCAG CTGGGATTGC AGCCATGCGC CACCACACCC GGCTAATTTT TGTATTTTAA
95281 GTAGAGACAG GATTCAACAT GTTGCCAGG CTGGTCTCGA ACTCCTGACC TCAAGTGATC
95341 CGCCAGCCTC GGCCTACCAA AGTCTGGGA TTACAGGTGT GAGACCTCGC GCCCAGCCAA
95401 ACTGTTTTTT TATGGGTGTA TTTATACCAC ACACATTTAA TGCAATTATT GATATCTTAG
95461 GGCTTAAGTT CATGAAGGGT AGTGTGGGAA CCATAGTCTC TTGGCCCACT AAATGTTTGC
95521 CAGAAATCAC TGACAAGGCA GATTGATTAA TAGGTGAAAA GGCAATTTTAC CTATTGTTTA
95581 ACGTGTCTAT GTGGGAGCAT TCAGAATTAA TTACCTAACT TCCCAATGAG TTATAGATGC
95641 TTATATACCA TTTTATGATC ACAGAAAGAA TTGGGGCTTA GATCTGGTA AAACAGGTTA
95701 TGGGAGGCAA AAGAGGTTTG GCTTGCAAAG GTGGCCTTGT TAGGTAGGTG AAGCCTCCCT
95761 CAGAAAGAAC AGATGGTAAA TGTTCTTTT ATGATTTTTA AGTGTGAGAC TCTCAGTCTC
95821 TCCTGGATCT GGGGAAAGGT ATAGAAAGGT GAGGAGGCAT GGCTGCATTA ATGGAGATTC
95881 TCTACAGATG TAAAATTTTT CCCATTTAAG GCAGCTTTGC AAGCCCCATT CTGCCTGCTG
95941 GCCAAGCAGC AGCCATTTCA AAATATGTCA AAGAAATATA TTTTGGGGTA AAATATTTTG
96001 ATTTCTTTTA GACTGGTGGC CTTATAAGAA AAGGAAGAGA CACCTGAGCT GACACACATA
96061 CCCTTGCTCT CTCAACATGT TATGATGCAG TAAGAAGGCC CTCACCAGAT ACTAATTCCA
96121 TGCCCTTAGC TTCCAGGTT CTAGAACAGT AGGAAATAAA TTTCTTTTCT TTTAAAGTTA
96181 GCCAGTCTGT GGTATTCTGT TATAGTATCA CAAAATGGAC TAAGTAACATA TATTATGATC
96241 ATCTTACATG ACTGATCCCT CCTACATCAT ACACATACAC AGGCCACATT TGGAACATTG
96301 TTAGAGGTTT CTCTGCCCAG TACAAATGTA CTACAAATTA TATATGTATT TTTAAATTTT
96361 TGAGTATCTT CAATAGTATA TTTTCGTTAA CTTTGTAGT CAAAATGTCA TTATAACATG
96421 TATTCAATAT GCATAATTAT TAGTCAGATG TTTTACATTC TTTCTTCATA CTAAGTGATA
96481 TGGTTTGGAT ATTTGTCCCC TCTAAATCTC ATGTTGAAAT GTAATCTCCA ATGTTGGAAG
96541 TGAAGCCTGG TGAAAGGTTT TTGGATCGTG AGGGTGAACC CCTCATGAAG CGCACTCTTC
96601 AGGGTAATCA ATGGGTTCTC ACTTTGAGTT CACAAGAGAT CTGGTCTTTT AAAAGAGTGT
96661 GACACCTCCC CCATCTCTCT CGCTCAGCTC TCACCATATG ATATGCCTAC TCCCTCTTCA
96721 CCTTCCACCA TGATTGGAAG TTTCTGAGG ACTTGCCAGT AGCAGATGCC TGCACCACAC
96781 CTCTGTACA GCCTGCACAA CCGTGAGCCA AAAAAAATTA CTTTTCTTTA TAAATTAGTC
96841 AGTTTCAGGG ATTCCCTTAT AGTAATGCAA GAACGAACATA ACACACTAAG TCTATTTTAT
96901 ATTTACAGAA TAGCTCAATC TGAAGTACCC TTTTCAACT TCACAGTAGC TACTTGTAGC
96961 TAGTGGGCAC TGATTGAGG CGTGTTCGAG GGTGAATTGT ATTATGCAAT TAACAGATTT
97021 TTTTTATTGT TTTGCGAAAC CACGAGGCAT AGATTGTCTT ACTTTCTCTG CTCCTGGTGT
97081 TGGAGTTGTT ATTGGGAAAC AACTTATTTT CCTCTTATAT TTATATGGAA TAAATAACCC
97141 CCAATATTTT CCTCCCAAT ATCTGCCTTT TGTATGTTTT TTGAAGGCAA GTGCCTAGAA

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97201 TTTACTGTTT TTGAAGCACT TACTGAAAGG ATTGCCATCA AGTTGTTTTG CTAATAGTAC
97261 ATGCCAGGCG CTTGTTGGTT TGCTTAATTC AAGGTAACCT GGATGAGAAG AAGAGTTTTT
97321 CTCATCCATG GCTCAGTGGA GTATAGATTA CTGATATTGT GACTGGATGT ACTCCTGCTT
97381 TCTAGTCTGA GTTTTTGAAG CTACCCTTAA TCTTGGTTTC AATTTTATCT AGCCCTGTAC
97441 ATATCCAAGG CTCTTTCCAA AATGGTCTAC GATTTGTTTA GGAAGTTAGA ATAGCTGTAC
97501 TTTCTGAACC ACGGTTCCCTG ACATTTTCTG GACTTCAAAC ACATCCAGCA TTTTATCGAA
97561 GTATTTATCC TTCCTACTTG GCTGGCTTCT TCCTTGCCCT CAGGTCTGAA TTCAAATGAC
97621 ATTCTCCTGA TGAAACTTTC CATCCTTATT TCTATTCTTT TTTCTTATCC CCTTCTTTA
97681 TTTTCTCCCA CAGCACTCAT CACTTATCTC TACATTTTCA TTATGTATTT ACCTTATTGT
97741 GCACCTCCCA CTACAAGACA AGTAGCACCG TAAGGAAACA GGTTGTCTGC TTTTCACTG
97801 CTATGCTCCC TGCACCTAGA ACACCTCTCG GCACCTAGCA GGTTTTCAGT AAATATATGC
97861 TGAACATAATA ATGCTGGATA TACATCTCCC TCATGAACTC TCTAAATCCT TCTAATTTAC
97921 ATTGATCAAT CTTCTTTTCC ATGTGCTTTT GTATGATTTA TTGCTCAAAA TCTTTATTTT
97981 ATATGCAGAA CGTGCACCTGC TATTTAATCT TCATGTACGT AAGTCCTCCC TTCTCTGAGT
98041 ATAATCTCTT CAGGGCACTA TCTGAGATAA CTTTTTAACA TCTCCATCAT GAATCTTGTA
98101 CCTTTTCAAA GAAAATGAGC CAGTGATTAC TGATGTTTAC GGCTATTGTT GAGGGTGAAG
98161 ATCATTATAA TTTTGAAGG GGAAGTTGAA TATTGTGAAG GGAAAGATAA CACTAGAGTC
98221 AGAAGACTTG GGAGAAGGCA AAAAACAAAC TAAAAATGAG CACTTTTAGT CTCCTGACAG
98281 TTTCTCTGAA TCAAATCCAT AGTTCGTGTA CAGCGTTGGC TTAGAAGCAG ATTTTTTTTT
98341 TTTTTTTTTT TGAAATGGAG TTTCGCTCTT GCCCAGGCTG GAGTGCAGTG GCACGATCTC
98401 GGCTCACTGC AACCTCTGTC TCCAGGGTTC AAGCGATTCT CCTGCTTCAG CCTATGGAGT
98461 AGCTGGGATT ACAGGCTCCC ACAACCACGC CCAGCTAATT TTTTGTATTT TTAGTGAAGA
98521 CTGGGGTTTC ACCATGTTGG CCAGGCTGGT TACGAACCTC TGTTCTCAAG TGATCTGCCC
98581 GCCTTGCCCT CCCAAAGTGT TGGGATTACA GGCATCAGCC ACCGTGCCCC GCCAGGAGCA
98641 CTTTTTTTCA CACTCATGTT TCTTTTCCCT TCTGTCATCC TGTTCAGTA TAAGCAGACC
98701 ACAGATAGAA GTAGTAGATA CCTCAGAAAT TCCTGGAATA ATTAATCCAC GTTTCATCTGT
98761 ACTCCATCTG CTCCTATCTC ATGGAATATA AAAGGAAAAA CACCAAGATT TCCCTAGGCA
98821 ATCTGTCTTG ATTTTAGGTT CCTCAACAGG AGAGCCAGAC AATGGCTGTA ATAATATTGT
98881 CCCGGCCAAG GAAAACTTC CCCTTTGCCC TCCCAAGGTT TATGGAAAAT TACTGGCAAA
98941 ACACAGATTA ACTGGAGAAA AGGCATATAT ATTTATTTCA TCACAATTTT ACAGGAGATT
99001 TTAGAATTAA GACTGAAAGA TACAGGGGAA ATTGCCCAT TTTATGCTTA GTTTCAACAA
99061 GATAAACAGC TGTATAGGGT ACGATCTAAT GCTAACAGAC TGAGTGGGGA AGCCCCGCAA
99121 GGCTTGTCTG TCAAGATTCT TCTTGACCTC TCAGTGCAGC ATTTCTTCCT TCTGGTTATA
99181 GGACAAGACT CTCTTTTAGA ATGGGGGGTC TTATGACCTA CAGGCAACA AGGTAGGTTA
99241 GAGTAATACT TTTAGGTTTT ATGGCTGGTT CTAGGGAAAA GGAGTCTGG TTTGTATGGC
99301 CTACCTTGAG GAGGAATTCT GGTTTCTATG GCTAGACTTT GGGGAGAATG GGACTTACAG
99361 ACAGGAAGGC AGAAGGTGGT CAGTGAACA CTTTTATAAT CATAATCCCA TTTTGAGTAT
99421 TTCTGTGTTA TGGAATGTT GTTCTCTCAT TTCCTGAAAG ATTCCAGAGA CTCCTCATT
99481 AGTGTGTGTA AAAAGTTCAG GAAATGCAAC TCAAAAATGT GCCACTTTGT TACGCTGATT
99541 TCTTTGAACT GAGGGCACCT AGGAAACAGT AAATTCAGG AAGGGCTTTC GCTGAACTCT
99601 AATCAAAAAT TTGAAAATTA AAAAAAATT CAAAAAGGAA TTTAGTTGTT AAGATTCACT
99661 TCCCTGGGGA ATCTCATCAA CCAGAGAAGA TTAAGTGTAT CACAGGAGAG GAGACTGGTG
99721 GTTAACACCA TCTAAACAGA CTTTGTACCA GCTGTCACCT ATTCTTTGAA ACACCCATTT
99781 ATTTTCTCC AAAATCATAT ACTCTCCCT AAGTTGCCTA CATCCCCCT CTTTCTCCCT
99841 TATGAATCAA GAGAGCTTAT AAGCTTCTAC AGTTCAGTGG GATTTGGGGT ATTCGCTTTT
99901 CTTCCCTCCC ACTCCCCCTC CCCTTTTTTT GTCTTTGAGA CACAGTCTTC TGGCTCTGTC
99961 GCCCACGCTG GAGTGTGGTG GCTCTATGTG AACTCACTGC AACCTCCTCC TCTCGGGTTC
100021 AAGCGATCCT CCCACCTCAG CTTCTCGAGT AACTGGAAC ACAGGCGTGC ACTACCAAGC
100081 CCGGCTTTTT TTTTCTTTTT TCTCCCCCGT TTCTTTTTTG GTTATTTTAC TGGAGACAGG
100141 GTTCTCCAT GTTGTCCACG CTGGTCTCGA ACGCCTGACC CGCCGTCCTC GGCCCTCCAA
100201 AGTGCTGGTA TTACGGGCAT GAGCCACTTG GCCCGATTG AAGGACCTCT TAAATATCTA
100261 TTTAGAAATT GGTCGGAGTC CACTCCCTTC CAAAAACATG AGTCACAATC CGGGAAAAGC
100321 ACGAGCGGCT GAAAGTCAAA ATAACCAGAA CAAAACCTCC ACTCATGCTT AAAAAAGGTA
100381 TTTTGACAAA ATCCTAATTC GGCCAATTAT TATTAGTATT CAAGTCGAAG GCTCGTCAAG

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100441 CCAGACTGGG GATTGGGTCA AACATAAACC TTACACCAGA CGGAAGGATT ACATGCAAAT
100501 GAAGGATGCA GATTCTGATT TCCCATTTGGG TATTTGACAT TAGCCAATGG GAGAATTCCT
100561 CACAGCCTAC CTCCAGTCAG TATAAATACT TCTCTGCCTT GCGTTCTAAT GTAGTTTCAT
100621 TACATTTTCT TGTGGCGATT TTCCCTTATC AGAAGTAGTT ATGTCTGGTC GCGGCAAACA
100681 AGGCGGTAAA GCTCGCGCCA AGGCTAAGAC TCGGTCTTCT CGTGCAGGTT TGCAGTTTCC
100741 TGTGGGCCGA GTGCACCGCC TGCTCCGCAA AGGCAACTAC TCCGAGCGCG TCGGGGCTGG
100801 CGCGCCGGTG TATCTCGCGG CGGTGCTTGA GTACCTGACC GCCGAGATCC TGGAGCTGGC
100861 GGGCAATGCG GCGCGCGACA ACAAGAAGAC CCGCATCATC CCGCGCCACC TGCATTTGGC
100921 CATCCGCAAT GACGAGGAGC TTAATAAACT CTTGGGGCGT GTGACCATCG CGCAGGGTGG
100981 CGTTTTGCCT AATATTCAGG CGGTGCTGCT GCCTAAGAAA ACTGAGAGCC ATCATAAGGC
101041 CAAGGGAAAG TGAAGAGTTA ACGCTTCATG CACTGCTGTT TTTCTGTCTAG CAGACAAAAT
101101 CAGCCTAACA GCAAAGGCTC TTTTCAGAGC CACCTACGAC TTCCATTAAA TGAGCTGTTG
101161 TGCTTTGGAT TATGCCGCCC ATAAAGATGT TTTTGAGGTG TTTTAAATGG CTTTGAGTGT
101221 GGCACCTTTA GTAATTTGTC CTGCAGAAAT TAGATCCATA GAAACCTCAG GAATTCTAGG
101281 TATGTGGGAG AAGTGCCATG CAGCACAAAA CATGTTTACA GGGGTGATTG GCGTTAAGTT
101341 TCACACACAG CAGTTACTAC ATTTTAGAGG AAGGAAATTA TACCCATGAG TGCATTCTTA
101401 ACTATCTTGA ATGGAAGTGT TAAACCCCGC ATGCCCCACA CAAGTTTGAA TATGTCATAC
101461 CATTTGCTGT AGCAATTAAT GGCATACACA ATTGAGAGCA CACACATTAC CACTGAACAT
101521 TTGAGTATGT ATTTCCCAA ATGAGCTTTT TTCCAGTTTG GGGATGTTTT GCTTTGTTTT
101581 GGGGTGGAGT CTCCCTCTCG CCCAAGCTGC AGTGCAGCGG CGTGATAACA GCTCACTGTA
101641 ACCTCGAACT CGGGCTCAAG CGATCCTCTT GACAGCCTTC TGAGTAGCTG GGATTACAGG
101701 CGAGAGCCGC CACGCCCGGC TAAGAGCATT TTTCTAATTG CCCACACTTC TTATGCGACA
101761 CCCAGAAAAA TACAATTTTA AATAAAGCGC ATATGCAAAT TTCCCTAATC GTCTCCAATA
101821 TCTCTGATT TCTTTTTTAT ATTTTAACTA GAAACAATTG GAGGTTTCCG CGTTGCTTTG
101881 TGTGTTGTA AATTTTAAGA CTTTCCAGT ACAAGACTTG TCCACAGTGG GGCAGGAGC
101941 ATATAGCAGC TAAGGGGTTA ACAAATGAC GTCAGAGTAG CTACGGTAAT GGCAGGAGC
102001 CTCTCTTAAT CTGCAACCAG GCACAGAGAT GGACCAATCC AAGAAGGGCG CGGGGATTTT
102061 TGAATTTTCT TGGGTCCAAT AGTTGGTGGT CTGACTCTAT AAAAGAAGAG TAGCTCTTTC
102121 CTTTCTCCA CAGACGTCTC TGCAGGCAAG CTTTCTGTG GTTTTGCCAT GGCTCGTACT
102181 AAACAGACAG CTCGGAAATC CACCGCGCGT AAAGCGCCAC GCAAGCAGCT GGCTACCAAG
102241 GCTGCTCGCA AGAGCGCGCC GGCTACCGGC GCGGTGAAAA AGCCTCACCG TTACCGCCCCG
102301 GGCACGTGTTG CTCTGCGCGA GATCCGCGCC TACCAAAGT CGACCGAGTT GCTGATTCGG
102361 AAGCTGCCGT TCCAGCGCCT GGTGCGAGAA ATCGCCCAAG ACTTCAAGAC CGATCTTCGC
102421 TTCCAGAGCT CTGCGGTGAT GGCGCTGCAG GAGGCTTGTG AGGCTACTT GGTAGGGCTC
102481 TTTGAGGACA CAAACCTTTG CGCCATCCAT GCTAAGCGAG TGACTATTAT GCCCAAAGAC
102541 ATCCAGCTCG CTCGCCGCAT TCGCGGAGAA AGAGCGTAAA TGTAAGTCA CTTTTTCATC
102601 AGTCTTAAAA CCCAAAGGCT CTTTTCAGAG CCACCCACTT ATTCCAACGA AAGTAGCTGT
102661 GATAATTTTT TGTGTCTTA ACAGAACAAA TTTCTAAGGA CCCCCCGGA AAGCATTAGA
102721 CTATGGTCTT AAAGTTGATT AACAGAAATA ACGGTTTGGT CAGTCTTGCA GTGTAGGTTA
102781 TTTCTGACCT TATTAAGGTG CTATTTGGAG AGAAGCTGTG TAAGTCCACT ATCATTACAGG
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102901 TGGTAAGTAG TTAAGTGGCG CTTACTAGGC ATTTTGTCAA AGCTTTGAAA AGATTAGAAA
102961 ATTGTGTCTT GCGAGTTCCA GTGCTTTCCT CAAAATGCTT AGGAAGATTT TCTCAGCTCA
103021 ATACATAGTC CCCTAGGTTT TCTCATATAT TATATATATA TATATATATA TATATACTGT
103081 TAAATTCATT TGGCTGTAA CATTAACTG AAATTTATTC TGGTGCAAAA TGTGAGGCAG
103141 GGATCTAACT GGCTCTCATT TTATCCATAG CTAGCTACCC ACTTTAAATC TGTCACTCTG
103201 TCGACCAAGC ATAATTTAAT CCCTTATATA TGAATTTTTA TATGTGTGGC TTTGCTTGTA
103261 AATAGTCTAT CTGGTTGCAT TGCTTTGTCT CCTCTAGGAC TATGCACCAT GACATGCCAC
103321 ATTCTTTTTT TCAGTACTTC TTGCCTGTAG TTATTAATTA CTAGAATTTA CAAGTTTTAA
103381 CCATTTTCTT TCTGTTGATC TTGCTTTTCG GTTTTGAGG TTGGGGATTG AGTACTGGAA
103441 GAAAATTTAG AGGGATGGGA ATACTGTACG CAAACAAAAG TAATATTTAT TTTAAATTTT
103501 TTATATTTTG TATTTTTTTA TCATATAGCT TTACATCAC ATTTTACAGA CTAACCTTAG
103561 AACAACCACA GAATGTCCAA CATTAAACT ACTAATTCCA AAGACCTTGC CTCACATTCT
103621 TTTTTACAAT AAATATTTTT TACACCTAAC ATCTTTTCTT GGCCTACATC TAGAATGTAA

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103681 ACTGATGTAC CATACTAAAA TCGCCTGACC AACTGTCAAC AACAACAAAT CACACACACA
103741 AAAGATTAAA TTTGAATTGC ATCGTTTACT TAAATTCATT TGTGTTCCAG CTTTTAATAA
103801 GGCAGTTTTT GGTTTATAAA GTAATATTG CATTTTAAAA ATTATGAAAA TGAATATGTC
103861 AGTTTGTGTT ATGATTTCGTT TTTCTTGACT CTTATACAAG CGACTCTAAC TGGCATAGAC
103921 ATTTGTATC CACAGACAGT ATAGATATGT TAGAGATGCC AATGGACTTG GTCTATGCCA
103981 AGGTGACTAC TCACAAGCTC TGGGCCGAGC TGAAGGTCAA GTATTTTTTT TCCAGTTATA
104041 GATGTGCTGG ATCTGATGTA TAGCGCTTGA CTTTTTATAT TTTCTTTATC TGTAGGAAAC
104101 AAATGTGTTG GAGGTACTGG GTCTGACGAA TAGCATAAAA GAATAAAGTT ACATTACTGT
104161 CTGAGGATCA GATGGACAGG GGGTGGTAGC TCAGTCCAGC TATTTTCCAC TCCCTCACTT
104221 ACATTCTTTG CCCCCTCCTC AACAGAACAA GGATTCTGCT GTAACCTCTC ATTGACAGTT
104281 GATATTTAAA AATTAACGAA TGGATGAAAT TCTCATTTGT GAAAGAAAAT TTATTGAGCA
104341 TTTTGTATTT GTGAGTAGTG CAAACATTTT AATATTATAT TAAGAATCTA TTGTTTTGTA
104401 TTAGAGGAGT AATTAAGGAG AGATTGGAGA CAAAAAGGGG GTGTTGTTTG CAGAATATAC
104461 CATCCAAAAA TAGACCACTG TGGGATCAGG ATTCTTTTGA GCTAAAAGCA CTTCAAAAAAC
104521 AGCATTCAAG AAGGGAATTC TTCTAAACTT TTCTTTCTGA AAACAGGAGA TAAAAGTTCC
104581 AATGTGAAAA ATGCTCTGCT TGTACCAGGT GAAAAGACAT ATTCTTCAGC CCAGAGGCAT
104641 AGATGAGATA ATTCTGCACA AACACAGCAG GGAGTCATAG CCGAGAGACT TCTATACACA
104701 AACAAACCTT GTTAAATAA TCATATATTC CTTTAACTC CTCATATGGT TTACTTTCCC
104761 ACAATTGCCT CTCTTAACT TAATGTGAAA GCATTTAGCT TTTGCCATTT CTTTGGGGCT
104821 TCACTTTTTT ATGAGGGTTC TCCTGTCCCA TAAAATTTAC ATTAATACA TTTGTATGCT
104881 TTCATTCTGC TAATCTGTTT TATGGCAAAT GAATTATCAG GTCCAGCTGG AGACCCTAAC
104941 AGAGTAGAGG TAAAATTTTG CCTCCCTACA AGATAGAGAT TGTGTGCATT AAATGTTGTT
105001 TGTTCCCACT TGTTCACTTT GTCAGCCTC TGAGCCGAAG CTAAGCCATC ATATCCCCTG
105061 TGAAGTGCAC GTATGCCTCT AGATGGCCTG AAGTAACTGA AGAAACACAA AAGAAGTGAA
105121 AATGCCCTGT TCCTGCCTTA ACTGATGACA TTACCTTGTG AAATTCCTTC TCCTGGCTCA
105181 TCCTGACTCA AAAGCTCCCC CACTGAGCAC CTTGTGACCC CCACCCCTGC CAGCCAGAGA
105241 ACAACCCCTT TTGACTGTAA TTTTCCACTA TCTACCCAAA TCTTATAAAA CGGACCCACC
105301 CCATCTCCCT TCGCTGACTC TTTTCGGACT CAGCCCGCCT GCACCCAGGT AGAATAAACA
105361 GCCTTGTGTC TCACACAAAC CCTGTTTGAT GGTCTCTTCA CACGGACGCG CCTGAAACAG
105421 TTTAACAGGG TTTTTCCTGC CCAGTCACAA CAAAGTGATG TTATGCTGCA GGCTGAAGTT
105481 TACAGCTAAT GCTGTTGAAG TCTAAAATCA GTTTTGGTTT GTTAGATTG GGTGAGATGG
105541 CTAAGATTCT CAGAGAAAAG AGTCAAGTTT GGGGTGCATT TTTCAAGCTT AAAAATTTAG
105601 CAGTAGCCCT TGCAGTTTTT CCAATAGAAG TGATTTAAGA ATGTTTTAG GAAATTTAAA
105661 ACAACAGTGA GAAGCGTGTA TGGAGAGTTG AACTACACTC CAGACTTGGC TATAGGAAAG
105721 CACGAATGCT GCTATTGTAT TGCACCTTGG AAAAGAGAAC AAAGGAATAT TTTCCGACAA
105781 TTTTAAACATG TCACATATGA AAAGCTAAAC GGAATCTGTC AACACCTTGT ACGTTATTAC
105841 AGGCTGTGAT TTTAAAAAAA CAATCCTTAC TAATACATAC ATAGTTGCTG CTAGCAATAT
105901 AGTGTGTTGGA GTAAAAACAC GAAAATGAGA GTTCAGGACA ATATCCCAAC TCTGAGCAGA
105961 TTTTTTTAAG TAGTAACATC TAAAATTAAC CCATATTATG TAATATTTAT TTCTTTTCCA
106021 CAGTCTCTTC TCATGCCTCG TTCACATTAG CTAATTAATA GTCCCTGAG TATCATATA
106081 ACCCGATTTA CAGATGAAGG CACGGTTGCA ATGAGCTATC ACCCTCTTCT GAATGAGACA
106141 GTACAGTGTG AAGGATAGCA AAATCCACT CCCATCCTCT TAGGGCTCTG GCTGGACCAG
106201 CAAATTAAAT TAATGTAAAA TGGATTAACA GGAGAAAGGT ATATGCATTT ATTTAACACA
106261 GGTTTTACGT GACACAGGTG CTCTCATAAG GTAATGAAAG CCAAAAAA GCAGTTAGCT
106321 ACTTATATAA TGAATTGGAC AATTAGTAAA ATGTAAAAAT GCGCTAAAGC AAAGGGATT
106381 AGGCTAGAAT ATATAACTGT GTAGAGAAGC GCCCAGCAAG GGCTAGTGCA AGGTTTGTAC
106441 AGAATTCTCT TGGCCTCAGC CTCCTATCCT TGAGAAGAAT GTTGCTTTT TTAACCTACA
106501 GTGAGAACAT CTTTCATATG AGAATTTTAC CTACTGCTTC TAAGAAACAG GTCAGCTTTC
106561 AAGAAAACAT AAGGCCAGAG TGATCTTTTC ACGCCTGCTC TTTTAAGTAC CTTTGAATAG
106621 TCAATATGTC TTCAAGCACT TGAAGACTT AAAAAGTTTA CCACTCCGGC ATATTAGTGA
106681 AAGCCCTTAA TATAAGCCCT TATTAAAAAT CTCAGTCGAG GGTATAAAT CAGATTCAAA
106741 TAGTAGTGTC GTAAACGGGA GGGAAAAACT AAAGGGATTA AAAAGTGAAT CTATTGTGTT
106801 CTCCTTCGCA GTCCTTAGGT CACTGCCCCC CGAGGGGCGG AGCAAAAAGT GAGGCAGCAA
106861 CGCCTCCTTA TCCTCGCTCC CGCTTCAGT TCTCAATAAG GTCCGATGTT CGTGTATAAA

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106921 TGCTCGTGGC TTGCTTTCTT TTCGCGTACC TGGTTTTTGT TGTCAGCTGG TTAGACATGT
 106981 CTGGTCGCGG CAAAGGCGGT AAAGGTTTGG GTAAGGGAGG TGCCAAGCGT CACCGAAAAAG
 107041 TGCTGCGGGA TAACATCCAA GGCATCACCA AACCGGCCAT TCGGCGCCTT GCTAGGCGTG
 107101 GTGGGGTTAA GCGAATTTCC GGTTTGATTT ATGAGGAGAC TCGTGGCGTT CTCAAGGTGT
 107161 TTCTGGAGAA CGTGATCCGG GACGCCGTGA CCTACACGGA GCACGCCAAG CGCAAGACTG
 107221 TCACTGCCAT GGATGTGGTT TACGCGTCA AGCGTCAAGG ACGCACTCTG TACGGCTTCG
 107281 GCGGTTAATC TTTTCGTCAG TTTTCTTCCA ATGGCCCTTT TCAGGGCCGC CCACCTCCCTC
 107341 TCAGAAAGAG CTGTGATTGT ATTCTTTCGG ATGGTAACAT CTCAATGGCT TTACTCGGCT
 107401 ATTCTGCCAT GTATGTAGAA CTATTATAAA CCAGTTGGGA GAGACCAGGT TGTTTGGTCT
 107461 GAGTGGCTGC TAAAGCAGAA ATCAGCTAAG TAAACGAGGT CTCCGAGATA AGTGAGCTAT
 107521 AAACCTCAAT GCTATAGTTT TGACATGTCA AGCAACTTAA CGTGCAGCGC GAGTCCGATA
 107581 AATGAGTAGC TCAGCTTTT AGTTTTAAAA ACGAGTTGTG CGTTATTTGT ACGAGAGCCT
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 107701 CAGGCGTATC TGACTTAACG TCAGCAAAAG CTGTACTTTT AGCTTCCCTG GTAACACCTG
 107761 CCGTCCTTAA CCGCCCCCTG CCGGTAGCGC CAGAAGCCTT TACTTCCATT TCTAGTTGAG
 107821 CTTGCGCTCC TGCTGAGTGA CGTCACCTCC CCCTTCTCTG GAGTAGGACT GGCGGTTAAA
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 107941 TTCGTAAATT CCCACTTAGT AGACTAAGGG AGTCTGTTTT ATAAATAAGG ACTCAAATTT
 108001 CTTCTGACTC CGAGGTCCGT GGCAGCAGCT ATAAGATGGA AGCCCCCTCT GATGTAAGAT
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 108121 AAATTGTAAA TTCCAAAAC GATTTAATTG TGAAAGTTTC AAACGTACG ACCTAGGAAG
 108181 TGTCAAAGTT AGGTGACCAG ATTTTGTAGAA GTCAGCCAAA TATTCAGCAT CTTTGATTAA
 108241 GTAACAAATA TATTGATGGC TACTTCAGCA AAAAAATCA ACTTTGTTTT CTGGTTACTT
 108301 TGTAAACAAG CTTCTCCTGA CAGGAGGATA TAGTGAATAG GCAGTTGAAT AAGTAGTTTC
 108361 GGGTGAGAGG TCTGAGCTGG AGATAAAAAAT GTGTGAGTCA TCAGCAGATA AATAAATGCT
 108421 GAGACCAGAT GAGATGGCTA AAAACTGAAA CATAATGTAG TGCAGCATTG TTTGTAATAG
 108481 TAAATGAGTG GCAACTGTAA AGTTTTCATC AGAAAGGACT AGAGTGATCT ATACATCCAT
 108541 AAAATAGAGT ATTTCTCTAC ACAGCCCTAC TAAAGAATGA GAAAGCTGTA CTCCACTACA
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 108661 CTCACCACTT ACATGCTCTG TGCTCTGTCA AATAGTTTGT TCAACAGAAC ACCACGGCCT
 108721 AGCTGTAAGT GCCACGTAA CTTCTAGCAA TGCCAAAGCC TGTGATAGTG GCAGCTTCGG
 108781 GCTGTTTCTC ATTCCCGGGA TGCCTAACCA CCTCTCCAAA TTCTATCAGT TTGCTTCCAC
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108901 CACGCTGTGA ATCCCGGCAC TTTGGAAAGC TGAGCCTGGT GGATCACCTG GGGTCAGGGG
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 109201 CCTGACCTTA AATCTCTAGA CTCATATACA ACTGCATATT TGATGTATCT AATTGAATAA
 109261 TGGGCATCTC GAACTGTGCC AAAATATGTT TATACGTAAA CACCAAGTCT GTTCTTCCTC
 109321 TGATATTTGT CATGTCAATC AATAGAATC CATTCTTCAA GCAGCTTGGG CCAGGAATTG
 109381 TGCAATATTG TTTGTCTGTA GCTTCTTACA ACTTTCACCC AATGCAGTCA GCTCTGTTGA
 109441 AAATCAATCA GAATACCTTT CATTGTTTTT TTTGCTGCTT CTCTAGGAGC AAGCTGCCAT
 109501 GGCGGTTTGT CTGAATGACC ACAGTGACCC CAACTGGTC TTTGTTTTCA CTTTAAATCC

109561 CCCTGTCATA CAGTTTTTTC TCTATCCAGC ATCAACAGTG ATCCTTTTTG AAGGTATTAT
 109621 GTCCACTGTC TGCTGAAAAG ATTCCACTGG CTTTCCATCA CCTTCATAAT AAAAACCAGC
 109681 ATCCTTATCA TAGCTTACAA GTAAGATGAC CAACCATTA AGTTGCCTG ACTCTCAGGG
 109741 GTTCTCAGG GTGTAAGACT TACAGTGCTG AAACCTAGAA AGTTCCAAGC AAACCTAGGAT
 109801 GAGCTGCTCA ACCTACTAGA TCTGTACTCT GGCTACCCCTC TGACCTCATT CTCTTCGAG
 109861 TTCTTTCTCT TCACTGACCT TGCTGTTTCT GGAATGGACC AAGCATTTCC AGCATCAGCA
 109921 CCTTATATC TATTCTTCT CCCTAGAAGG GTCTTGTCTT GGATATCTAG ATGGCTCTAG
 109981 ATCTCATTTT ATTCAAGCCT CTCCTCAAAT ACCAACCCTA CGAAAGAGAC CTCCTATAAT
 110041 CATCCCTTGT AAAATAAGCT TTTCTGCTCA TTTAGCATAT ATATATATAG TTGACTATCC
 110101 TCAATAGCAT ATATATATAA CATTTCCTCA CCTAGAATTA TATATGTAAT AATATATTTA

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110161 ACAAAAAATA CATATAACTA GATATATTTT ATTTTGTGTT TGTTCCTCTCT CCCCCAACTG
110221 GAATATATTT TTTGAAGGTA GGGACTTTGT TTTGTCCCAG AAGTATCCCT AGCACCTTGA
110281 ACAGGGCTGA CGTTTAAACAG GTAGTTTATG GAGGTTTGT GAATGAAAGG ATGTGTGAAT
110341 TTTCTATGTA AGTCTCCAGG CTCTCCACTA AGCCCACCAG AATGCTAACA CAATCAATTC
110401 CCCATCTCAT TCCTTGACCT GCCACTGCCT GAAGCAATCA GCGTGCACTT TCTCTTTAGA
110461 AAATCTGGGG GATAGTCTAG GGGTTGCAAA TTAAGCAACA TTATCTTTGT TCTGAACAAG
110521 GACTGCATGA GTGTTAGGAC TGAAGAAGGC CCAAGGTGGT GGTGGGTATG CCTAAGATGA
110581 GTATGACATA TCAGCAATGC TATGAACATA GCAATGCTAT GAAAGGCCAG GCAAAAACGTA
110641 ACAGGAGCTA GTCGTGGCTT ATTGTTACAA CGACTATACC TCCCATATGG GTAATCGATA
110701 TCCACACACC CCTCTACATT GACTCTGGAA TTCAGGAAAG GGAATTAAAA TTTTCTAACT
110761 TATGTACCCC AATGATTTC ACAAATATCTG GCATATGAGA TCAATAAATA TCTTTAAAT
110821 ACCAACTAAG AAAGACATAA AATGACCAC CCTCCATACC AGGCTCATT TTGCTCCTCT
110881 GATTCTGAA ACTATCCAGA ATGCAGCTAT GAATTCTCTC CATTTGTCAGT TTTAAATTAA
110941 GCCAAGCTGG GTACTTGTGT AATTCCTCAA GAAATCCTGG ATGAAAACCTG TCAGGTGGAA
111001 AACAGGACCT CAAAATAAAG AGACATCCAT CACTGAAGCT AACATCGTGA GGCTGAAATC
111061 AGTCTTATAA CAATGGTACC AAAAAAGACA CAATGAGAGG CATTTGTGAA TATTTACTCA
111121 GATGAGAGTA AGATATTTCC CTATCAGCTA ACCTGAAGTT CACATCCCTT TTCCAGCTGA
111181 GTTCTGAAGC TAGATGTACT TAACTGGAAC ACATAACTGC ATCAGGAACA TCCTTTAAAA
111241 CTATGGCTAC CATGGCTTGA CTGGACAAAC CCCAGGCTTC CAGGTTTAGC ACAGGTGGCC
111301 CTTACAGAC CAACATTGCC TATGTACCA ACCTCATGTC CTACCACCTT GCTTGCATCA
111361 TTTCTCTCTC TGCATATATA AAAATATATG TGTATGTATA TAATCAGCTT TATTGATATT
111421 TAATGTACCA CAAAATTTGC CCACCTTAGG TACAGTTCAA TGAATTTTAC CGTGTTTTCT
111481 TAGTTGTACA ACCATCATCA CAATTTAATT TCGGAATATT TCTATCACCC AAATTTCCAT
111541 TTCTCGTAA AGGGGGAAAA AAAAAAGTTA ACTGCTGAAG GCCGCGGTAA CACTGAAAAA
111601 GGTGCCTTTT CTCTCTAAAA CAGATTTTAA TCTCCCTGA ATTTAGTGTCT CTGGGTATTC
111661 CAGGAGTCTG AATAGGGTTT CAATTTTCAG GGTCTTTTTA ATAGAGTAAA ACTGTATTGG
111721 TGGCGATAAA TTTAGTATTG CTCTCAGTAC ATGATTGAGG GATACTTAAA TGTCTCTGTG
111781 ATTTTATTTT ATAATCGCTA AAAGATGGTT TTTTTTTTTC CTAAAACAGG GTTTTTGTIT
111841 TTTCTCAATA AGCTTCTTAG CTTCCTCTCC GGCTCCCTGG CTTGCCTCAG GAAATATTAG
111901 CTCATCAGTT CTGATTGGTT GACAGCTACG AATGGCCCTC ATTGATTGGG CAGCGCTTCT
111961 TTGTCCCTTG GAAACTAATA CAAATTTTTA AACTACTTT TTTTCCACTC TTTCTTCAGA
112021 GTTGAATAT CGTTGCTCCC CTACCATAT GTAGTGAGTG GAGGGCAAAC TTGGAGTTCC
112081 CCTAATCTTT CTTTTTAGG ATCTCAGCTC AGTATCATT ATCTTAATTA ACATTTGAGC
112141 TTCTTGACTT AATGATACA GCTCTTCTTT TGTTTAGTTG GGCGGCCCTG AAAAGGGCCT
112201 TTGGTTTACA AATGCAAGCT GTGGAGAAAT CAGCAACCTT AACCGCCAAA GCCATAAAGG
112261 GTGCGTCCCT GCGCTTAAG CCGGTAGACC ACGTCCATGG CAGTGACTGT CTTGCGCTTG
112321 GCGTGCTCCG TATAGGTGAC AGCGTCACGG ATCACGTTCT CCAAAAACAC CTTGAGCACC
112381 CCGCGAGTCT CCTCGTAGAT CAGACCAGAG ATCCGCTTCA CACCGCCACG CCGGGCCAGA
112441 CGCCGGATGG CCGGCTTGGT GATGCCCTGG ATGTTGTAC GCAACACCTT GCGGTGGCGC
112501 TTGGCACCCC CCTTACCAA ACCCTTCCCG CCCTTACCAC GTCCAGACAT GACTTCCCAA
112561 GAAGTGAACC AAGAGCAAGT GAGAGAATAG GAAACCGATC TTTATATATC TACGTTACCC
112621 CTGCCCCAC CTCCAGCGGA CACTGAGACT GAAAAGCGCG CAGGCGGGAA ATGTGACGCC
112681 TACAGTCCGC TCCTTTAACC CCTCTCCA GCGCCAGGAA ATGGCGGGAG CAGCGATTGG
112741 GGGAGGGTGG GGAGATGAGG GTGGGACCAA GCAGGCTTGA CCAATGGCCT TTATTTTCTT
112801 AACAGAGCTA CAGGCTTTGA GGAACCTGGT TAAGAATTAA ATGTAAACCC ATTCTGACTC
112861 CAGAATTATT TTAAGTCGAA CTTTTTTTTT AACCGAATCT CTCTGTGCGC CAGACTGGAG
112921 TACATTAGAG CCATCTCGAT TCACTGAAAC CTCTGCCTCT CAGGTTCAAG TGTTTCTCCT
112981 GCCTCAGCCT TCAGAGTGTA GCTGGGATTA CAAGCGCTCG CCGTCGCGCC CGGCGTGTIT
113041 TTGTATTTTT CGTAGAGACG GGATTCGGCC ATGTTGGCCA GGCTGATCCC GAACTCCTGA
113101 TTCTGGTAA TCCGCCCGCC TCAGCCTCTC AAAGTGCTTG AATTACAGGC GTGAGTCACC
113161 GCGACCGGCC GAAATCGATT GGTTTTGAAG CCTTCAGTAG CATTAACACG AAAAGTGTCTC
113221 CCAATGCATT CCCTTTTGTG TTAATTTGGT TTCTTACAGC TACTTTACTT GAAAAGGTGG
113281 TGGCTCTGAA AAGAGCCTTT GCTTGGACCG TCAGAGAGAC CACAGTAATC ACGCCCTCTC
113341 TCCGCGGATG CGGCGGGCGA GCTGGATGTC CTTGGGCATG ATAGTGACGC GCTTGGCGTG

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113401 GATGGCGCAC AGGTTAGTGT CCTCAAATAG CCCTACCAAG TAGGCCTCGC ACGCCTCCTG
113461 CAGAGCCATC ACAGCGGAGC TCTGGAAACG CAGGTCTGTT TTAAAGTCCT GCGCAATCTC
113521 GCGCACCAGG CGCTGGAAG GTAGTTTACG AATAAGCAGT TCAGTGGACT TCTGATAACG
113581 GCGGATCTCG CGCAGAGCCA CGGTGCCCGG CCGGTAGCGG TGGGGCTTTT TCACGCCGCC
113641 GGTGGCCGGA GCGCTTTTGC GGGCTGCCTT AGTGGCCAAC TGTTTGCCTG GCGCCTTGCC
113701 ACCAGTAGAC TTCCGAGCAG TTTGCTTAGT GCGAGCCATG ACGGAAAAAC AGCACAGCGG
113761 AACACCCAAC ACTAGCGCAA ATACGCCCAT GAGCTGCTCT ATTTATAGTG TGTAAGTGC
113821 AGTGATTGGA TGATAGAAGA CGCTAAATAT GACGTTACAC ACTCTGATTG GTCTATCTTT
113881 AAGCCAGCAA CAATCGTGCA GTTTCACCGG CTACTATATT CTATTCCAAC TCTACAGATG
113941 ATTATTTAAG TGGTATTTTA TTACTACTAT TATTTTATTT TACTTTTGCT TTGTTCCCA
114001 AGCTGGTCTT AAACCTTGGG TCAAAGGATC TTCCCGCCTC AGCATCCAGA GTAGCTGGGA
114061 TTACAGGGGA GCCCCACTGC GCCGGCTTGG ACTTTAATTT TTAAACTTG TCCTCTTCTA
114121 CATCTGGTTT TCATAACCTG AAGGCTGTGT TTATTTTCCA TAAAACAAGG CATTGATTCC
114181 AAAGGTATTA TAATTCCTCA ATTCCGTATA ACCTTCAGCT CTTTAGGAAA AAAAAA
114241 AAAAAAAGG GAGGGAATAC TGCTCACCTC CTCTCCGGA ATGTACCCTT TACGGGAATT
114301 TCTGAAACCT TTCACAAGAA TTGGATTCCCT TTGTAATGCT TTAATTGACT TAGGAGTGT
114361 ATTGAAATCT ACAAAGCATC TCAAACATAG TAGGATTACA CTATTACTCA GAAACATTTT
114421 CTATGAGACG TCTTTCTCTT GATTATGCTC TTTGAATCCT AAACCTTGCA CGTTCTGCAG
114481 CTTTTGTTTT CTAAAGCCTA GGTGTACTCT GCCAGTCACA AAATGGCGTT TCTCCAGCAC
114541 TGCCGCCAGG TACCACCAGC TGGGAGTTGT TCCTCTTGC GAGCAGGAGG TGGACTTGGC
114601 CCAAGAGAAA CTGGATAGTG GTTCGCAAGG AACATAATT AGCATTGCCA AGAGCTAATG
114661 CAATCATTTT GAAAATCTCA AAACACTGAA AAGTGGATTG TGACCTTTT AAATTACAA
114721 GAGACAGGCC ACATTCTATC TTTTGATTGG TTTAGGCTAT TTTCTTGAAC AGCCATTAG
114781 AAAGCAGATC TATCATCCTT CATTGTCATG GAGCGTCCC ATTTTATTG AAACAGTTT
114841 AACCCTAATG AAAAAAGGGA GGCAGAACCC ATTATTTAAA GTGGAAACTC CTGAATCAGA
114901 TAATTAGGAG TATTTCTTTT TCAAAGTTG CGTTTTTTCA GATACCTCGC TTATTACACT
114961 AAGAAAGGTT TATATCTTTC ACAAAGGTT TACTTACAAA AATCTTCAA TTTTGTATAC
115021 CTGTGTTTCA TAACTGACTA GCCGTCAAAC CAAGATGTAG AGTTTCCAAC CGTTATTTTC
115081 CAAATTTTTA GAAATTACGT GAAATATTG AATGCATGCC TTCTCAATAA AATGGGACGT
115141 AGGAAGCACT GGTGCAGAAG ATGGGTACAA TACTTATCTG GGACCACTCC ATTATTTGGT
115201 TGGCACGTTG TTTGAACAAA AAGGGGAAAA GCTCAGGTTA CTTAGCATGG TTCGGACTTA
115261 TTTGAAAACT ACCACAGCAG GAGCGGAAAT AAGACCGCAT TACCTCACTC TCTGCTGTGC
115321 TGTGCTAGGG GGTATCCAG AATAGGATTG TAGAAGTGGA TGTCGATTTA ATAGTTTTTT
115381 ATTCTCCCAT TAGCTGAGTC TCTGATTGGC AATGTGAGAT CGTTTAGCT TATTGATACT
115441 TTGAAATGCA CTTAACAGCC ACAAACAAGT TAAAGGGTTG TTACCATAAA ATCTTATCCC
115501 CAGGGTGTGC TTGCATTTAT CACCCGTGTT TGCTTTCACA CTAAGTGGAC TTAACCCCC
115561 AGCAGAATGC CTGTCAGGGA ACCGTTTCG TGGACCCAGC ATTTAACGCC TTTTCGAGGC
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115741 GTATGGATGA AAAGGGCATT GGAAATTCCT GAAGTGCATC CCACATTGGA CTGTGGAAAT
115801 AAGTTGCAAG TGCAGAAACG TTCCACACT TGCAGTTGA GTATTAATTG CAGCGTTGT
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115921 TCGCTCTAAA ACATTGCCAG AAAATGTAAT AGAGTTGATG ACAACTGGCC CTAACACGGC
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116101 CGGATGCTTG TGGCACTGCA TTGTAAACC GCCCCCTCTC AACCTACTCC CTAATAAAGA
116161 GCTGCTTTTT GAGAGAGAAG CCGTACCCTC TGATGTTACT GGGCGGCAGT CTGCCTACAA
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116461 TTATACCACT TTATTTGGTG TGCTGTGTTA GTCACCATGT CTGAAACAGT GCCTCCCGCC
116521 CCCGCCGCTT CTGCTGCTCC TGAGAAACCT TTAGCTGGCA AGAAGGCAA GAAACCTGCT
116581 AAGGCTGCAG CAGCCTCCAA GAAAAACCC GCTGGCCCTT CCGTGTGAGA GCTGATCGTG

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116641 CAGGCTGCTT CCTCCTCTAA GGAGCGTGGT GGTGTGTCGT TGGCAGCTCT TAAAAAGGCG
116701 CTGGCGGCCG CAGGCTACGA CGTGGAGAAG AACACAGCC GCATTAAGCT GGGCATTAAAG
116761 AGCCTGGTAA GCAAGGGAAC GTTGGTGCAG ACAAAGGGTA CCGGAGCCTC GGGTTCCTTC
116821 AAGCTCAACA AGAAGGCGTC CTCCGTGGAA ACCAAGCCCG GCGCCTCAAA GGTGGCTACA
116881 AAAACTAAGG CAACGGGTGC ATCTAAAAAG CTCAAAAAGG CCACGGGGGC TAGCAAAAAG
116941 AGCGTCAAGA CTCCGAAAAA GGCTAAAAAG CCTGCGGCAA CAAGGAAATC CTCCAAGAAT
117001 CCAAAAAAAC CCAAACTGT AAAGCCCAAG AAAGTAGCTA AAAGCCCTGC TAAAGCTAAG
117061 GCTGTAAAAC CCAAGGCGGC CAAGGCTAGG GTGACGAAGC CAAAGACTGC CAAACCCAAG
117121 AAAGCGGCAC CCAAGAAAAA GTAAATTCAG TTAGAAGTTT CTTCTAGTAA CCCAACGGCT
117181 CTTTTAAGAG CCACCTACGC ATTTACAGAA AAGAGCTGTA GTACACAGAT GAAATCCCCC
117241 AAGCAAATGC AACACGCCCT CAATTATATT AGAATCACTT GGAGAGTCGA TAGAATTTTA
117301 ACATAGCCTC ATCTAGTAAG AATTTACTAC TCAATCTATC AAAGATAGCA AGGTGAATTC
117361 AAATGCACCG AGTTAAAAATC GAGTTTTAAA GTCACCTGGG TTTCGGTAGC CGGAAGTCCC
117421 GCGTCTCAGC ACTCCAAGCT AATTAGTCAT AACCGTATTG AACCAAGGTT GAAGCCCAGT
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117601 TGGCAAAATA TATGGCTTAA CCACGCCCTC TCCACAGGAG TGGCTAGCGA GCTGTCTGTC
117661 CTTGGGAAGG ACGGTGACCC TGCTGGCGTG GCTGGCGCCC ACGTTGGCGT CCTCTGAAAG
117721 CCCCCCAGG TAGGCCTAGC TCGCTTGCTT TCTGCAGCGC CATCATGACA AAGCTTTGAA
117781 ACGCAAAATG CTTTCTTTGT GCAGCGCCTT ACCATGGGTG CACTTACGGG CTGTGCACTT
117841 GGTTTAGGCC CTTGTCAGGA CAAAGGAGCT TAGTTTGTG GAGTTTGTAG GCTGCAACCC
117901 AAAATCCCTT GCTCGGTTTC TCTGTTTTTA GAAACGGAAG CGCCCTGATT GGATATTTGA
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118141 TATATGATGA GCCAAGTTTA CTCACCTTTA CTTAGTGCAG TTCAATTCTA AAAGTTTATT
118201 TTTGCGTGTG TGCATATGAG TTAATAATCA GTTGATTTTT TCAAACGGTC TTTTTTCAAT
118261 TGTTTTGCTT AGCTCCTTCC ATCGTCTAAA GTCAGGGATA CAGGCACATC ACATCCCTGT
118321 TCCCCCTTCC TCAAACCTAAT ATGTAGCTAC CTAGGTTTAT CCTTTAAAAC AAAAATTCTC
118381 ACCTATTTTT GTGAGAAATA TACATGTTTT TCTTTGAACT AAGTATTTTA CATAACCTA
118441 TCTATATACA TGCATACTTG TGGTTTTGTT TTTTAAAAA AAAAAAAAAA AAAACACGTT
118501 ATCTTTTGAG ACTGGGTCTC AGTCTGTTGC CCAGACTGGA CTGCACTGAG ATAATCACAG
118561 CACACTGTAA CCTCCAATC CTGGGCTCAG GCTATCCTGC AGCCTCAGCA TCCGGAGTAG
118621 CTGGGATTGC ATGCACGCAC CACCAAGCCG GGCTTTTGT TTTTATTTTT TGTGGAGACA
118681 GTCACACCAT GTTGTTCAAG CTGGTCTAGA AATGGCCTCA AGTGATCATC GACCTCCCAA
118741 AGTGTGGGA TTACGGTCAC TGTGCTGGC CTTGTATGCA TAATTGTTTT GTCTTTTGAT
118801 TAGGGTTATT AATTTAAAAA ACAAAGCCTG GACGCAGTGG CTCACATCTG TAATCCCAGC
118861 ACTTTAGGAA GCCAGATGGG CAGATTACTT GAGCTCAGGA GTTCAAGACC AGCCTGGGCA
118921 ACATGGTGAA ATCCCATCTT GACAAAAAAT ACAAATAATT AGCAAGGCCC AGTGGCACGC
118981 ACTTATAGTC CCAGTACTT GGGAGGCTGG GGTGGGAAGA TGAAGGGAAC CTGGGAGGTA
119041 GAGGCTGCAG TGAGCAGAGA TCGTGCCACT GCACTCAAGC CTAGGTGACA GAATGAGACC
119101 CAGTCTCAAA ACAAATAA TAAAAATTTT TTACAACGAT GTTATATACA CTTCTGCATG
119161 TTGCTTTTCT CTTAACCAAA CTTTCTAAA ACCCTGTCAT GAAAAAGAA ATCCTTCACA
119221 TGGAATAGCA TAAGTTATTC ATCCATTTCT TATTGATAAG CATTGATGTT TCCAGTTACC
119281 ACTGCTGAAC ATGGTGCAAT TGAATAGAAT TCCAGGGCTG AGATTGCTAG GTTTTAGGTT
119341 GTATTTTATT ATTTTATTTA TTTATTTATT TATTTAGACA GAGTCTTACT CTGTCACCCA
119401 TGGTGGAGTA CAGTGCCATG ACCTCAGTTG CAACCTTTGC CTCCTGAGTT CAAGCGATTC
119461 TCATGCTCTT GGTCTCCCGA GTAGCTGGGA TTACAGGCAC CTGCCACCAG GCCTGGCTAA
119521 TTTTGTATT TTTAGGAGAG ATGGGGTTTC ACCATGTTGG CCAGACTGGT CTCAAACCTC
119581 TGGCCTCAAG TGATCTGGCC ACCTCGGCCT CCCGAAGTGC TGGGATTACA GGTGTGAGCC
119641 ATGGCGCCAG ACCTGGACTT TGTCTTCTGT TTCATCAGTC CTTCTGTTGG TTCAAGCACA
119701 GTATCACACT GAAGACTGAT GATTCTATAT AAATATGGTA AAGACTGTAC ACCCTAAGTG
119761 TTCTTATTTT TTAATTTTAA GGCAATTTTA GATTCCAGCT TTCCAAAGAA TTGTGGAATG
119821 CTTAGAGCTA GAGAAGCCTT GGAAGTCATT TAGTTTTTGT TTTGTCAGAG AAAATTCTGT

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119881	AGAGACTCTG	TCCTGCTCTC	ACTGAATACC	ATCCCATAGT	ACCCCCCAAC	AGCTTTAAAG
119941	GGCAATAATA	CCTTATGGAC	AGTATGCTTT	TCCTCAAATA	TATTCTAAGC	CATGGTCAAT
120001	GCAAAAGAGT	GAGAAGGAAA	GTAAGAATAAG	TTATCTAAGA	ATCAGTGGGT	GCTCTCTTTA
120061	AACTGATTTA	TCACTCCCCC	TTCCAAACTC	TCTTGAAGGT	CACTCTGCCT	CCCTTTCTAC
120121	ATAAGAACTC	CTAACTCCAA	GGGAGGAAGG	TAAGTTATTC	TTATTCCTTG	CTTAGAAAAA
120181	GAGAAAAATAG	GTTTGGTAAG	CATCCGCTTT	CTGCTACCAT	TCTCTGTGTT	TCTGTGTTTT
120241	TTATAGGATC	ATTCAATTAT	TGGTTGGCTC	TTGAGAGGGA	ATGCAAGGTT	CAAGGACACA
120301	AGCCTAGATC	TTGCCTGTAT	AGAACCTCAT	GATGTTATGC	TTCTCTAAAA	TGAGGCCTGG
120361	AGGAGACATG	TTGAAAGTGA	CCCATAAATC	TGCAGTATCT	CATGTCTCTC	AATGGGGACA
120421	AGGAGTACCA	TGGGAAATAG	CATTAGGTCA	ATGACAGTAA	CAACTCCCAG	GTGAGTTGAT
120481	TTATTCTTTT	ATTTATAAAG	TGTTAATAT	GCTACATAGT	CCCTAATTTT	GCCACAAATA
120541	GTCATTATTT	TAATTTTCATA	TTTCACTATT	GATAAATGAA	GGAAAAAATG	AGTAGCAGTT
120601	AAGCAGTCCA	TAAACCTACA	TATAAAGCAA	ATTGGAGATT	TTAAAATTGA	TTCTGGATGC
120661	TTAAAATCCT	TCTCATTGAA	AAAAAATTTT	GTATTAGAAG	ATTTCAACAT	TCTTTAAACT
120721	GAGAAGCATA	ACATATAAAC	AGAAAACCAC	AGCAAAACAA	AAATGCAAGG	CTCAATAAAT
120781	GAACACAAAG	TGAACACCAT	AATAATTGCC	ACACAAGTAA	AAAAACAGAA	AATCAGCCAA
120841	CCCTCCCGA	GCCGCCTGAT	GCTTGCTTCC	AGTCACATTA	TCACTCCATC	TGCCCTAAAC
120901	ATAACCCCTA	TTTTGATTTT	CAATGCTGTA	ATTTAGTATG	CCTGTTTTTG	AAACATATAA
120961	AATGGAAATA	AAACAAATGT	AATCCTATGT	ACCTGACATA	TTTCACTCCA	GAACATTAGG
121021	TTTGAATAGA	TTCATCTGTG	TTGCTGTGTA	TAACTTTAAT	TCATTTTTAT	TGTTATGTAA
121081	TATTCCATGT	TATGAGTGCA	ACAATTTAGG	TGTCTACTGT	TGATGCATAT	TTGCTTCCCT
121141	TTTTTCAGCTA	ATATAAACAA	TACCGTGAAT	ATTCCTGTGT	ATGTGTCTTG	GTATATATAG
121201	GAATACATAT	TTTGTGTTGA	TACCTAGGAG	AGGAATTGTT	GGGTCAAATG	CTAAACTCTT
121261	TTTGAAAGTG	GTGATATTAG	GTTTACATGC	GATGAAATGA	AAATTAAAAA	CACAGTTATA
121321	AACAGCATGG	ATGAACCTCA	CAAACCTAAT	GTTGATGGAA	TCTAGCTGGG	AATTCCTGTT
121381	CTTCCATATA	CTTCCCAATA	TTTTTTTCCA	ATTAAAATTG	TTAATCTTTT	GAAGATGTTA
121441	TCCATTGTGG	CAGATGTGCA	GTATTATCTC	ATTATGGTTT	TATTTTACAT	CTTTTGCCCA
121501	TTTTTTCTTA	ATTGGATTGT	ATATCAGTCG	ACTTGGGCTG	CCATAACAAA	AATACTAGAC
121561	TAGGTAGCTT	GAACAAAAGG	AGTTTATTAC	CTCACAGTTC	TAAAGGCCAG	GCCAGAAATC
121621	CTAAATTGAG	GTGCCAAGAG	ATTCACTTTC	TAGTGAGGGC	TCTCTTATTG	ACCTGAAGAT
121681	AGTTGCTGTC	TTAGATTGTT	TGGTGCTGAA	CAGAATACCA	GAGACCAAAT	AATTTATAAA
121741	GAATACAGAT	TTATTTCTTA	CAATTCCTGGT	GGCTATAAAG	CCTATGGTCG	AGGGGCCAC
121801	CTCTGGCAAG	GGCCTTCTTA	CTGTATATGC	AGATGTGAGA	TGTCATCTCA	TATTTCAAAC
121861	ACAGCAGTCG	CCTTTTGTGT	CCTCATGTGG	CCTCTTCATA	TGCCCATAAA	ATGACCTCAT
121921	GTCTCTTCCT	TTTCTTATAA	GGACACCAGA	TCTATCAGAC	TACTGGCCTA	CTCTTATGAC
121981	CTCATTTAAC	CTTAAATATC	TCCATAAAGT	CCCAAATCC	CTATCTCCAA	ATATAGGCAC
122041	ATTGGGTGTT	AGAGTTTCAA	CATCAATTTT	GGGGGAACAC	AATTTAGGCC	AAAAAGATTG
122101	TGTTTTTTCT	TGTTGGTTTA	AGATAGCTGT	CTTTTTGTCC	TTTTTGTCTT	TTCTTTTTTT
122161	TTGAGGTGGA	CTCTTGCTGT	GTCACCCGGG	TTGGAGTGCA	GTGGCGCTGT	CTCAGCTCAC
122221	TGCAACCTCC	ACCTCCTGGG	TTCAAGAAAT	TCTCCTCCTC	CCAAGTAGCT	GGGACTACAG
122281	GTGCATACCA	CCGCGCCCTG	CTAATTTTTG	TATTTTTGAT	AGAGACGGGG	TTTCACCATG
122341	TTGGCCAGGC	TGGTCTCAAA	CTCCTGACCT	CAGGTGATCC	ACCTGCCTCG	GCCTCCCAAA
122401	ATGCTGAGAT	TACAGGTGTG	AGCCACCAAA	CCTGGCCTGT	CTTTTCTGTT	TTAAGTTTTT
122461	AAATTTTGCT	CACGAACCCT	TTATCCATTT	TATGTGTTGC	AGGTATTGCC	TCTGTAACTT
122521	GTCTTCACTC	TGTCAGAGGC	TGGAGTGCAG	TGGCACAAATC	ACAGCTCACT	GCAGCTCCA
122581	CCTCCCAGGA	TCAAGCGATC	CTCCCATCTT	ATCCTCCTTA	GTAGGTGGGA	CTACATGTGC
122641	AGGCCACCAT	GCCCAGCTAA	TCCTTGATAT	TTTTTGTAGA	GATGGTGTCTG	TTGCCCAAGT
122701	TGGTCTCAAA	CTCCTGAGCT	CAAGCAATCC	ATCAACCTTG	GCCTCCCAAA	GTGTTGGGAC
122761	TAGAGGTGTG	AGCCACCACT	GCACCCAGCC	AATGATATCT	CATGATGCAT	TAAAGTCATT
122821	AAATTTAGTG	ACTCAAATTA	AGCAACCTGC	CCTTTTATGC	ACAACCTTTT	TTGTATCTTA
122881	TTTAAAAAAT	CATTTTCTAT	TTCAAGGTCA	TGAAGATCTT	ATTTTATAAT	ACCTTCTTGT
122941	GAAATTAGTT	CTCAAGACTA	CCCTCACTTC	TAACACCAAT	TATAAGTTGG	GAGGTCTGTG
123001	GTTCCCAATC	AACCTTAGGT	TAGTAATTTG	CTAAAAGGAC	TCACAGAACT	TGCTGAAGCT
123061	GTTAGCCTCA	TGGTTACAAT	TTATTATAGG	ATATATAGCT	TATTATGTCA	TTCCAATGCA

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123121	ATGTAAAATT	ATACAACTAC	TTTTAAAAAG	ATTTTAGCAT	TTGACCCAAC	AATTTCACTC
123181	TGAGGTATAC	AAACAGCAGA	TATGTGTGCA	CATATATACC	AAGACACATA	CACAGCAAAA
123241	TTCATTGTTT	GTAATAGTTG	AAAAGGGGAA	ACAACTCAAG	GAATAAAGAT	TAAAAATCAGC
123301	TGAGAAAAGA	AACACACAAG	GCAGTATTAT	GGATCGAATT	GTATGCAGAT	CTCCCTTGCC
123361	CCCAGAAGAT	ATGTTTAAAG	TCCCAACTCC	CAGTACCTCA	GAATTGTGGC	CTTATTTGGA
123421	AATAGGATAG	TTGCAGATAT	AATTAGTTAA	GATGAGGTTA	TAGTACAGTA	TGATGGGCTG
123481	GTGACTTAGA	AGAAGTAGTA	TATATATATT	TTTTAATAGA	ACTAGTATTC	TTCTAAGGTG
123541	GTCACGTGAA	GACAGACACA	CACAGGCAGA	GACTGAGGTT	ATGCAGCTGC	AGGTCAAGGA
123601	ATGTCAAAGG	TTGCCAGCAA	GTACGAGAAG	CTAGGAAGAG	TCAAGGAAGG	ATTTTCTTAC
123661	AGGCTTCAGT	GGAAGCATAG	ATCTAATGAT	ACCTTCATGT	CAGATTTCTA	GCTTCCAGAA
123721	CTACAAGAGA	ATATATTTGT	TGTTTTAAGC	CACCCTAGCT	TCTAGCTCTT	TGTTACAGCA
123781	GCCCTAGGAA	ACTAATATAG	GCACAATCCA	GGCAAGTTCC	AAATATGAGC	TTCCAGTTGT
123841	CCTCTCCAG	TAATATGAAC	AGTATTACTT	TCCCAGCATT	AATGTGTGAC	AATACACATG
123901	ACGTACAGAG	CAGTCCCCAC	TTATGCACAA	AACATATGTT	CCAGGACCTC	CAGTGGATGT
123961	CTGAAACCAT	GGATAGTACT	GAACTCTATA	TAGCTGTTTT	TTCTTATACA	GACACAGCTA
124021	TGATAAGGCT	TAATTTATAA	ATTAGGCACA	GTAAGAGATT	AATAACAATA	AATTAGAATA
124081	ATTGTTAAGA	ATATACTGTA	TAAAAGTTAG	GTGAATGTTT	ATTTCTGAAA	TTTACCGTTT
124141	ATTATTTTTG	GACTGCAGTA	GACCACAGGA	ACTAAAACCA	TGTAGAAACC	GTATACAAGA
124201	GAACTGTATT	TCACCCGAGC	CTCAGTGTGC	AGTTTTAATG	GCCTGCCATG	GTTGACTGCT
124261	CACATGGCCG	ATCTTTTAGT	CTACCTCCAC	AGGTAGAGCT	GATACTGTGT	GGCTCAAAGT
124321	TCCTATTATA	AATCACATTG	TTGACTGTGT	GGTGGTCAA	ACCTCCAGGT	AAACAAAGAC
124381	ACACTTATCA	GTGAGAACAT	TTCAAGGGTC	TAAAATTTCAT	CTCCAGTAG	CTGAGGGCAA
124441	AGGCTAGACC	TCTTTTGGG	TAAAGATAAT	TTTTTACCAT	ATACTTTATT	TTGCTTTTCA
124501	TGTTTAACTT	TATTTTGCTT	TTTCATGTTAG	TTCCCCTGGA	ATTGTTTTTT	GTGTATAGTG
124561	TGAAGTAGGG	GGTCAAGTTT	CTTTTTTTTT	CCTTTTGTG	CTTTTCTGT	TTAAAAGGCT
124621	ATACAATTGT	CCCATGCCAT	TTATTTACAA	GAGTCCTTTC	ACCATGTGTT	TATGGTGCCA
124681	CTTTAGATGT	AAATCAATGT	CCATATTTGT	TTGAGCCTGT	TCCATTGCTT	TGTCTATTTT
124741	TGGACAACAC	TGCCCTGATT	ATTGTCATTT	TATCAGTTTT	GATATTTAAT	AAAGCAACAG
124801	ATTTGTTTAT	TTTGGGCCCT	TGGATTTGTG	TATTAAATTT	GAACCCTGTT	TGTCAATTTT
124861	TATAATAAAG	CTTATTGGGA	ATCTGATTAG	GATTACAATG	GTTTGTGAGA	TCAGTTTGGG
124921	GACAATTAAT	ACCTTTAAAA	TATTGACCGC	TTCAACTGTA	AATATACTCC	TCCATTATTT
124981	AGTTTTCTCT	TTTAATTTAT	CTGAGTAATA	CATTATAGTT	TTCTTCGTAG	AAGTCAGATA
125041	CGTAGAAAAT	TCAAAGCCCC	AGTGCAATAG	CTCATGTCTG	TAATACCAGC	ACTTTGGGAG
125101	CGCGATGTGG	GTGGATCACC	TGAGGTCAGG	AGTTTGAGAC	CAGACTGGCC	AACATGGTGA
125161	AACCTCATCT	CTAGTAAAAA	TACAAAAAAT	AGCTGGGTGT	GGTGGCGGGC	ACCTGTAATC
125221	CCAGCTAATC	AGGAGACTGA	GGCAGGAGAA	TCGCTTGAAC	CCAGGAGGCA	GAGGTTGCAG
125281	TGAGCCAAGT	TCCTGTCACT	GCACCCACCC	CTGGGCGACA	GAGCGAGACT	TCGTCTCAAA
125341	AAAACAAAAA	AAAGAACATT	CAAATAATCA	ATGTAGATAA	TTCAAATAAC	TAAAAATGA
125401	ACAGTTATTA	AAATATCAGG	ATATAAAAGC	AAAAAAATCA	ATAACCTCCA	TATATACAAA
125461	ATGGCCAGTT	AGAGAAAAAA	AAAAGAATAG	GCGAGACTTA	AAAAGGCTGG	GAATCTCCCT
125521	GAAAATCTTT	GAGAGCCTTG	GCCCTGCCCT	CAGGGATTTC	TCTGGCTTCA	TGCCCAGATA
125581	CGGGTACAGT	TCCTTGTTTA	AAAAAATTTT	GCTCCATCAA	TCAACAAGGG	GCTCCTTCCT
125641	CAGAGCACAA	GGACCTCCAT	AACACCGGAC	ACTAGATGTC	TAAGGGACAC	CTCTTAAGGA
125701	AGTTAGACTT	CCAAAGAATG	GTGTTTCCTC	TGTCCCAAA	CTCTGGAAC	CACAGCACAA
125761	CTGCTCCTTG	GAGTTCGGTT	TCAAATCTAC	AAGGCTGTCA	TGGAGGTTGC	AGACCAAGTC
125821	CGTGGCCTCA	GTGTCCGGAT	GTACGGTGGC	CTTGGCACCT	GAATGTGAGA	ACATGACCTC
125881	CCTGAAACCA	CCACAAGTAT	TGTTTCATGT	TATGTATGTT	TTTTCTTATC	TGAAATTCCT
125941	TTTCTTTAAA	AATTCAAATT	ACATATTTTG	CAAGCCCCTG	AACAAGCTTC	ATGAGCATTT
126001	ATTGAACCCA	CAGCTTTTAA	AACCTACTGA	ACACTTTGCT	CTATGTTGTC	ATTCACTATC
126061	CACCAATTAT	TTAATTATTG	ATCAATATTG	TTTCCTTAGT	GTTGGGATCA	TTTATGCATG
126121	TATTTCTTTT	ATATTGCATA	TTTATATTTT	CTGCATTACA	GTTATTACAT	ATTACTTTTG
126181	CTACAGTAAT	AGTTCAAAAA	TGTACATCCA	AAATTTAGCT	GTGAAGTGGA	TGGACTGAGG
126241	CAGAACTGGA	GGCAAGAAAA	TGTCACAGTA	ATTCTAAAAA	AGATGATGTA	CAATTAGAGC
126301	AAGAGAGTAG	CACTGAAATT	GAAGAAAAAT	AGATGCGTTT	GAGAGAAAAA	TAGGAGGTAG

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126361 AATCAACAGA TTAGATGTAG GGATGAGAAG GGTCAAAGAT GACACTAGGG TTTTAACTG
126421 GAGCAAGTAG GTAGACAGAA CATTTCTTCC TGAAAGGGCA GGTGAGATCA TGTGTTGTCT
126481 CAAAGGGCAT GAAGAGTAGA AAGCCTGGGA CAGATCCTGA GATGACCAAT ACCCATGGTG
126541 CAGGGAGAGG GAGGGAGATC TGCTAAAAAG ACTGCAAATG TCAGGATAGT AGAAAATCAT
126601 GAGTGTGTGA TGTCTGGAA GTTGAGACAG TATCACATTT GAGAACATTT AAATTGGTAA
126661 CTCTGACAAA AAGCTGGAGG CCAACTGTGA ATGCCCATGA GAGTGAGAA GGATCCTCTT
126721 TTTGTGGGCA TCAGAAAGCC CACCAGGTTT CTGCAGTGAA GATCTGAGAA GGATCCTCTT
126781 GTGGCTTTGG CAGGGAGAGA AGAATTATTA TGAAATACAC CCCAGAACCT TCTTCAAAAC
126841 AAAGGCCTAC TCTCAAGGGG AAAACATTTT GCCAGAGTCT TATCCCAGCT GGGAGAAGGT
126901 AATTCTTCCC ACTGCAGCCT CATCTAGGCT TTCTGTCTCA CTTAAGGGAA GAAAATTAGT
126961 CAACAGGGAT CAGAGCTTCA TGAAAATAAA TTGGAAATGG TGCAGCCAGG AAAGGAGCAA
127021 AGGTCTGAGG AGGAGGAGAA GGAGGAAGAG GAGTTGTATC ATTATAAATA CTTGAGGAAG
127081 AGGAGGAGAA GGAGGAGGAG GAGGAGTTGT ATCATTATAA ACACTTGAGG AAGAGGAGGA
127141 GGAGAAGGAG GAGGAGGAGT TGTATCATTAA TAAACACTTG AGGAAGAGGA GGAGGAGAAG
127201 GAGGAGGAGG AGGAGTTGTA TCATTATAAA CACTTGTGAC GGTCCCAGCC CCAAGATATA
127261 GGCATGCTAA TAAACTGAGG CTAAACATTT TGAACACAGA ATGCTGCTTC TCCCTAACAC
127321 CATCAAGGCT CCAACTGAAT AACAATGAAT TATGAATGAA AGAGCTGTAA GGAGAGACAA
127381 AAGTTAGAAT GAGACAAGTA TTGTTATCTA GAGATGCCAA GAAGGCAAGG AAGATAACTA
127441 AAAAGGCACT CTGGATTAGT AAATAGGAAG TCATTAGTGA CCTTGTAAT AATGGAGCCA
127501 GAGGAATACC AAGGGCAGAA GCCTCACTAT AGTGTGTTGC ACCTGTCAGA GGTGAGGAGG
127561 TGTAAGTAC TCTCCACAG TGTGGCTTTG GAAGAGAGAA GTCAGCAGCT GCATGGAGAT
127621 TTGGGAGAGG GAAAGCTTTT TTTTTTTTTT TTTAATTGGA AAAGACTGAG CTATGTGTAA
127681 ATAGAATAAG ACAGGAAGAG GTTAGACACA GGAAAGAGGG CAGACAAAA CAAGTGCACA
127741 GTTATCTAAG GGAAACAATG GGATCAAGCT GCAAGTATAT AAACCTGTCT TGATAGTACA
127801 ATCCTTGATC TGGTTTATTC AGTGTGTTGGT CCAAACCCAC ATCCCTGTTT TGCCTGTCTC
127861 TGAAGTGTCT TGTGCCCCAG AAGCCCAGCT TCTACAGATA GCATTAGCTG GGCAGCCCTG
127921 CCCTCTTGCA ACAGCTGGAT TTGGCCAGTG ATCAGCCCAG CAGGAATGTA GATGGCAAAG
127981 GAGAGAGAGG TTAGTGTACT TATCCCTGCT ATCAGCCCCC TGCTTGGTGG GCAGCTCTTC
128041 CTCCACAGTC CCAGCTCTGG CCTAGCTCTG GTTACAGGTT CCCTCCATT GCCTCTTCAG
128101 ATTTAAAGGT GTGTCTGTCA GGGTATAACT GGGAGCTAGA AATTGCACTG AAATTGAACA
128161 AAGAATTTTA TGGGAATGGT TGTAACTAG TTATAAGAGG ACTGAAATG GAAAAGTGGA
128221 CAAACGTATC AGAGATAGTA ATGACAGAAA GCAACTACCA CCTCCAGGTT TAGGAGAACA
128281 AGGAAAGAT TCTTTGAAGA GATCCCCAGA ACTGGACCT CTGAGGAGTG TATGCTGGAC
128341 CACTGATGAT GATATGTCTG TAGATAGAGG CATGATGAGG CTGATTTTAG GAGCATGGAA
128401 GATCTCCAAA CTGAAGCCAA CTGCTGTTAC TGGATTCAAC TGCCACTGCC AGGTTGAAGA
128461 ACCCATCTG TGAGGATGTC AACAAACAAA GTGGGAAATC TTTTCACATC CTTCCAGCCC
128521 TCTAGTCTTC CTCCAGTGCT TTCTATTGGT AGGGTTTGGG GAGGTGGCTA GCAAAGCGGT
128581 ATTGGAAAAG ATAGAAGAGA CTAAATCTTC ATAACCAGCA CAGGGTGACA CTGGATCACT
128641 ACTGTTGCTG ATCTTGGGCT GCCTCATATC CCCTGTTCTT CCCATTAGCC CTGTCAACAAC
128701 TTTGTAGATA TCCCTTCATT ATATGCCCTT CATATATTCT TTTGGTTTAA CTTTTTCTGT
128761 TGGAAATCCTA ATATGGCACT CCTCCATTTT TCAGGACCAA AAGAGTATAA AAGATTATCT
128821 TTTACCAAAA AAAAGACAAA AAACGTATCT AATTCCTGAT TTGATCATT CACAATCTAT
128881 ACATGTATCA AAATATCACA TAGTACCCCA TAAATATATA CAACTGTGTC CATTAAAAAT
128941 AAAAATTAAG GAAAAGATGG TAAATATAGC TCTGTCAGGC AGTGGAGGTT TTACCACGAT
129001 GGCTGTATT TCCCCATGA AGGGGGGAGT GAGGGAGCAG CTGAAAGTAG GTGCTTATAG
129061 GGGTATAGAG GGGCTCAAAG CTTTGAGAGA GGAGAATGTC TGAAAGAGCT GCCAAATAGC
129121 ATGCAGGTCC CATGGGGGCA GAGCCTCTGC TCATTACCA GTGCCTCTTC AATATCTACA
129181 CTTAAGCCTA ACACAAAGTG TGTGCTTAAT AAGTATTTGC TGAGTATGTA AAGTGGAAC
129241 AGAACCAATC TGGCAAACTT TGTAGGACTG GTGGGCAATG AAGATCAGTC AGGTAAAATC
129301 TGTGATATA AATTTATAT GATCAAAAAA TTCAAGGTTA GGTGTTTTTC TTCAGTCATG
129361 CTCACGATG CTTACGCCAT GCTCAACTCT TCTGTAGCCA CAGAAAAAAG TTTACCCATA
129421 ATCGAGCTGT GTCTGTGTCT GAATAATGAA AAGACCATGA TGCAAGGGAG TTGGAGACAC
129481 AGAAACAGTG TTTGAAGTAA TGGGTAATGG AAGCATGCTA CCAGGGAAAG GAAAGAAGTG
129541 GCAATAGGAA GGAACAGAGA TCTGTGTCTC TATGTCCCTT GAGCATATTC ACATGTTAAA

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129601 GCTAATTCAG TTTTCAATCA TCATTAAAAAT TTTGTTCCCTA AATATATGGC CATTATTTTC
129661 CACAACCACA CTAAACTTT ATTACCTCTG GCAAGTGACT ATGCAAGTAA CTAAGAGCAA
129721 AAATATCCAC AACTACCATT TGAGCTATCA ATTTAGGGAA AGTCATCTGG CTATAATCTA
129781 AGTGACCCCTC CACTGAATGT CAGTATCTTT GCATATGTGA TTTAAATCTG GGCCTTCGCA
129841 ACACCATGAA CTGTTCTTGT CTTGAATATC CAGATTGAAG GAAATAATCT GAGTAGTTAC
129901 GAGTCTGAA GCTAGAAAGA TGGAAACCCC ATTTGCTCAT CAGAAAGCCT TAGAGCTTGG
129961 GCGCTGGCGG GTCCTGTCTC ACCGGGACAG AGGGGCTCTT TCCTCCCCAT CTGATAGTCT
130021 GATAACTAGA GAAGCCGCC AACTTATTCT CCAAGAAGGA GCCATCTTAG TTCCTCCTGA
130081 AATGTTTATA TTTAGAAATT ATTGTTTGTC AGTAATTTAA CCCCTTAATG GGCTTGCTT
130141 GTGGTCCATA CCACTGAGTG CAGAGCTTGC CTGGAAGAAT TGTGAGGGCC ATTCCATCTT
130201 CCAGGCAGTA GAGTTCAGTA CTTCTTTAAA ATTGCTGCTG AACTCTGTAT TTGAAAAGAA
130261 AGAATCATTT GGGTGTGGTA GCTCACACCT GTAATCCTAG CGCTTTGGGA GGCTGAGGTG
130321 GGAGGATCAT TTGATGCCAG GAGGACCACT TGAGACCACC CTGGGTAACA TAGCAAGACC
130381 CTGCTTTTAG AAAAAAAAAA TACAATAAAA TAAATACAAAT AAAAATAAAA GCAAAAAGAA
130441 AGAGTCCATC TTAGGGACAG ACTGTAACTA CTCCTGGAG CTTACCTTTA CATAGTTCAG
130501 GATCAATTAT AATAAAACAC TTTTGTGACAG ATTCAATAGG ATTATTTTAA TCCCCATCAT
130561 CTCTCTGAGT TTCCAGTCAG TTTCTCTGCA TGTAGACACC CTTCTCCAGC CCACCATTGT
130621 CTCTCCTCCT ATAGCTCCAC CAACAAATCA GAACTTTTTC TAACTGCACC TAGTGCACCT
130681 AGAGTCTACT CCAGAATGCT CATGGAGAAA GTTCTGAAA GGTAAACTC TGAATGATAT
130741 TTGTAGCTAA AGGGAGACTT GCTAGAGACA ATAAGCTAAT AGTTGTAGAC TTCAGTAGAA
130801 GAGGAATGAC ACTGCAATGT CAGGGTGCAG GACTTCAAGA GGGCAGAGTA TGGAAACCCA
130861 ATGGGAAAAA TGCTCACCAG GAACATGAAG AGAAGGAATT ACGTGTAAGG ATTTCTCAAT
130921 GTGTTCCCAA ATTTGCCAG CAGAGGGAGG CCTCGGGTTG ATGGCAGGCT GACCACACAA
130981 TTAAGAAGG CTGAACCTGG GGGCTTTTAA CAACCATCGT GGGCTCTACT GTAAGCATTT
131041 AGAAAAAGAA AGTTATCCAT TCAAAAATAT ATATATTTT AAAACTCAGA ACAAATTAT
131101 GAAGAGCTAT ATTTACTTTT CTACATTTCTA ATTTTATAA ATCTGAGTAT ATTTGCATA
131161 TATTGTTATA GTACATATTC AATTTTGAT TTTGCTGTTT TCACTTAACC ATTTTACTA
131221 GATTACTCTG TGTTTATAAT AATCACTTTT TTAACACTTT TATTTTATT TATTTATTTT
131281 TTTTTTGAGT CAGAGTCACA CTCTGTCGCC CAGGCTGGAG TGCAGTGGCG TGATCTTGGC
131341 TTAAGTCAAC TTCCACCTCC TGGATTCAAG CAGTTCTCCT GCCTTAGCCT CCTGAGCAGC
131401 TGGGATTACA GGTGTGCACC ACCAAGCCCG GCTAATTTT GTATTTTATG TAAAGACGGG
131461 GTTTCACCAT GTTGGTCAGG CTGGTCTCCA ACTCCTGACC TCATGATCTG CCCACCTTGG
131521 CCTCCCAAAG TGCTGGGATA ATCACTTTT ATGCTGCATA ATTCTTCAGA TTTGTGAGTA
131581 CGACTGTATT TACACTCAT TGTTTTATTA GAAAGAAATC CAGAATATT TGGCTGCCCT
131641 AATTAATTTT ACAATTAATA TGATTTTGAA ATTGGGTATT GGCTCCTTCT GAATGGTTT
131701 ATTAAATAT ATTCTAATGT AATTTATGAC ATTTTCATCA TATTAGCATA TTTATTCTGT
131761 TAGAATTTCA TAATTTATAA AGCTACAAAC TGTATGTGAT ATAGCTTGTA ACTTTATCTC
131821 ATAACCTTAT GCAGTTACAA GTAGAAATAA AATGTTCCCC TCAAGATTGC TTAATAATTT
131881 ATTATAAACA AGTGTAACAA ACAAAATCAC TAAAACACTC CCTCTTTTTT CCCCCAAAT
131941 GCATGTTTCC ATTTTAAACAG AACCCGTATT TAATCAGCAG ATTTCTATGG TGGCTAGATT
132001 TGTAAGCTAA ATATTAAGAG TCCCAAAGCA AATGCATTTT TCTCTTAAAT TTTACTGACT
132061 TTTTTTTTTT TTCTTTTCT GAGACGGAGT CTGCTCTGT CGCCAGGCT GGAATGCAGT
132121 GGCACAACTC CGGCTCACTG CAACCTCCGC CTCCCGATT CACGCCATTC TCCTGCCTCA
132181 ACCTCCCGAG TAGCTGGGAC CACAGGCGCC CGCCACCAG CCCAGCTAAT TTTTGTATT
132241 TTTAGTAGAG ACAGGGTTT ACCGTGTTAG CCGGGATGGT CTCGATCTCC TGACCTCATG
132301 ATCTGCCAC CTCAGCCTCC CAAAGTGCTA GGATCACAGG CATGAGCCAC CGCGCCCCGC
132361 CTACTGACTT TTATCCAAAG AAAATATAAG AGCTCTTCAT CATAACGTAT GTTCTTGCT
132421 CTTGTTATTA AATATGACAC ATTTAGACTT AAAGTATTT GAAGGTTTAT GACATTGTTT
132481 AAGTTATTAC ATAATTAATT CATAAGATA ATGACTAGTT TGAAGTACTG ACAGCTCACA
132541 CATCATCAGT TGAACAGCAG AAAGCTTACT AAGCTACTTT CTTATGTTT TGTCTCCAG
132601 CTACTAAAAG AAACGAAACC CTTCCAGGTG TTAAGGCAAA ACTTTCCTCC CCCTTCTTC
132661 TATAAATCTG ATTCCATGTT AGTGAAATTT CTACTGATGG CTTTGGTTT CTCTATAGTA
132721 GAATAGAGAT CCTATGGCAA AAGTCATGTC TGACATGGTA GCAAATAGAA ATGGGGAAAA
132781 GGAAGGTCTG CAAGAGCCAA TGTGGGAAAT GGGGAGAGGA CTGACTACAA AAACCCAGCA

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132841 GGAATTCCAG AAGAAAACCTC CTCAGGACGG GCACATTGGC TCATGCCTGT AATCCCAGTA
132901 CTTTGGGAGG CCGAGGTGGG CAGATCACTT GAGTCCAGGA GTTTGAGACC AGCCTGGTCA
132961 ACATGGCGAA ACCTCATCTC TACAAAAAAT AAAAAAATTT GTCAGGCGTG GTGGCATGCA
133021 CCTGTAGTCC CAGCTACTCA AGAGACTTAA GTGGGAGAAT CACTCGAGCC TTGGAGGTGG
133081 AGGTTGGTGA GCCGAGATCA CGCCACTGCA TTCCAGCCTG GCGGACAAAG TGAGACGCCA
133141 TCTCAATCAA TCAGTCTCCT CGAAAAGCAA CATTATGGAG AGACAGGATT CCGTCAAGGC
133201 CTGGGGCACA CAGGAAAATA TTAAGGCAGA AGAGAGTTTC CTCCCCACAC CACACCGTAT
133261 CCCACAGGCA CTGCGGATGT GCATATGCAA GAGGGGTTGA TCCTAAGAAT TTAGAGTCAC
133321 AGAGGAGGAG GCACCAAGCA GACTGTGGAG AAAGTCATGA CCAGAAAGGG ACAGAATGTA
133381 AAGCTTCAGC TGATTATCTG GCCTCAGGGA TTCCAGAGGA ACTGGTCCCA ATGGTCTCCT
133441 GGTGATGTAG GTTCTTAGGT TTCTTTTACA GGGGTTTTCT GGGAGATCGT TGACCCAGTT
133501 AGCATTCAAG CAACTTCCAC CCTGCACTTT TATTCTTTCC CCTTCACCTG CTTAGGTTTT
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133621 TAAAGATGAT GCCTTCTAAC TCCTCATTCA ACAGATACAA AAACATTACA ATAAAATGAC
133681 TCATGCAAGA CACCCAGGTA GTTTATAGCA GCTAATAAAA ACAGAATAAC TATAAAATAT
133741 GGTAAGTTTA TAAAAGTTAC ATTGAGTATA CTTTATAAGA ACTGCTTATT GAGTTTGCCT
133801 AATAACCACA CAGCACAATA ATAATATGTA TATATTTTTA AATATGTGTA AATATGTGTA
133861 ACACAACTT GTAGAAGGTA TATCTGAGTA CAACCCTATT CTGTTTGGTT ACCTTTTCTA
133921 GTTCATTATG TAAGTGGCAT AGCTACCTAA GGACTTATGC TTATAAATGT TACTCAAAAA
133981 AATACAGAGG ACATATGTGG ATAGATAATG GAAGAGATAA GATAGGTAGG TTGAAGGGTT
134041 GGGCTGCCCC TCCACACCTG TGGTTGTTTC TCGTTAGGTG GAATGAGAGA CTTGGAAAAG
134101 AAAGAGACAC AGAGACAAAG TATAGAGAAA GAAAAAAGG GGTCCAGGGG ACCGGTGTTC
134161 AGCATACGGA GGATCCACAC GGCCTCTGAG TTCCCTTAGT ATTTATTGAT CATTATTGGG
134221 TGTTTTCTCG AGAGGGGGAT GTGGCAGGTT CAAAGGATAA TAGTGGAGAG AAGGTCAGCA
134281 GGTAACACG TGAACAAAGG TCTCTGCATC ATAAACAAGG TAAAGAATTA AGTGCTGTGC
134341 TTTAGATATG CATAACATA AACATCTCAA TGACTTGAAG AGCAGTATTG CTGCCAGCAT
134401 GTCCACCTC CAGCCCTAAG GCAGTTTTCC CCTATCTCAG TAGATGGAAT ATACAATCGG
134461 GTTTTACACT GAGACATTCC ATTGCCCAGG GACGAGCAGG AGACAGATGC CTTCTCTTG
134521 TCTCAACTGC AAAGAGGCGT TCCTTCCTCT TTTACTAATC CTCCTCAGCA CAGACCCTTT
134581 ACGGGTGTCG GGCTGGGGGA CGGTCAGGTC TTTCCCTTCC CACGAGGCCA CATTTTCAGAC
134641 TATCATATGG GGAGAAACCT TGGACAATAC CTGGCTTTCC TAGGCAGAGG TCCCTGTGGC
134701 CTTCTCAGT GTTTTGTGTC CCTGAGTACT TGAGATTAGG GAGTGGAGAT GACTCTTAAC
134761 GAGCATGCTG CCTTCAAGCA TTTCTTTAAC AAAGCACATC TTGCACAGCC CTTAATCCAT
134821 TTAACCTGA GTTGACACAG CATATGTCTC AGGGAGCACA GGGTTGGGGC TAGGGTTAGA
134881 TTAACAGCAT CTCAAGGCAG AAGAATTTTT CTTAGTACAG AACAAAATGG AGTCTCCTAT
134941 GTCTACTTCT TTCTACACAG ACACAGTAAC AATGTGATCT CTCTCTCTTT TCCCCACAGG
135001 AGGTGATGGC CGGAAGAACA TGGCAGAGGG CAAAACAAA CAGCATTGGG AACAAAGCTCT
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135121 ATGGAAGACA AATGTGTACT GCGTGAGTTT TAAGGCAATA GGAGTAGTGG GACCTAGGGC
135181 ACACCAGAGA GCATATTAAC TCTCAAACCT TTAACAAACAT TATATCTGCT GGACACAGTG
135241 GCTCACACCT TAATCCTACA ACTTTGGGAG GCCGAGGCGG GCGGGTGTAG CTTGAGCCCA
135301 GGAGTTCGAG ACCAACCCTG GCAACATGGC AAAATCCCGT CCCTACAAA CAAACAAACA
135361 AAAACAAAAA TTAGCCAGGC ACGGTGATGC GTACCTGTGG TCCCAGCTAC TCAGAGGCTG
135421 AGGTGGGAGG ATCGCTTGAG CCCCAGGAGG TTAAGGCTGC AGTGAGCCAT GATAATGCCA
135481 CTGCATCTCA GCCTGGGCAA CAGAGGGAGA ACCTGTCTCA AAACAAAAAC AAAACACAC
135541 CATACCCAAC CACAATGCAT CTGTCTTAAG TACCAGTACC ACACCCCTCT ACTCACTACT
135601 AAATAGGTGA GTTCCCAATC CCTGGTAGCA GGTTTAAGCA TGTTATATTA AAGGTCTTAG
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135781 AAATGGAGAT GTTTTAGGCA TCTACTCATC ATTCTGAGCT CCATCTTTTG TGACTGTAGT
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135901 TGCCCAAAGG ATCCATCCTG ATGGCCCTGT CTGCTTACCT TACCTGCCTG CCTTTGCAGC
135961 ACCGCTCTGC TCTTCTGCAG GACTTCCCTT ATCCTTTGGG GTCTTGCTGC TCTTAGGCTG
136021 CTCTGCTTGT TTTGATCTGC TTTGCATCAC ATGTATGTAA AGGTCCTTTC CTTATTTACC

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136081 CATGACCAAG GTATTATGAG ATTCTGGAAT TTCCCCAAAC CACATTGATT GCTGGGAGAA
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 136201 AATCCATTTA GAGAGACCTT TCTCCAGTGG TGACTCAAAG ATGCAGCTCC TTTCATCCTG
 136261 TGGCTTGGCC ATCTTCAGCA CATGGCTCCC AAGGATGTCC TCAGGATGGT CTCTAATCCA
 136321 AGGAGCCTGA AGAGAAAAAA AGGCATGGAG TATTGTGAGT GGTAGGTGGT TATGGACCAG
 136381 TTATGGAAGA ATACACATCA CTTTTGCCCA CCTTCTACTA ACCAGAAGTC ACACAGCCAT
 136441 AGACACTGAC AAGTAGGACT TAACAAGAAT CTAATTTTGA GTCTAGGAAT ACGACTGTAG
 136501 CAAATATTTA ACAGCTTCAA ACACAGGTGC ATTGCTATCA CTATGCTTGG CCCAGGCCTG
 136561 TCTCCCTTTC CTGCCATGTC ACAGGGGCCA GCATTTATGT CTAGATTGGG TTGGTTGGGA
 136621 TATTAAGACA ATAATGAACC AATACAACAT CTTGAGCATA AAACCAACTG ATACAATGAT
 136681 GTACAAGTCA GATGATTCTG ATGATTATGA ATTATGTCAA TAAAAGAAAT GTGATAACTA
 136741 AGGTAATTTT TGTTTTGGCA AATTTTTGTT TGTTTCATGAC AGGATGAAAT CCTGTCATTT
 136801 GTAGCAACAT GGATGGAATT GCAGGATATC ACATTAAGTG AAATAAGCCA GAAACAGAAA
 136861 GTTAAACACC ACATGTTCTC ACTTATATGC AGAAGCTAGC TAACTAAGTA AATAAGTTTA
 136921 TCTCATTGAA GTAAAAAGTA CAACAGAGAT TACTAGAGGC TGGGAATGGT AGGGGAAAGA
 136981 GATGATAAAG AGAGATTCGT TAAAATAAGT TACAGCTAGA TAAGAGCAAT CAGTTCTAGT
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 137101 AAAAGAGGAC ATTGAATGTT TCCAACACAA AGAAATGAGA AATGCTTGAA ATAATGGATA
 137161 TTCTAATTAA TTACCCTGAT CTGATCACTA TACACAGTAT GTATAAAAAAT AACACTATGG
 137221 GCTGGGCGCA GTGGCTCACA CCTGTAATCC CAGCACTTTG GGAGGCCAAG GTAAGCAGAT
 137281 CACTTGAGGT CAGGAGTTAG AGACCAGTCT GGCCAACATA GTGAACTCC ATCCCTACTA
 137341 AAAATACAAA AATCAGCCAG GCGTGCTGGC ATGTGCCTGT AATCCCAGCT ACTCAGGAGG
 137401 CTGAGGCAAG AGAATTGCTT GAACCCAGGA GCGGAGGTT GCAGTGAGCC GAAATCGCGC
 137461 CACTGCACTC CAGCCTGGGT AACAGAGCAA GGCTCTGTTT CAAAAATAAA TAAATACATA
 137521 AATAAATATT TTTTAAAAAA AGAACATCAC TATGCACCCC ATATATACAT ATAATTATTA
 137581 TGTCAATTG AAACATAATT TTGAAAAATG AAAAAATGAA ACACAAATAT GAATCAATCC
 137641 TCTCCAAGTT GATATACTTA AAAGGAAAAA AGTCCGAGGG CTAAACTAT TCAATCAAAA
 137701 TTTTATTAAA ATGCTATAGT AATCTGAAA GTATTTTACA ATGAATTGGT ATAAGGTTAG
 137761 ACACAAAGAT CAGTGAAACA AAACAGAGAA CCCAGAAATA GATTCACACA TCTATGGACA
 137821 ACTGTTTGTG ACAAAGGTGT CAAGGCTATT TAATAAGTAA AAAAATCGTC TTTTCAGTAA
 137881 ATGTTTCTTG AACAAGTAGA CATCCGGTGT GGGGGAGAGG AGCAGGAGCC TTACCTCAAA
 137941 CTTTATGCAA AAATTAATCT AAAATAGACC ATAGACTTAA ATGTAAAAGC TAAAAATATA
 138001 AAACCTCTTT AAAAAATAGG AGAAAATCAT CAACACCCTA GGATTAGCAA AGATTTCTTT
 138061 AAAACAAAAC AACAGGTTTA TAGTTTATAA AACATAAATA ACAAATGAT AAATTTCTATC
 138121 AAAAGTGAAA ATTTGCTTTT CAAAAACAT TATAAAATGA AAAGCAGGAG GCTGAGGCAT
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 138301 AAAAGAAAAA GAAAAATCAC AGGCTGAGAG AAAATATTTA TAATACATGT ATCTGACAAA
 138361 GGACTCGCAC CTGGAAAATA TAAGGAACCT TATACTTAG TAAGATGACA AGCCAAAACA
 138421 AAGAGTAAAA GTTTTCAACA GACATTTTAC AAAAGAAAAC ATACAAATGG CCAGTATGCA
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 138541 ATACTTCACA TTCAACAGAA TAGCTAATGT TAAAAGGACT GACAATCCCC AGGGTGAGCA
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 138661 TTTGAAAAAA GTTTGGCTGT TTCTAACATA AAATTAAACA CTTATACAGC CCAGCAATAT
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 138781 TCATACTGGC TTTGTTTCAC AATGCTATAA ACTGGAAACA ACCCAGGTGT CCATCAACAG
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 139021 TGTAATCCCA GCTACTCGGA AGGCTGAGGC AAGAGAATCA CTTGAACCGA AGAGGCGGAG
 139081 GTTGCACTGA GCCAAGACCA TGCCATTGCA CTTCAAGCTG GGCAACAAGA TGGAAACTCC
 139141 ATCTCAAAAA AAAAAAAAT TGCAATATAT CTATATCTTG GAATATTATA AAGCAATAAA
 139201 AGGGAATAAA CTAATGATAT ATACACAAAA TGGATGAATC TCAAAAATGT GAAGGAAAAAT
 139261 AAAAAATACA TATGATATAA ATTCCATTCA TATGAAATTT TAGGAATGGG AAAACTAAGC

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139321 TGTAATTATG GAAAGTACAT CAGTGGCTGC CTGGGGCCAA GAGGATGGAA GAGGCGGCAC
139381 AGGTGATACT ACAAATGGAA ACTATCTAGG TTGACGGAAG TGTTCTGTAA CTTGATTACA
139441 GTAGTAACTG TTTGGGTATA TAAAACGCAT CAAATTGTAT AATTAATACA GGTGTATTTT
139501 ACTGTGTATA AATTATTCCT CAATAAAGTT GATTTTTCAT TAAATATATT ATTTGCTAAA
139561 ATGAGGAGAG ACAACTATTA TCTTAAATA GTTAAGCACA ATAAAAATAC TACAATCAAC
139621 TCATTATATA TGGAAATTAA AGGAGAAAAA TAGTGGTATG ATTAATTAAA ATAAAAAGAA
139681 AACCTTCTAA ATTTTATCTT AGCTCATAGT TGTAAGAGCT GCCATCCCTA ACCAAGGCCA
139741 CCCTTGACCC TTTCTCATGT TCCATCTTTC TGTTTGTTC ATAGTTTATG TCTCACCAAA
139801 ATCTATCAGA TAAACGTATT CATATGAAGA TTAAATATA TTACATGTTA AGCCTTAGCG
139861 AATACTTCAA TATCTAAAGA AGGTACAAAC AAAACAAAAA TCAACACTTA GTTATAAGAG
139921 ATTACATACT CTCCAGGGAA GACCTGAAGA CTAGCCCTT TCTGGATCCC ACTAGCCCTT
139981 CATCCCACTC CAAGCCCTCC CCTCCAATCC CATATGCACT GGGCATTCTT ACAAATAAGA
140041 CCATCAGCTC TGGATATCTG TACTGATTGA TGCTCCTGCT AACTACCTGA ATGATTGCGA
140101 TGTAAGGACA GCACTGCCTG AATCCTATTT ATCTCTCGCT ATGCCATAGC GGCCTTCCAT
140161 GCTGATGGCG TGTTTGAGGA TCCAGAGGGG TCTTTGGTTG GCAGGATTGT TTTATTTCCC
140221 CAAGAGGAGA GCCTTGATGC AAAAATAGGT GAAGAAATCA GTACAACAAA ACAGAAAGCC
140281 TAGAACTAC TATGAACACA ATAGAGCAGA AGTAGCCTTA AGAGTTGGTG GAGAAAGGAT
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140401 AGCTATACCC CATATCATAC ACAAAGTTT CTACATCTAA CAAAGACACA GATAGAAAAT
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140581 TCTGGGAGGC CGAGGTAGGT GGATTAGTGG AGGTCATGAT TTCGAGACCA GCCTGGACAA
140641 CATAGTGAAA CCCCATCTCT ACTAAATAC AAAAATTGGT AGGGTGTGGT GGCTCACGCT
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140761 GTTGCACTGA GGGGAGATGG GCCTCATGCA CTCAGCCTG AGCAACACAG CGAGACTCTG
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140881 TCGTTTAAAT GATATGACAC ACTACATCTA ATATTGGAA AAGTACTTCT TAATACTTTT
140941 AATAAAAAGA GCGCTGAGA GCATACAACC TATCCTCAGA AGAGTGTGTT ACCTCTAGGA
141001 GGGACGCAAG CGCGTTCTT CTTCATTTTA ACTGGTCATT TTCATTTATT TCAGGAACAT
141061 CTGAAGTAAA CACAGTCACA CGTTAACCTT TAAAAATCTA GGAGGTGCGT ACGCATAGTT
141121 CCATTACTTC AATTTTGTG CTTTTCGATT TTAATATATC ACAGGGAAGC TCGGTACAGC
141181 TTCAAGGCTA GGAGGGGTGG CTCTCTCTTA AGCCCTGTCC CCGCCAGCCC CAGACCTCTC
141241 GTCCCGCCCC CATTGCCAG TCCCACCCT CACTTCCCCA TTTCCCCCT CCCCGGTCT
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141961 CTTTCAGAAC TTTAACCTGT TTGCTGAAGT ACGTCAGTAA CAATGGCAGG GAAAGGGTAT
142021 CTTAAATTTT ACCACAGCCT CAAAGAGGCC ATTTCTGTGA TCCGCTGAGG CTTGGAGTCG
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142561 ACGAAAATAA AAATTAAAAA AAATTTTAAA AAAAGAAAC AAAAGCTCTC TAATGACCAA
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144121 GGCCAAGGAG GGAGGATTGT TTGAGCCCAG AAGTTGGAGA CCAGCCTGGG CAACATAGTG
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144241 TTGAAAGCCA TTTTCTGCAA ATACATAGTG AATTGTATCA GTAATTTTCT TCCAACAGTG
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144721 ATACAAGACC TTGCTAACAA TAGCAAAGAT CAATTAATTC AAAATTTGAA AAAGTGAAT
144781 TTATTTAGCT TTAGAGTACT CTCGTGATAT GAGATTGCCA AATTAATACT TTGGGTGCAT
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145081 TGTCAATTAGG GAACTGCAA TTAAGACAAG TAGATAACCAC TGCATACCTA GTAGAATGAC
145141 CAAAATTTAG AACACTGTCA GCACCAAAGG TTGCAAAGAT ATGTAGCAAT AGTAACCTGT
145201 TCATTACTGG TGAGAATGCA AAATGTGCAA TCACTTTGGA AGACAGTTTG GTGGTTTCTT
145261 ACAAAGTAA CCATACTTTT ACCATAAGAT TCACCAATCA CACTCCTTAG TATTTATCCA
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145621 GATATGAGAA TCGTTTGAAC CTGGGAGATG GAGGTTGCAG TGAGCCAGTG CCACTGCACT
145681 TCAGCCTGGG CAACAGAGCA AGACTCCTCT GTCTCAAAAA AAAAAAAAAA AAGAAAGAAA
145741 AGAAAAAGA AAAAGAAAA GAAAGAAAC GATCAAGCCA TGAAACACA TGAAGGAAAC

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145801 TTAAATGTAT GTTACTAAAA AGCCAACCTG AAAAGACTGC ATACTATATG ACTCCAACCTG
145861 ATGCAGGGCA AGCAAGCCAA AAATTAGGGC TTAGCCCGGG AAGAATTCAA GGGTGAAGTG
145921 GTGGTGTAG CAACTTTTAC TGAAGCAGCA GTGTACAACA GCAGAACAGG TACTGCTCCT
145981 TGCTGAGCAG GGCTAACCCA TAAGTAATGT GCCCAGAGTA GCAGCTCAGG GGCAGTTCTG
146041 CAGTAATATA CCTGCTTTTA GTTAAGTGCA TGTTAAGGGG GATTATGCAG AAATTTCTAG
146101 AAAAAGAGTG GTAACCTCGG AGTAGGTACA GAGGAAAGAA GTCGATAATG TCCTGTTGTT
146161 GCCATGGCAA CGAAAACTG ACATGGCGCT GGTGGGCGTG TCTTATGGAG AGGTGCTTTA
146221 ACCTCGTCCC TGTTTCGGCT AGTCTTCAAT CTGGTCCGGA GTAAAGTCCC TGCCTCCGGA
146281 GTTCACTCCT GCTTCCTGCT TCACAACCTG ATGACACTCT AGAAAAGACA GTAACATATG
146341 ACACAGTCAA AAGATTAGTT GATAGAAATT GGGTGACAGG AAGTGTTGAA AAGGCAGAAC
146401 ACAGGATTTT TAGGGCAGTG AAACCTCTGT GATACTATAA TGGTGAATAC ATGACATTAT
146461 ACATTTGTCA AAACCCATAG AAAGCACAAC ACCAAGAATA AACCCATAATG TAAATTCAG
146521 ACTTTCGTTG ATAATGACGT GTCAATGTAA GTTCAATTGT AATAAATGTA CTACTGTGGT
146581 GCTGGATGTC TATGGTGGGG GGACATTTTT GCTTCAATAG TTACAGTTGA AGTAAATGTT
146641 TGTGTTTCCC ACAATGCATA TGTAGAACT CTCACATTCA ATGTGATGGT CTTTGGAGGT
146701 GGGCTCTTTG GGTGATAGTT AGGTTTAGTT GAGATCCTAG CAGATCGAGT CTTTCATGATG
146761 GGCATGATGG GACTGGTCCC TTATAAGAAA AGACCAGAAA GCTAGCTCTC TCTTTGCCAT
146821 GTGAAGACAT AGCAGGAAGG TAGCCATCTG CAAGCTAGGA AAGGGCCTTC ACAAGAATC
146881 AACTCAGACC TCAGAACAGT GAGAGATAAA TTGTCGTTGT TTAAGTCACT CAGGCTGTGG
146941 TATTTTGT TT CAGCAGCCCA ACCTAAGACT GTTAATTGGA TTAGAAATTT CTTTTTGGGG
147001 ATGGTGTGTG GCGGGCGGGG GCGGGGAGT ACCTTTGTTA AGCTTTTATA TCAATGAGTT
147061 TGTAGGCTTT TCTTTTTTGG TCATTGACTA GGACAGTTTA AATAGTATGA GTGTGAAGGA
147121 GATTGTTGGT CATCTATTCT ATGTCCCTTC TCTGTTTTTT AATATGAGAA CTCCTGATTT
147181 TCAGCCAACT ACCCTGGAAG AAAAGCTAAT CTTTCTGACT TCTTAAGTGT GGCCATGTAC
147241 TAAATCTGG CTAATGCAAG GCAAGCCAAA GGTTTTATGA TAGGTTTATG GACACTAGAG
147301 TAAAGAGAG CTGTTGCACA CATGCTCTTC ACCCTACTTT TGTGTCCITT TTTCCATCCT
147361 ACAACTTGGG TTGTGAGTAT GATGGCTGGA ACTTTAGTGG CTCTCTTGGG TCCCAGGGGT
147421 AATTGAGGGG TGGCTGGAAG GAATCTGTGA TTTTCTGGAG TTTCCATACA CAAACAAGAC
147481 CTGGATTTTC TGGGCTTCCC AGACTTCCAC ATCTAGACTT GCTTTAAATG GGAGATAAAT
147541 AAACCTGTTT CAGCCACTGT CATTTTGGGC TATTTTATAG AACTTAATCT AATCTTCAAG
147601 GGTACATGAA TTGCTTTTCC TTAATAAAAA AATCAGCCAT AAAATCATCT TCTTTTTTCT
147661 TTTGTTCCCC ACATTATTTA GTTGGAGCTC TGTAACCTTT TTTTTTTTTT TTTTGGAGAC
147721 AAGGTCTTGC TCTGTCACTT AGGCTGGAAT TCAGTGCCAT GACCATGGCT CACTGCAGCC
147781 TTGCCCTCCT AGGCTCAAGC AATCCTCGTC TCAGCCTCCT GAGTAGCTGA AACTAAGGCA
147841 CATGCCACCA TGCCAGCTA ATTTCTTTTC TTTTAGAGAT GGGAGCCTTG CCCAGGCTAG
147901 TCTCAAACCT CTAGCCTCAA GTGATCCTCC CATCTCAGCC TCCCAAAGTG ACAGGATTAC
147961 AGGTGTGAGC CACCATGCCT GGCTGCTCTG TAAGTGTCTG AATTTTCAAT TGTATTTATC
148021 AGTCTGTTTA GATTTTCTTT CCTTCTTGG GTCAGTTAGG CCATTGGTGT TCTTTTAAAG
148081 GTTTTCAAAT TTATTTGCAT CTAATCTTTC AAATTACTCT CAAAATTATT CCAGTATATA
148141 TTCTTTTGT CTTATTTTCT TCTGTATTCT TTATTAATAA AGCTAATGAT TTATCTAGCA
148201 GGACTTATAT TCTTTCCATA ACTTTCTGCT ACCCCAATTA ATCTCCAATT TTATATTTCT
148261 TCTGGCCTTC CTTATAGTTT CCACAGGTTT ATTTTATTCA TTTTTTAAAA CTTTTATTTA
148321 ATTGTTTATT TTATATCAT TCTTTCTTAT TCAGCAATCT AAGTGCTTAG GGATATAGAA
148381 TTTCTCTTAA GCAGCATATG CTAGGCTTTA ACAATGTTAG GGAGGCCTCC CTTTTCTGGG
148441 GAAGACCACA CTTACATTAA CACAGGACTG TGGGATGCCA AGAGGTAGAG AAGAGCTTAT
148501 GAATATCCAG ATTACATCTT CACTGATCCT GCACAAAGGT GGGGTTCCCTC GGTACCAC
148561 TGGGTCCTAT TACCCAAGTC TGGGTCAGCA TACCGAGACT ACGGTTATAT AGAACAAGTG
148621 CAACTGGCGA TAATCCTTCT GTTGGGGAGA AAAATCTTTT TTTTCTATTC ATCTTAGGTT
148681 CTCCATCTGT GGCCCTATCA AGTAGACTAA CAAAAGACAG ATTGACAAGA CAGAAACAAA
148741 GCATGTGCAT TGTACAAACA CAGGGGAGTA CTGAGATGAA TACTCAAAG AGGATTTAGA
148801 ACTTGGGCTT ATATAGCATT TTAAGAAAAG AATACATTTT TTAAGTGACA AGGAAGACGA
148861 AAAGGACTTT GAGTTTCTAG TGCAGTAAAT TGTGGGAAGG CAACTTTTTC TTTCCCTTTT
148921 TTTTTTTTTT TTTTTAAAAA AAAAGACTTC TCTGGTGCTA TGTCCAGGCT GATAAGAGTC
148981 TAAAGTCTCT GGTGACTAAC TTTTGTCTCT CCCCAGGTAA GAAGACACCT TCACAATTTT

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149041	ATATCCTGCT	TTTAGGCAAA	TAGGGAGAGG	GCAGAGGTGT	TTGTTTGT	TTAATCTATT
149101	TTTTTCTCA	ATTGTCTTCA	ACTCAAAATA	CTTCTTATGC	CAAAGATGGC	ATATTCTGCT
149161	ACCCTTCACT	TACTACTTAC	AACCCAGCCT	CTATCATCAT	AATTAGAACT	TCTGACCCTG
149221	GGGAACATGG	GCAATAGTTT	GAACCTTTTT	ATATCTCCCT	TAGGCAGAGA	TGGAGGCCCA
149281	GCCATGCCTC	TGACATCTAG	ACACAACTGT	TGCTTCATTT	CTCCTATTCT	CAGAGGTGAT
149341	GTTGTAGGAC	TTCAACAAAT	ATCAGTAAAC	ATTAATTTTT	TTTTTCCTTG	AGGCACAGCA
149401	TGATCTTGGC	TTACTGCAGC	TGCTGCAGGC	TCAAGCAATT	CTCCTGCCTT	GGCCTCACGA
149461	GTAGCTGGGT	TACAGGCCCC	TACCACCATG	CCCGGCTAAT	TTTTGTATTT	TTAGTAGAGA
149521	CAGGGTTTCA	CCATGTTGGC	CAGGCTGGTG	TTGAACTCCT	GACCTCAAGT	GATCCACCTG
149581	CCTCAGCCTC	ACATAGTTCT	GGGATTACAG	GCGTGAGCCA	CCATGCCTGG	CCATCAATTT
149641	TTATGTCAAC	TCTAAATTAT	AACATTAGC	AAATTTGTGA	CTTTTTATGG	TCATCAATTAA
149701	TGTTGTTTAT	GTTTGTAGTT	TAGTCTGTGC	ATTACTCACT	CGGGTATGGT	AAATTTGTCT
149761	TTTTCAAAAT	GAAGTTAAGG	TCTATTTGCT	CTTCTCTGAA	TCATAATAAG	AACTGCCAAC
149821	AGCCATTTCA	GCAATAACTA	TTTACTGAGA	TTTTAAATA	TTTCAAGGTA	ATTGGTCTTA
149881	GCAGACTGGA	AAATACCAAA	TTCTTTTCCA	GAAGTGAATC	CCCCATCAAA	GTTCAATTTT
149941	ACTCATAATT	CCCTTTTCAT	TTGAAGCATC	TCATTGTAAG	CCAGTCTTAA	CCCTTCTCTC
150001	ACACTTTGCT	TGGCTGTTTC	TCAGGTAGAA	CTCAGTAAGT	CTGGTAGCCT	CCAGGACTGC
150061	CGCTTAGATT	ATTAAACAAC	ATGTCAGTGG	TTGGAAGAGT	CAATGTTATT	TTGATTTTTT
150121	TGTTTGTGTT	TGTTTAAAT	GCAGTTGGCG	GATAATTGCA	GCTTTCTTTC	ATTCCTTACA
150181	TGAGTTCAAA	TGGCAGCAAA	CAAGTTAGGA	GAACGCAGAC	CTTCTGACTT	GTGGGTACCC
150241	CTACTCATCA	CCTGAAGACC	CTTGGAATC	AAAGCCCTGA	CCCATTAAAG	ACGGATGGAG
150301	ACAGCAACAT	ACGATCATCA	CTATTATCTT	GCTTTGCCCC	AGTCCAGGTT	AACCATCTGT
150361	GGTATTTTTA	GTTGCTAAGT	CCATATATTC	AACATAAATC	AATTATATAT	CCACTAAAT
150421	CTCAGCACTA	GTCTAACTAC	TAAGGAAATG	ACAGCGAAGA	AAACAGACCA	AACGTCTGCC
150481	CTTATGGGAT	TTATATTATT	TTCTCTGTGC	TGGTTAAACC	AAGGAGCTTC	TGCTCTTTTC
150541	CTTAGTCACC	TGGGGGAGGC	AGAAACAAAG	GAGAATATTG	ATAAACCTGG	AAATAGGGCC
150601	GGAGAGTATC	AGAGAAGGAA	GCCTTCGGGA	AAGTAAAGAT	GTGGCAGCCA	GTATTCCTGT
150661	TATAAAAGGA	TACAACTCCG	GCCTCATAGT	CCAGAAAAAT	TCCCACAAGC	AGGGGCTGCT
150721	CATGCAGATG	AAGGGAAGTT	GGGGGAGAAG	TAAGTGCTAC	ATAGCCTTTC	TTTTTGCACA
150781	GCCTGAGGGT	CCAGAATCCA	GACTGAGGCT	CTTGCTTCAT	GCCAGTGCCC	CTCTGCACAT
150841	TTTCCATACA	AACTCCTAAA	TCCCATCCGG	TTCCTTCGCC	AACATCCACT	TCAAAGTAAC
150901	GTCTTCCTGA	GGTGAAGCCT	TCACAACCCA	AGACACAGGG	GAAGGCAGTA	AATCTCCTGG
150961	AAGATGTGTC	CTGATTCTCC	TGGGTGTATC	CACGAGTCAC	TTGTCTCCGA	TCCTCAGAGA
151021	GAATTAGTTC	GTGATGAGCT	GTATCTGGAT	CCAGAGTCAC	ACTAAGTCGA	AAACAAAACA
151081	AAACAAACAA	AAATAATTTT	GTTGCTGTGA	AGAACACAGG	TTATTTTATT	TTATTTTATT
151141	TTGAGATGGA	GTGTTGCTGT	CACCCAGGCT	GGAGTGCACT	GGCACTATCT	CAACTCACTG
151201	CAACCTCCAC	CTCCTGGATT	CAGGCAATTC	TCCTGCCTCA	GCCTCCGGAG	TAAGTCCGAC
151261	TACAGGTGCG	CACCACCACA	AGTGGCTAAT	TTTTTTAAAT	TTTCTGTAGA	GATGGGGTTT
151321	CGCCATGTTG	GCCAGGCTGG	TCTCAAATC	CTGACCTGAA	GTGTTCCACC	CACCTCGGCC
151381	TCCCAAAGTG	CTGGATTACA	CAGGTGTGAG	CCACCATGCC	CAGCCACAAG	TTATTTTCAA
151441	TAAAACCAGC	CTGTGTTCAA	ACCCAATAT	TGTTTCTTAT	AACTGGGTG	AGCTTAGGCA
151501	AATCATTTAA	CTTCTGAGC	CTCAGTTTGT	TAAGTATAAA	GTGGAAATTA	CCGTATTTGT
151561	TGCAGAGAAT	GGTGGGTAGG	ATTGAATAAG	CTTATGTTTG	CTTAATGCTT	GGTAAATTC
151621	CTGGTACATG	GTAACCACT	AATAAGTGGT	AGTTGTTGGG	GTGATCAGGC	CCAACACCAG
151681	GCCGTGGGGG	CTACAAAGTC	CGGCGGGGTC	AAAGGAATGA	GAAAAGACAA	GTTAAGAGTG
151741	CATAAAGTGG	GTCCAGGGTG	CCAGCACTAG	ATTGGAGGCT	GCAAAGGCC	TAAGCTCTGG
151801	GAGCCACAC	TATTTATTGG	TGATCAACAA	AAGAAGCAGG	TGGTGAGGAC	GTGAGGGTAA
151861	ACAGGTGAGG	GCATGAGGAC	ATGGGGGTAG	AAAGGTAGTG	GTGCATTAAG	CGTAGCTGTG
151921	ACAGTTTAGC	ATTTTCTTTG	ACACATGTAG	AATATACTCT	GCTGCTTGAG	ATAGTAGAGG
151981	ACACGTTTAT	GAGTGAAAAG	CAAGGAACCA	ACAAGTCTGT	GCACTTTCCA	GAGGCTATGA
152041	GGGGTTTTAT	GCCCTGAGCC	CTGGGTCCA	TCCAAGCCAC	AAGGGGTTTT	ATGCCCTAGG
152101	CTTAGATTTG	TGGTGCGGCA	GGGCAGCCTT	CCACCATTTG	GCACAGAGCT	TGGTGTCCA
152161	AAGGCCACGA	GGGGTTTTGG	ACCCTGGACC	CCGGACATCT	TCCAAGACTC	TTTTACATTA
152221	TGACAGACAA	GCCAGTCTCT	CTTCAGCTCT	TCTAACAA	TGTAGTAATA	ATGATATCAT

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152281 CAACATCATC TTCGTCTTAA TTATTCAAGG ATGCCAAGGT ACAGAACTAA CCTGTTAATA
152341 TGGTTACCAT CCTGTCCAAA GTTCTTCTCC CATGCAGGAC TTCCAGGAAT CATGAGACAG
152401 TTGAGCAGAA AGATACCTTT TCCCTTCTCT ACTGAATAAC CACCAACATT GAGAATCAGA
152461 GAGGGAAAAT GACTCAGCTA ATGTCTTAGC TTGTTATTGG AAGACCCAGG TCTCATGACA
152521 CATGCCTAGT CCCATGACTT TTAATTGTAA GCTCTTCTCT TCCCCCTCAG ATAATGTTCC
152581 ATAAGCATTG GTATGAGATA ATAATACACT GAGGACCAAT ATACATGAAA AATATCAGAC
152641 TAGAATCAAA CAAGACAGAA AAAAGATCTG ATAACCTAAA GTGAGATACT GAACAGTATG
152701 CAGTTTAAAA AATAAAAAAT GGTAATAGGA TGTCTAACA AGAGAGTTAA GAAACCACTG
152761 TGCTACTGAG TTAAATGTTG ATCAGTTGGT CTGTGACAAT TAAGGAATTC AAGTATTGAG
152821 AAACACTTCC TGTGCTGGAT GCTCTCTGTT TGTCTTCCA AATAATCCCT CACTTTTCCC
152881 TGTCTTGCTC TGTGCCCAGG AAGGCTGACA TGGACAGATT AACCAGGCTT TCCGCCCTCT
152941 GGCTTGGTTC AGCCAATGGG AAGCACCAGA GGAGACCATA GGGCACAAG AAGCAGCCTT
153001 GGGAGTATTC AGTACCCAG TCCCACGCTA TGATTTGGAG GGTCTGCATT CCTCTGCCTC
153061 TGGGCACACT CTAGTATAGT TACAGCTCCC TACACCTGCC ACTTGAGGCC CAGAGGAGGT
153121 GATGGCTCTC TAACTGTTCC TAGTCTGGG TGCTTCTGT TCCTTGTTGA TTTCCCAACT
153181 CCTCACCTTT GTAAATACCC TCCTTTTCA AACTCTATT AGTTAGCTTT TATCAGCCTG
153241 ACTCAGAGAA GTTTGGGGTT TCAATTCTA TTACCTGAAT GACCCAGGAA AACCCATGTT
153301 GAGAAATTAA AATGTTTACG GGTGGTGAAT ACCACTTAAG AGAAAAATA TCAATTGGAT
153361 TTTTAAAT CCACCTATCT ATTGGTGTGA CACATCAACA AAAACATATA GAAAGATTGG
153421 AAGCTAAAAG ATAGATAATA TAGTCATATA CTGTTATAGT ATTATATCAA AAGATATTA
153481 GTCAGAGCAT TATTAAGAAT GGAAGAAGGG CCAGGTGTGG TGGCTCATGC CTGTAATCCC
153541 AGCACTTTGG GAGGCCAAGG CAGGCGGATC ACTTGAAGCC AGGAGTTCAA GACCAAGCCTG
153601 CCCAACATGG CAAAACCCTG GCTCTACCAA AAATACAACA ATTAGCTGGG CATTGTGGCA
153661 CATGCCTGTA ATCCCAGCTA CTGGGAGGCG TGAAGCACA GAATCACTTG AACCGGGGAG
153721 GCAGAGGTTG CAGTGAGCTG AGATTTCCGC ACTACACTAC AGCCTGGGTG ACAGAGAGAG
153781 ATTCTGTCTC AAAAAAAAAA AAAAAGAAAG AATGAAAGGA GTCACCTAAA AAAGATAACA
153841 CAATTTTAAA CATAATGTA CTACATTATT AGTGAATTCA TGTTTAGAAT TGTGTTAATA
153901 TACAAAGCAA AAATTGTAGA ATTATGGAG AAATGGACAA ATCTACAATC ATCATGGGAT
153961 GTTTTAACAT TCTTCTTTCC ATAATTGATA GATCAGGCAG ACCAAAAGAA AGAAATAAGG
154021 GAAGATACGG AAGGTCTGAA CAATCTAAGA AGCGCAATCT CATAGTCAAT ACATAAAGCT
154081 CAGCAATTGT TTAATAATAG TAAGCAGAGA ATATGCAGTT TTCTCAGGTA TAGATGGAAC
154141 ATGCACTAAC TGAGTAAATA CTAGGCAGAA AACAGTCTGA ACAAGTTTCA ATAAATCTGT
154201 ATTACACAGA TCATTTTCTC TAGCCTCAAT ATAAGATTAT AAACCAATAA TAAAAAGATG
154261 ACTAAAAAGA TTCTAAATAT TAGGAAATGT AAACACTATA TAAGTCATTA GAAGATGTAT
154321 AGAATGGAAC AATAATAAAA AGTTATTTAT AAAATATAC AATGAAGCTA AAGCAGAATT
154381 TTAAGGAAAA TTTGTAGGCT TTAATGCTT ATCTTAGAAA AATTAAAAAG CTGAACATTA
154441 ATGAGCCAAG CATCTAATTT AAATTTTAAA AAGAACATAG AAAGCCAAAT ATAATTTTTT
154501 AAAAAGAAAA AATAGATATT AAACAATATA ACAGTGAAGT TAAAGAAAAC AAGAATGCAA
154561 TAAAGAGGAA AAACAAACAA AAAAAAGGT AGCTTCTTTT AAAAGAAATT TAATAAAATA
154621 GACATACCTC CAATGAGATT TATCAAAGTA AGACAGAAGG CACAAATGGA ATGAATACAG
154681 AAACTTTTTA AATATTACAG AACTTTTATA TAAATCTTAT GCTACTAATA AAATTGAAAG
154741 TACTGATAAA ATTATTACTT CCTAGAAAAA ATATTCTGTA GTAAACTCA CTCAAAAAAC
154801 AAATAAAGCA TGGGCAGACC TAACATTTAA GAAATGAAAT CACTACTTTA AATTTTACCG
154861 ACAGATAATA AAACGTGCAT CTTTATCAAG CAAAAATGGA ACTTGTCAGT TTTATAGGAA
154921 ATTTAGAAGT CAAGGCATGA GTAATGCCAA TCTCATACCA AATCCTACAA AGAATAGAAA
154981 ATTATGGCTC CCGCTTATAG ACATAGATAT AGAACTCCTG CACAAAATAA TATAAATAAC
155041 AAACCAAATT TTATATTTGC AACTATACAT ATTATATGTG TATGTATTAT ATATGTTAAC
155101 ATATACATAT ATAATATGTA TAGCATATGT TCTACATATT ATATATGTAT AGTGTATGTA
155161 TTTTACAATA TATAAATGAA AACCCAATCT TTAATATATT CATCTAGATT GTCATATATG
155221 ACATATATAA TACATTACAT CAAAATGTG TACAATAATC AGGCCAGGCA CAGTGACTCA
155281 TGCCTGTAAT CCCAGCACGT TGGGAGGCTG AGGCGGGTCA ATCACTTGAG TCCAAGAGTT
155341 TGAGACCAGC CTGGTCAATA TGGCCAAATT CCATCTCTAC AAAAAATATG AAAAAATTATC
155401 CAGGCATTGT GGTGCACACC AATAGTCCCA GCTACTCGGG AAGCTGAGGT GAGAGGATCA
155461 CTTGAGCCTG GGAGGTGGAG ATTGCAGTGA GTCGAGATTG CGCCAGTGCA CTCCAGCCTG

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155521 GGTGGCAAAG GGAGACCCTG TCTCAAAAAA AAATTAAAAA ATTAGCCAGG TATGGTGGCC
155581 TGTTCCCTGTA GTCCCAGCAA CTGGGGAGGC TGAGGTGAGA AGATCACTTT AGCTCAGGTG
155641 GTGGAGCCAT GATCGCACCA CTGTACCACT CGGCTTGGGC AACAGAGTGA GAGCCTGTCT
155701 CGAAAAACA AATATATACA CACAGTAATC AATATATATA TTATATGTAC CAATCAATGC
155761 TTCACTTTTA TATATAATAT AGATTACATC TTATTAGATA TATAGTATTC CTTCTCCATA
155821 GATAGATAGA TACAGATATA GACATAGTAT CCTCTATCCA TATTAGAGAG AGGATACTAT
155881 ATATATCTAT AGCATATAGA GATGCTGTCT CAAAAAAATT TAAACATCAG CCAGATGTGG
155941 TGGCCCCTGC CTGTAGTCCC AGCTACTGGG GAGGCTGAAA TGAGAGGATT GCCATTGATC
156001 CTCTCATTGG TTGAGCCATA ATCGCACTAC TGCACCACTC AGCCTGGGAG ACAGAGGGAG
156061 ACCTGAGGTG GAAGGATATA GATATAGATA TATAAATAAA TATGTATAGA GAGAATATAA
156121 TATATGTGTG TATGTGTATA TATATATATT ATGAAGACAC TGGGAGAGAA TACTATATAT
156181 ATATGTGTGT GTGTATATAT ATATTATGAA GACACTGGTG GGATGGTTTC ATTACCAATT
156241 GGACCAAGAG TCCAGGTATG GAGCCAACAT GCAATGTTGT TGTGACTGA GCTGGCAGAG
156301 CACTGGTCAT AGTTACGGGA AAAGAAGGTC TCCAATGAGA CATACTTAAC AAAATATATG
156361 AACTTGCCAT ATACGTGGAG AGTTCTGGTG TGTATATAGC CTTCTCTCAC CAACCTAGCA
156421 ATTGTCTTCA TCATCATTAT AATGCTATCA GAGCAAAGAT GACAGCTAAA TTTTTTTGTC
156481 CCTTCTTCT TCTTCTCTT CCTTCCCCTC CCCACCTCT TTCTCTTCT CCTCCTCCTT
156541 CATCTCTCT CTTTTTTTTT TTGAGATGGA GTCTTACTCT GTCGCTCAAG CTGGAGTGCA
156601 GTGGCACAAT CTCAGCTCAC TGCAACCTCT GCCTTCTGGG TTCAAGCAAT TCTGCCTAAG
156661 CCTCCAGAGT AGCTAGGACT GCAAGTGCAC ACCACCACAC CTGGCTAATT TTTGTATTTT
156721 TAGTAGAGAT AGGGTTTCAC AATGCTGGCC AGGCTGGTCT CAAACTCCTG CCCTCAAGTG
156781 ATCCTCCTGC CTCGGCCTCC CAATGTGCTG GGATTACAGG CGTAAGCCAC TGTACCCGGC
156841 CTCCTCCTTT AATAGACAGG GTCTAGCTCT GTTGCCAGG CTGGGTACAG TGGCGTGATC
156901 ATAGCTTACT GCAGCCTCGA ACTCCTGGGC TCAGGAGATC CTCCTGCCCT AGTCTCCCCA
156961 GTAGCTGGAA CTACAGGCAT AGCACACGGG GCTAATAAAA TTAATTAGGT GATAAAATTC
157021 ACTGCCCCACT GATGACTAAG CTCTTTGGAC ATAAAAGACA CAGACCTTGA AGGAAAATGT
157081 GTCTACTTAA TTTTGAAACC CTATTTATCA AAAACAGGA TGAAAATGCA AAATGCCATC
157141 CACATGCCAG AAGATATCAG CTATAATAAG TTCCCATAAA TCAATAAGGA AAAGAACCCA
157201 ATAAAAATTA TTAAACCACA GTAAATCATG GGTAAATCAC AGAGGCCCTGA AGGGCTAATG
157261 GACATACAAA AAGAATCTCA ATCTCACTAG TGAAATCAGA AAAGCACAAA TTAAGTACAC
157321 AATTAGGTAC CATTTTAAAT CTGTAAGACT GTCAAAATCA TAAATTATAT AAGTAAAGAC
157381 TCAGGGAGTT TTGGAGGAGT GAGAGCTCTT ATATTGCTTG TGGGGTAGAA TTGGAACAAT
157441 TTCAGATCT GTAGTATCTG GTAAAATTAT GATATGCATC CCTCACACCA GCATGTCATC
157501 CCAAGGTATC TCCCTGGAGG GAACATTTAC GGGACACAAG GAAGCATGGA TAAGAATGTT
157561 CACAGTAGTA TTGTCTGCAA CAGCAACAAC AACAAAAAAA CCCAATAACA CACAACCTCA
157621 ATGCCCAGTC CACAAGGCAA TGGATTAAAT AAACCTCAGG CCGGAGATGG TGGTTTATGC
157681 CTGTAATCCC AACACTTTAG AAGGCCGAGG CGAGAGGACT GCTTGAGCCC AGGAGTTCAA
157741 GACCAGCCTG AACAAAATAA AGAGATAGTG TTTCTACAAA AAATTTTAA AAAATTAGCC
157801 AGACGTGGCA GTGCTTGCCT GTGGTCCCAG CTACTGGGGA AGCTGACGTG GGAGGATTGC
157861 TTAAGCCCAG GAATTTAAGG CTGCAGGGAG CCATGATGGG GCCATTGCAC TCCAGCCTGG
157921 GTGACAGAGT GAGACCCTGT CTAAGAGAGA TAAGTAAATA ACAACTTTGC ATTTTCTGCC
157981 ACATTGCAAA ATGGTGAGAG AGTGGTTTCT AGACTCTAGA CTCTTTCTAT GACTACCTTC
158041 TAGTTATGAG ATCCTACAAC ACTCACCTAA CCTCTCTGTG TCATATTTCC TCCTCTATAA
158101 AGCAAAAATG CCCCATATAG AGAGGACTGT GATATAAAAC AAGAACCAG AAAAGTAAAG
158161 CTTTTCTAAT CTGTCACAGA CTAAGAGTGT CTCAGTATAT GTGAGTCATT ATTCCTGGTG
158221 CTGGTAGGAG TGTATGTTAC AACTTTGAGT CAAGTAATAT GGTACCATAT ATTAAGATTA
158281 ACAACAACCT CGGCAATCCC AGTTTGGGGT ATGTTCCCAA AAGAAATGAA AGCACCAGGA
158341 TATAAGGATG CATGGACTAG AAAGTTATTG TAGCAACATT GTAATACTA AGTTCTAAAA
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158461 TATTAGACAT AAAAAGTAAC GAGTAACATA GAAGAGACAG TGTATATATG TTACGTTTGT
158521 ACAAACCTAG GGAAGATAT AGATCACCTT ACCTAGAGAA GTCAGATTGG AGACGGGTGG
158581 GAAAAACCTT GAACCTTCTC CTTATATCCT TTATATTGTT TGAAGTATTA AAATGTATTT
158641 GTTGCATCTG CTTGAAGGCA ATGTAAATA AAATAACAT ACATTTAAAA ATAAAAATAA
158701 AATTTATTCC TATCACTTTT GTAATAAAGC TGGGCACAGT GACTAACACT TGTAATCCTA

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